

SEQUENCE LISTING

<110> Pompejus, Markus
Kroger, Burkhard
Schroder, Hartwig
Zelder, Oskar
Haberhauer, Gregor

<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
INVOLVED IN DNA REPLICATION, PROTEIN SYNTHESIS,
AND PATHOGENESIS

<130> BGI-130CP

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<160> 430

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<211> 965

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1) .. (942)

<223> RXN00625

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Thr Val Lys Pro Val Gly Glu Ser Arg Ile Phe Asp Asp Ala Ala Phe	
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acc ggc acc gca cgc cag cca ctc gca cag gaa ttc cag cca ctc aac	144
Thr Gly Thr Ala Arg Gln Pro Leu Ala Gln Glu Phe Gln Pro Leu Asn	
35 40 45	
gac agc gag aaa tcc ttc gtc ggc gta gtc aac cac ttc aag tcc aag	192
Asp Ser Glu Lys Ser Phe Val Gly Val Val Asn His Phe Lys Ser Lys	
50 55 60	
ggc tct gtc act cgt gga gac gcc gac acc ggc gac ggc caa ggc aac	240
Gly Ser Val Thr Arg Gly Asp Ala Asp Thr Gly Asp Gly Gln Gly Asn	
65 70 75 80	
aac gcc aac gtt cgc gtc gca cag gca cag gca ctc atc gac cac ctg	288
Asn Ala Asn Val Arg Val Ala Gln Ala Gln Ala Leu Ile Asp His Leu	
85 90 95	
gaa aac cag gac gac tgg gca tcc aag cca atc ttc atc ctc ggc gac	336
Glu Asn Gln Asp Asp Trp Ala Ser Lys Pro Ile Phe Ile Leu Gly Asp	
100 105 110	
acc aac tcc tac gcc aag gaa acc gcg atg acc acc ctt tac ggc gct	384
Thr Asn Ser Tyr Ala Lys Glu Thr Ala Met Thr Thr Leu Tyr Gly Ala	
115 120 125	
ggc tac acc aac atc gcc acc gaa ttc gac gct ggc tac agc tac cag	432
Gly Tyr Thr Asn Ile Ala Thr Glu Phe Asp Ala Gly Tyr Ser Tyr Gln	
130 135 140	

ttc tcc ggc cgc att ggc agc ctc gac cac gca ctc ggc aac gaa gca 480
 Phe Ser Gly Arg Ile Gly Ser Leu Asp His Ala Leu Gly Asn Glu Ala
 145 150 155 160

 gcc atg aag cac gtc atc gac gcc gag gtc tgg gac atc aac gct gac 528
 Ala Met Lys His Val Ile Asp Ala Glu Val Trp Asp Ile Asn Ala Asp
 165 170 175

 gaa gca atc gca ttc gaa tac tcc cgt cga ctc aac aac acc tcc gac 576
 Glu Ala Ile Ala Phe Glu Tyr Ser Arg Arg Leu Asn Asn Thr Ser Asp
 180 185 190

 gta ttc gag aac aac gtc ttc cgc tcc tcc gac cac gac ccg atc aag 624
 Val Phe Glu Asn Asn Val Phe Arg Ser Ser Asp His Asp Pro Ile Lys
 195 200 205

 gtc gga ttc aac ctc agc gag acc act gag ccc acc att ccg gta gag 672
 Val Gly Phe Asn Leu Ser Glu Thr Thr Glu Pro Thr Ile Pro Val Glu
 210 215 220

 ccc act gat cct gca gaa cct acc gat cca act acc cca gtt aag cca 720
 Pro Thr Asp Pro Ala Glu Pro Thr Asp Pro Thr Thr Pro Val Lys Pro
 225 230 235 240

 act gat ccg gta gag acc acg gat cca tct gag cca acc gac cct gca 768
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 245 250 255

 gaa cct act gat cca gct gaa cca act gac cct gag gaa acg aag aag 816
 Glu Pro Thr Asp Pro Ala Glu Pro Thr Asp Pro Glu Glu Thr Lys Lys
 260 265 270

 cca gag gag ccg aag aac cct ggt tcc tcc aac gga agc tcc caa tac 864
 Pro Glu Glu Pro Lys Asn Pro Gly Ser Ser Asn Gly Ser Ser Gln Tyr
 275 280 285

 gcc acc att gca gca atc atc gca gca atc cta ggt gcc att gct ttg 912
 Ala Thr Ile Ala Ala Ile Ile Ala Ala Ile Leu Gly Ala Ile Ala Leu
 290 295 300

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<212> PRT

<213> Corynebacterium glutamicum

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65					70					75					80
Asn	Ala	Asn	Val	Arg	Val	Ala	Gln	Ala	Gln	Ala	Leu	Ile	Asp	His	Leu
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Glu	Asn	Gln	Asp	Asp	Trp	Ala	Ser	Lys	Pro	Ile	Phe	Ile	Leu	Gly	Asp
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Thr	Asn	Ser	Tyr	Ala	Lys	Glu	Thr	Ala	Met	Thr	Thr	Leu	Tyr	Gly	Ala
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Gly	Tyr	Thr	Asn	Ile	Ala	Thr	Glu	Phe	Asp	Ala	Gly	Tyr	Ser	Tyr	Gln
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Ala	Met	Lys	His	Val	Ile	Asp	Ala	Glu	Val	Trp	Asp	Ile	Asn	Ala	Asp
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Glu	Ala	Ile	Ala	Phe	Glu	Tyr	Ser	Arg	Arg	Leu	Asn	Asn	Thr	Ser	Asp
			180					185					190		
Val	Phe	Glu	Asn	Asn	Val	Phe	Arg	Ser	Ser	Asp	His	Asp	Pro	Ile	Lys
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Val	Gly	Phe	Asn	Leu	Ser	Glu	Thr	Thr	Glu	Pro	Thr	Ile	Pro	Val	Glu
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Pro	Thr	Asp	Pro	Ala	Glu	Pro	Thr	Asp	Pro	Thr	Thr	Pro	Val	Lys	Pro
				225			230					235			240
Thr	Asp	Pro	Val	Glu	Thr	Thr	Asp	Pro	Ser	Glu	Pro	Thr	Asp	Pro	Ala
				245					250					255	
Glu	Pro	Thr	Asp	Pro	Ala	Glu	Pro	Thr	Asp	Pro	Glu	Glu	Thr	Lys	Lys
			260					265					270		
Pro	Glu	Glu	Pro	Lys	Asn	Pro	Gly	Ser	Ser	Asn	Gly	Ser	Ser	Gln	Tyr
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Ala	Thr	Ile	Ala	Ala	Ile	Ile	Ala	Ala	Ile	Leu	Gly	Ala	Ile	Ala	Leu
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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(339)

<223> FRXA00625

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Glu Pro Thr Ile Pro Val Glu Pro Thr Asp Pro Ala Glu Pro Thr Asp	
20 25 30	
cca act acc cca gtt aag cca act gat ccg gta gag acc acg gat cca	144
Pro Thr Thr Pro Val Lys Pro Thr Asp Pro Val Glu Thr Thr Asp Pro	
35 40 45	
tct gag cca acc gac cct gca gaa cct act gat cca gct gaa cca act	192
Ser Glu Pro Thr Asp Pro Ala Glu Pro Thr Asp Pro Ala Glu Pro Thr	
50 55 60	
gac cct gag gaa acg aag aag cca gag gag ccg aag aac cct ggt tcc	240
Asp Pro Glu Glu Thr Lys Lys Pro Glu Glu Pro Lys Asn Pro Gly Ser	
65 70 75 80	
tcc aac gga agc tcc caa tac gcc acc att gca gca atc atc gca gca	288
Ser Asn Gly Ser Ser Gln Tyr Ala Thr Ile Ala Ala Ile Ile Ala Ala	
85 90 95	
atc cta ggt gcc att gct ttg gcc ttc cag ttc ttc cat tca agt tct	336
Ile Leu Gly Ala Ile Ala Leu Ala Phe Gln Phe Phe His Ser Ser Ser	
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Asn	

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20 25 30	
Pro Thr Thr Pro Val Lys Pro Thr Asp Pro Val Glu Thr Thr Asp Pro	
35 40 45	
Ser Glu Pro Thr Asp Pro Ala Glu Pro Thr Asp Pro Ala Glu Pro Thr	
50 55 60	
Asp Pro Glu Glu Thr Lys Lys Pro Glu Glu Pro Lys Asn Pro Gly Ser	
65 70 75 80	
Ser Asn Gly Ser Ser Gln Tyr Ala Thr Ile Ala Ala Ile Ile Ala Ala	
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Asn

<210> 5
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 <222> (101)..(1768)
 <223> RXN02943

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 Met Ser Arg Ile Ser
 1 5
 gcg cgc act ctg gca atc gca ctt gcc ggt gca acc gcg gcc agc ctg 163
 Ala Arg Thr Leu Ala Ile Ala Leu Ala Gly Ala Thr Ala Ala Ser Leu
 10 15 20
 gca gtt gtt cca gca gca aca gct aat cct gcc gga acc gct cct gtc 211
 Ala Val Val Pro Ala Ala Thr Ala Asn Pro Ala Gly Thr Ala Pro Val
 25 30 35
 atc aac gaa atc tac gaa ggc ggt gga aac agc gga tcg ttg ttc tcc 259
 Ile Asn Glu Ile Tyr Glu Gly Gly Gly Asn Ser Gly Ser Leu Phe Ser
 40 45 50
 aac gac ttc att gag ctc tac aac cca acc tca ggg gac att tcc ctc 307
 Asn Asp Phe Ile Glu Leu Tyr Asn Pro Thr Ser Gly Asp Ile Ser Leu
 55 60 65
 gac ggt tgg agc gtt acc tac tac gca gcc aac ggt aac tcc ggc gga 355
 Asp Gly Trp Ser Val Thr Tyr Tyr Ala Ala Asn Gly Asn Ser Gly Gly
 70 75 80 85
 acc aca aac ctg acc gga aac atc cct gcc aac ggt tac tac ctc atc 403
 Thr Thr Asn Leu Thr Gly Asn Ile Pro Ala Asn Gly Tyr Tyr Leu Ile
 90 95 100
 cag caa cgc gca ggc agc aac aac acc ggc gct ctg cct acc cca gac 451
 Gln Gln Arg Ala Gly Ser Asn Asn Thr Gly Ala Leu Pro Thr Pro Asp
 105 110 115
 gcc acc ggt aac ttg gca atg ggt gcc tcc caa gga tca gtt gca ctg 499
 Ala Thr Gly Asn Leu Ala Met Gly Ala Ser Gln Gly Ser Val Ala Leu
 120 125 130
 acc gac aac tct ggc cta acc gct gac ctt gtc gga ttc ggt ggc acg 547
 Thr Asp Asn Ser Gly Leu Thr Ala Asp Leu Val Gly Phe Gly Gly Thr
 135 140 145
 tcc atg ttt gaa gga aca gct gct gca cct gag acc agc aac aaa ttg 595

Ser 150	Met	Phe	Glu	Gly	Thr 155	Ala	Ala	Ala	Pro	Glu 160	Thr	Ser	Asn	Lys	Leu 165	
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Ser	Val	Gln	Arg	Lys 170	Glu	Val	Gly	Ala	Asp 175	Ser	Asp	Asn	Asn	Ser	Val 180	
gac	ttc	gag	act	gga	gct	cca	act	cca	acg	tcc	tcg	gga	gga	tcc	gct	691
Asp	Phe	Glu	Thr 185	Gly	Ala	Pro	Thr	Pro	Thr 190	Ser	Ser	Gly	Gly	Ser	Ala 195	
cct	gtt	gac	cca	ggc	gag	cca	gaa	act	cca	gta	aac	cct	ggg	gaa	aca	739
Pro	Val	Asp 200	Pro	Gly	Glu	Pro	Glu	Thr 205	Pro	Val	Asn	Pro 210	Gly	Glu	Thr	
gtc	tcc	atc	gca	caa	atc	caa	gga	acc	ggg	ctc	gct	acc	cca	ctc	gag	787
Val	Ser	Ile	Ala	Gln	Ile	Gln	Gly	Thr 220	Gly	Leu	Ala	Thr 225	Pro	Leu	Glu	
ggg	cag	acc	gtc	acc	acc	gaa	ggg	att	gtc	act	gcc	gtt	tac	gca	gaa	835
Gly	Gln	Thr	Val	Thr	Thr 235	Glu	Gly	Ile	Val	Thr 240	Ala	Val	Tyr	Ala	Glu 245	
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Gly	Gly	Phe	Asn	Gly 250	Tyr	Tyr	Ile	Gln	Thr 255	Pro	Gly	Ser	Gly	Thr 260	Ala	
cca	aag	gtt	gct	ggc	gac	gca	tcc	gac	ggc	atc	ttc	gtc	tac	gtg	gga	931
Pro	Lys	Val	Ala	Gly 265	Asp	Ala	Ser	Asp 270	Gly	Ile	Phe	Val	Tyr 275	Val	Gly	
agc	aat	ggg	tcc	tac	cca	gag	ctc	ggc	gca	tct	gtc	acc	gtc	act	ggc	979
Ser	Asn	Gly 280	Ser	Tyr	Pro	Glu	Leu 285	Gly	Ala	Ser	Val	Thr 290	Val	Thr	Gly	
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Lys	Ala	Thr	Glu	His	Tyr	Glu	Met 300	Thr	Gln	Leu	Gly 305	Asn	Ser	Ser	Phe	
acc	gtt	tcg	gac	acc	gca	ttc	gag	cca	gta	acc	cca	ctc	gaa	ctg	gac	1075
Thr	Val	Ser	Asp	Thr	Ala	Phe	Glu 315	Pro	Val	Thr 320	Pro	Leu	Glu	Leu	Asp 325	
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Thr	Val	Pro	Thr	Gly 330	Asp	Asp	Ile	Arg	Glu 335	Ala	Tyr	Glu	Gly	Met 340	Leu	
ctg	aag	cca	acc	ggc	gct	cac	acc	gtg	acc	aac	aac	tac	gca	acc	aac	1171
Leu	Lys	Pro	Thr 345	Gly	Ala	His	Thr	Val 350	Thr	Asn	Asn	Tyr	Ala 355	Thr	Asn	
acc	ttc	ggg	gaa	att	gcc	ctc	gcc	cca	ggg	aac	gag	cct	ttg	tac	cag	1219
Thr	Phe	Gly	Glu	Ile	Ala	Leu	Ala 365	Pro	Gly	Asn	Glu	Pro 370	Leu	Tyr	Gln	
gcc	act	caa	atg	gtg	gca	ccg	gga	gcc	gaa	gcg	att	gcg	tac	gag	gcg	1267
Ala	Thr	Gln	Met	Val	Ala	Pro 380	Gly	Ala	Glu	Ala	Ile 385	Ala	Tyr	Glu	Ala	
gaa	aac	gtc	gca	aag	caa	att	acg	ctg	gat	gac	gga	cgc	tcc	ggc	aac	1315
Glu	Asn	Val	Ala	Lys	Gln	Ile	Thr	Leu	Asp	Asp	Gly	Arg	Ser	Gly	Asn	

390	395	400	405	
tac act cgc ggc gac tcc agc acg cct atg gca tgg ctt gtg cag gac				1363
Tyr Thr Arg Gly Asp Ser Ser Thr Pro Met Ala Trp Leu Val Gln Asp	410	415	420	
ggg ggc gag acc atc aag tcc atc cgc acc ggc gac cag gtg gaa ttc				1411
Gly Gly Glu Thr Ile Lys Ser Ile Arg Thr Gly Asp Gln Val Glu Phe	425	430	435	
cag gca cca gta atc ttc gat tac cgc tac gac ctg tgg aaa ttc cag				1459
Gln Ala Pro Val Ile Phe Asp Tyr Arg Tyr Asp Leu Trp Lys Phe Gln	440	445	450	
cca acc acc cct gtc acc ggc aac acc gca agc tcc gac ctt cct atc				1507
Pro Thr Thr Pro Val Thr Gly Asn Thr Ala Ser Ser Asp Leu Pro Ile	455	460	465	
acc tgg gat gac acc cgc gcg gct gag cta gct tca atc aat gac gtt				1555
Thr Trp Asp Asp Thr Arg Ala Ala Glu Leu Ala Ser Ile Asn Asp Val	470	475	480	485
gct ggc gaa ttc cac atc gca agc ttc aac gtg ctc aac tac ttc acc				1603
Ala Gly Glu Phe His Ile Ala Ser Phe Asn Val Leu Asn Tyr Phe Thr	490	495	500	
tct ctc ggc gaa gat gaa cca ggc tgc agc gca tac agg gat atc aac				1651
Ser Leu Gly Glu Asp Glu Pro Gly Cys Ser Ala Tyr Arg Asp Ile Asn	505	510	515	
aac acc cca gtc acc gcc aac aac tgt aac gtc cgt ggc gct tac acc				1699
Asn Thr Pro Val Thr Ala Asn Asn Cys Asn Val Arg Gly Ala Tyr Thr	520	525	530	
gaa gaa gca ctc gaa gat cag cag agc aag atc gtc gaa gca atc aac				1747
Glu Glu Ala Leu Glu Asp Gln Gln Ser Lys Ile Val Glu Ala Ile Asn	535	540	545	
cgc ctt gac gtc gat gtt ctt				1768
Arg Leu Asp Val Asp Val Leu	550	555		

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<212> PRT

<213> Corynebacterium glutamicum

<400> 6

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Gly Ser Leu Phe Ser Asn Asp Phe Ile Glu Leu Tyr Asn Pro Thr Ser	50	55	60	

Gly Asp Ile Ser Leu Asp Gly Trp Ser Val Thr Tyr Tyr Ala Ala Asn
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 Gly Asn Ser Gly Gly Thr Thr Asn Leu Thr Gly Asn Ile Pro Ala Asn
 85 90 95
 Gly Tyr Tyr Leu Ile Gln Gln Arg Ala Gly Ser Asn Asn Thr Gly Ala
 100 105 110
 Leu Pro Thr Pro Asp Ala Thr Gly Asn Leu Ala Met Gly Ala Ser Gln
 115 120 125
 Gly Ser Val Ala Leu Thr Asp Asn Ser Gly Leu Thr Ala Asp Leu Val
 130 135 140
 Gly Phe Gly Gly Thr Ser Met Phe Glu Gly Thr Ala Ala Ala Pro Glu
 145 150 155 160
 Thr Ser Asn Lys Leu Ser Val Gln Arg Lys Glu Val Gly Ala Asp Ser
 165 170 175
 Asp Asn Asn Ser Val Asp Phe Glu Thr Gly Ala Pro Thr Pro Thr Ser
 180 185 190
 Ser Gly Gly Ser Ala Pro Val Asp Pro Gly Glu Pro Glu Thr Pro Val
 195 200 205
 Asn Pro Gly Glu Thr Val Ser Ile Ala Gln Ile Gln Gly Thr Gly Leu
 210 215 220
 Ala Thr Pro Leu Glu Gly Gln Thr Val Thr Thr Glu Gly Ile Val Thr
 225 230 235 240
 Ala Val Tyr Ala Glu Gly Gly Phe Asn Gly Tyr Tyr Ile Gln Thr Pro
 245 250 255
 Gly Ser Gly Thr Ala Pro Lys Val Ala Gly Asp Ala Ser Asp Gly Ile
 260 265 270
 Phe Val Tyr Val Gly Ser Asn Gly Ser Tyr Pro Glu Leu Gly Ala Ser
 275 280 285
 Val Thr Val Thr Gly Lys Ala Thr Glu His Tyr Glu Met Thr Gln Leu
 290 295 300
 Gly Asn Ser Ser Phe Thr Val Ser Asp Thr Ala Phe Glu Pro Val Thr
 305 310 315 320
 Pro Leu Glu Leu Asp Thr Val Pro Thr Gly Asp Asp Ile Arg Glu Ala
 325 330 335
 Tyr Glu Gly Met Leu Leu Lys Pro Thr Gly Ala His Thr Val Thr Asn
 340 345 350
 Asn Tyr Ala Thr Asn Thr Phe Gly Glu Ile Ala Leu Ala Pro Gly Asn
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 Glu Pro Leu Tyr Gln Ala Thr Gln Met Val Ala Pro Gly Ala Glu Ala
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 Ile Ala Tyr Glu Ala Glu Asn Val Ala Lys Gln Ile Thr Leu Asp Asp

385		390		395		400
Gly Arg Ser Gly	Asn Tyr Thr Arg Gly Asp Ser Ser Thr Pro Met Ala					
	405			410		415
Trp Leu Val Gln	Asp Gly Gly Glu Thr Ile Lys Ser Ile Arg Thr Gly					
	420		425			430
Asp Gln Val Glu	Phe Gln Ala Pro Val Ile Phe Asp Tyr Arg Tyr Asp					
	435		440			445
Leu Trp Lys Phe	Gln Pro Thr Thr Pro Val Thr Gly Asn Thr Ala Ser					
	450		455		460	
Ser Asp Leu Pro	Ile Thr Trp Asp Asp Thr Arg Ala Ala Glu Leu Ala					
	465		470		475	480
Ser Ile Asn Asp	Val Ala Gly Glu Phe His Ile Ala Ser Phe Asn Val					
	485		490			495
Leu Asn Tyr Phe	Thr Ser Leu Gly Glu Asp Glu Pro Gly Cys Ser Ala					
	500		505			510
Tyr Arg Asp Ile	Asn Asn Thr Pro Val Thr Ala Asn Asn Cys Asn Val					
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Arg Gly Ala Tyr	Thr Glu Glu Ala Leu Glu Asp Gln Gln Ser Lys Ile					
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Val Glu Ala Ile	Asn Arg Leu Asp Val Asp Val Leu					
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<210> 7

<211> 1369

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1369)

<223> FRXA00538

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gcg	cgc	act	ctg	gca	atc	gca	ctt	gcc	ggc	gca	acc	gcg	gcc	agc	ctg	163
Ala	Arg	Thr	Leu	Ala	Ile	Ala	Leu	Ala	Gly	Ala	Thr	Ala	Ala	Ser	Leu	
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gca	gtt	gtt	cca	gca	gca	aca	gct	aat	cct	gcc	gga	acc	gct	cct	gtc	211
Ala	Val	Val	Pro	Ala	Ala	Thr	Ala	Asn	Pro	Ala	Gly	Thr	Ala	Pro	Val	
			25				30						35			

atc	aac	gaa	atc	tac	gaa	ggc	ggc	gga	aac	agc	gga	tcg	ttg	ttc	tcc	259
Ile	Asn	Glu	Ile	Tyr	Glu	Gly	Gly	Gly	Asn	Ser	Gly	Ser	Leu	Phe	Ser	
		40				45						50				

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aag gcc acc gaa cac tac gag atg act cag cta ggc aac tcc tcc ttc 1027
 Lys Ala Thr Glu His Tyr Glu Met Thr Gln Leu Gly Asn Ser Ser Phe
 295 300 305

acc gtt tcg gac acc gca ttc gag cca gta acc cca ctc gaa ctg gac 1075
 Thr Val Ser Asp Thr Ala Phe Glu Pro Val Thr Pro Leu Glu Leu Asp
 310 315 320 325

acc gtt cct act ggc gat gac att cgc gaa gca tac gaa ggc atg ctg 1123
 Thr Val Pro Thr Gly Asp Asp Ile Arg Glu Ala Tyr Glu Gly Met Leu
 330 335 340

ctg aag cca acc ggc gct cac acc gtg acc aac aac tac gca acc aac 1171
 Leu Lys Pro Thr Gly Ala His Thr Val Thr Asn Asn Tyr Ala Thr Asn
 345 350 355

acc ttc ggt gaa att gcc ctc gcc cca ggt aac gag cct ttg tac cag 1219
 Thr Phe Gly Glu Ile Ala Leu Ala Pro Gly Asn Glu Pro Leu Tyr Gln
 360 365 370

gcc act caa atg gtg gca ccg gga gcc gaa gcg att gcg tac gag gcg 1267
 Ala Thr Gln Met Val Ala Pro Gly Ala Glu Ala Ile Ala Tyr Glu Ala
 375 380 385

gaa aac gtc gca aag caa att acg ctg gat gac gga cgc tcc ggc aac 1315
 Glu Asn Val Ala Lys Gln Ile Thr Leu Asp Asp Gly Arg Ser Gly Asn
 390 395 400 405

tac act cgc ggc gac tcc agc acg cct atg gca tgg ctt gtg cag gac 1363
 Tyr Thr Arg Gly Asp Ser Ser Thr Pro Met Ala Trp Leu Val Gln Asp
 410 415 420

ggt ggc 1369
 Gly Gly

<210> 8

<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 8

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Thr Ala Ala Ser Leu Ala Val Val Pro Ala Ala Thr Ala Asn Pro Ala
 20 25 30

Gly Thr Ala Pro Val Ile Asn Glu Ile Tyr Glu Gly Gly Gly Asn Ser
 35 40 45

Gly Ser Leu Phe Ser Asn Asp Phe Ile Glu Leu Tyr Asn Pro Thr Ser
 50 55 60

Gly Asp Ile Ser Leu Asp Gly Trp Ser Val Thr Tyr Tyr Ala Ala Asn
 65 70 75 80

Gly Asn Ser Gly Gly Thr Thr Asn Leu Thr Gly Asn Ile Pro Ala Asn
 85 90 95

Gly Tyr Tyr Leu Ile Gln Gln Arg Ala Gly Ser Asn Asn Thr Gly Ala
 100 105 110
 Leu Pro Thr Pro Asp Ala Thr Gly Asn Leu Ala Met Gly Ala Ser Gln
 115 120 125
 Gly Ser Val Ala Leu Thr Asp Asn Ser Gly Leu Thr Ala Asp Leu Val
 130 135 140
 Gly Phe Gly Gly Thr Ser Met Phe Glu Gly Thr Ala Ala Ala Pro Glu
 145 150 155 160
 Thr Ser Asn Lys Leu Ser Val Gln Arg Lys Glu Val Gly Ala Asp Ser
 165 170 175
 Asp Asn Asn Ser Val Asp Phe Glu Thr Gly Ala Pro Thr Pro Thr Ser
 180 185 190
 Ser Gly Gly Ser Ala Pro Val Asp Pro Gly Glu Pro Glu Thr Pro Val
 195 200 205
 Asn Pro Gly Glu Thr Val Ser Ile Ala Gln Ile Gln Gly Thr Gly Leu
 210 215 220
 Ala Thr Pro Leu Glu Gly Gln Thr Val Thr Thr Glu Gly Ile Val Thr
 225 230 235 240
 Ala Val Tyr Ala Glu Gly Gly Phe Asn Gly Tyr Tyr Ile Gln Thr Pro
 245 250 255
 Gly Ser Gly Thr Ala Pro Lys Val Ala Gly Asp Ala Ser Asp Gly Ile
 260 265 270
 Phe Val Tyr Val Gly Ser Asn Gly Ser Tyr Pro Glu Leu Gly Ala Ser
 275 280 285
 Val Thr Val Thr Gly Lys Ala Thr Glu His Tyr Glu Met Thr Gln Leu
 290 295 300
 Gly Asn Ser Ser Phe Thr Val Ser Asp Thr Ala Phe Glu Pro Val Thr
 305 310 315 320
 Pro Leu Glu Leu Asp Thr Val Pro Thr Gly Asp Asp Ile Arg Glu Ala
 325 330 335
 Tyr Glu Gly Met Leu Leu Lys Pro Thr Gly Ala His Thr Val Thr Asn
 340 345 350
 Asn Tyr Ala Thr Asn Thr Phe Gly Glu Ile Ala Leu Ala Pro Gly Asn
 355 360 365
 Glu Pro Leu Tyr Gln Ala Thr Gln Met Val Ala Pro Gly Ala Glu Ala
 370 375 380
 Ile Ala Tyr Glu Ala Glu Asn Val Ala Lys Gln Ile Thr Leu Asp Asp
 385 390 395 400
 Gly Arg Ser Gly Asn Tyr Thr Arg Gly Asp Ser Ser Thr Pro Met Ala
 405 410 415
 Trp Leu Val Gln Asp Gly Gly

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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101) .. (880)  
<223> RXA00823
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tcatttctaat gatgaatcaa atccgcgccta acttaagggt																	
											atg	ggg	tcc	att	act		115
											Met	Gly	Ser	Ile	Thr		
											1				5		
ccg cag aag cgg cct cgc gtg ggg tct cac atc gcg aac aag ggt caa																	163
Pro Gln Lys Arg Pro Arg Val Gly Ser His Ile Ala Asn Lys Gly Gln																	
10 15 20																	
gag act gat atc ggg cga aaa cgc cga gct cga cgc atc aat cgc aca																	211
Glu Thr Asp Ile Gly Arg Lys Arg Arg Ala Arg Arg Ile Asn Arg Thr																	
25 30 35																	
ctc acc gtg gca tat ccg gat gcg cac tgc gaa tta gat ttc acc aat																	259
Leu Thr Val Ala Tyr Pro Asp Ala His Cys Glu Leu Asp Phe Thr Asn																	
40 45 50																	
ccg cta gaa ctc acg gtc gcc acc att ttg tcc gcc cag tgc acg gac																	307
Pro Leu Glu Leu Thr Val Ala Thr Ile Leu Ser Ala Gln Cys Thr Asp																	
55 60 65																	
gtt cgc gtg aac cag gtg acg ccc gcg ttg ttc aag cgc tat ccg acg																	355
Val Arg Val Asn Gln Val Thr Pro Ala Leu Phe Lys Arg Tyr Pro Thr																	
70 75 80 85																	
gcc aca gat tac gcc aac gcc gat cgc acg gaa ttg gag gag ttc atc																	403
Ala Thr Asp Tyr Ala Asn Ala Asp Arg Thr Glu Leu Glu Glu Phe Ile																	
90 95 100																	
cgt ccg aca ggc ttt tac cgc aac aag gcc act tct tta atc ggc ctg																	451
Arg Pro Thr Gly Phe Tyr Arg Asn Lys Ala Thr Ser Leu Ile Gly Leu																	
105 110 115																	
ggg gag gca cta att tcg ctt cac gac ggc cag gtc ccc ggt acc ctt																	499
Gly Glu Ala Leu Ile Ser Leu His Asp Gly Gln Val Pro Gly Thr Leu																	
120 125 130																	
gag cag cta gtt gag ctg ccg ggg gtc ggg cgg aaa acc gcc aac gtg																	547
Glu Gln Leu Val Glu Leu Pro Gly Val Gly Arg Lys Thr Ala Asn Val																	
135 140 145																	
gtg ctg gga aat gct ttc ggt gtt ccg gga atc acg gtg gat aca cac																	595
Val Leu Gly Asn Ala Phe Gly Val Pro Gly Ile Thr Val Asp Thr His																	
150 155 160 165																	
ttt ggc agg ttg gtg cgt cgc ctg aag ctc act gat gaa gaa gat ccc																	643

Phe Gly Arg Leu Val Arg Arg Leu Lys Leu Thr Asp Glu Glu Asp Pro
 170 175 180
 gtc aag gtg gaa aaa gtg atg aac gaa ctc atc gaa aag cct gag tgg 691
 Val Lys Val Glu Lys Val Met Asn Glu Leu Ile Glu Lys Pro Glu Trp
 185 190 195
 acc atg ttt tca cat agg ctg atc ttc cac gga cgt agg ata tgt cat 739
 Thr Met Phe Ser His Arg Leu Ile Phe His Gly Arg Arg Ile Cys His
 200 205 210
 agt cga cgc gcc gcc tgt gga gcc tgc atg ctg gca gct gat tgc cca 787
 Ser Arg Arg Ala Ala Cys Gly Ala Cys Met Leu Ala Ala Asp Cys Pro
 215 220 225
 tcc ttt ggt ttg gag ggg ccg tca gat cca ttt gag gcg caa aaa ctc 835
 Ser Phe Gly Leu Glu Gly Pro Ser Asp Pro Phe Glu Ala Gln Lys Leu
 230 235 240 245
 att aaa agt gat gat agg gag cac ctg ctg aaa atg gca gga atg 880
 Ile Lys Ser Asp Asp Arg Glu His Leu Leu Lys Met Ala Gly Met
 250 255 260
 tagaaaacaa atgacaagca gtg 903

 <210> 10
 <211> 260
 <212> PRT
 <213> Corynebacterium glutamicum

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 Ala Asn Lys Gly Gln Glu Thr Asp Ile Gly Arg Lys Arg Arg Ala Arg
 20 25 30
 Arg Ile Asn Arg Thr Leu Thr Val Ala Tyr Pro Asp Ala His Cys Glu
 35 40 45
 Leu Asp Phe Thr Asn Pro Leu Glu Leu Thr Val Ala Thr Ile Leu Ser
 50 55 60
 Ala Gln Cys Thr Asp Val Arg Val Asn Gln Val Thr Pro Ala Leu Phe
 65 70 75 80
 Lys Arg Tyr Pro Thr Ala Thr Asp Tyr Ala Asn Ala Asp Arg Thr Glu
 85 90 95
 Leu Glu Glu Phe Ile Arg Pro Thr Gly Phe Tyr Arg Asn Lys Ala Thr
 100 105 110
 Ser Leu Ile Gly Leu Gly Glu Ala Leu Ile Ser Leu His Asp Gly Gln
 115 120 125
 Val Pro Gly Thr Leu Glu Gln Leu Val Glu Leu Pro Gly Val Gly Arg
 130 135 140
 Lys Thr Ala Asn Val Val Leu Gly Asn Ala Phe Gly Val Pro Gly Ile
 145 150 155 160

Thr Val Asp Thr His Phe Gly Arg Leu Val Arg Arg Leu Lys Leu Thr
 165 170 175

Asp Glu Glu Asp Pro Val Lys Val Glu Lys Val Met Asn Glu Leu Ile
 180 185 190

Glu Lys Pro Glu Trp Thr Met Phe Ser His Arg Leu Ile Phe His Gly
 195 200 205

Arg Arg Ile Cys His Ser Arg Arg Ala Ala Cys Gly Ala Cys Met Leu
 210 215 220

Ala Ala Asp Cys Pro Ser Phe Gly Leu Glu Gly Pro Ser Asp Pro Phe
 225 230 235 240

Glu Ala Gln Lys Leu Ile Lys Ser Asp Asp Arg Glu His Leu Leu Lys
 245 250 255

Met Ala Gly Met
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<210> 11
 <211> 1740
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101) .. (1717)
 <223> RXA02145

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tcattgagcc actcggccct gcattctggg agcgttaagtc atg agt cta gct acc 115
 Met Ser Leu Ala Thr
 1 5

gtg gga aac aat ctt gat tcc cgt tac acc atg gcg tcg ggt atc cgt 163
 Val Gly Asn Asn Leu Asp Ser Arg Tyr Thr Met Ala Ser Gly Ile Arg
 10 15 20

cgc cag atc aac aag gtc ttc cca act cac tgg tcc ttc atg ctc ggc 211
 Arg Gln Ile Asn Lys Val Phe Pro Thr His Trp Ser Phe Met Leu Gly
 25 30 35

gag att gcg ctt tac agc ttc atc gtc ttg ctg ctg act ggt gtc tac 259
 Glu Ile Ala Leu Tyr Ser Phe Ile Val Leu Leu Leu Thr Gly Val Tyr
 40 45 50

ctg acc ctg ttc ttc gac cca tca atc acc aag gtc att tat gac ggc 307
 Leu Thr Leu Leu Phe Phe Asp Pro Ser Ile Thr Lys Val Ile Tyr Asp Gly
 55 60 65

ggc tac ctc cca ctg aac ggt gtg gag atg tcc cgt gca tac gca act 355
 Gly Tyr Leu Pro Leu Asn Gly Val Glu Met Ser Arg Ala Tyr Ala Thr
 70 75 80 85

gcg ttg gat att tcc ttc gag gtt cgc ggt ggt ctg ttc atc cgc cag 403

Ala	Leu	Asp	Ile	Ser	Phe	Glu	Val	Arg	Gly	Gly	Leu	Phe	Ile	Arg	Gln	
				90					95					100		
atg	cac	cac	tgg	gca	gcc	ctg	ctg	ttc	gtt	gta	tcc	atg	ctg	gtt	cac	451
Met	His	His	Trp	Ala	Ala	Leu	Leu	Phe	Val	Val	Ser	Met	Leu	Val	His	
			105					110					115			
atg	ctc	cgt	att	ttc	ttc	acc	ggg	gcg	ttc	cgt	cgc	cca	cgt	gaa	gca	499
Met	Leu	Arg	Ile	Phe	Phe	Thr	Gly	Ala	Phe	Arg	Arg	Pro	Arg	Glu	Ala	
		120					125					130				
aac	tgg	atc	atc	ggg	gtt	gtt	ctg	atc	atc	ctg	ggg	atg	gct	gaa	ggc	547
Asn	Trp	Ile	Ile	Gly	Val	Val	Leu	Ile	Ile	Leu	Gly	Met	Ala	Glu	Gly	
	135					140					145					
ttc	atg	ggg	tac	tcc	ctg	cct	gat	gac	ctg	ctc	tct	ggg	gtt	ggg	ctt	595
Phe	Met	Gly	Tyr	Ser	Leu	Pro	Asp	Asp	Leu	Leu	Ser	Gly	Val	Gly	Leu	
150					155					160					165	
cga	atc	atg	tcc	gcc	atc	atc	gtt	ggg	ctt	ccg	atc	ata	ggg	acc	tgg	643
Arg	Ile	Met	Ser	Ala	Ile	Ile	Val	Gly	Leu	Pro	Ile	Ile	Gly	Thr	Trp	
				170					175					180		
atg	cac	tgg	ctg	atc	ttc	ggg	gga	gac	ttc	cca	tcc	gat	ctg	atg	ctg	691
Met	His	Trp	Leu	Ile	Phe	Gly	Gly	Asp	Phe	Pro	Ser	Asp	Leu	Met	Leu	
			185					190					195			
gac	cgc	ttc	tac	atc	gca	cac	gtt	cta	atc	atc	cca	gct	atc	ctg	ctt	739
Asp	Arg	Phe	Tyr	Ile	Ala	His	Val	Leu	Ile	Ile	Pro	Ala	Ile	Leu	Leu	
		200					205					210				
ggc	ttg	atc	gca	gct	cac	ctg	gca	ctt	gtt	tgg	tac	cag	aag	cac	acc	787
Gly	Leu	Ile	Ala	Ala	His	Leu	Ala	Leu	Val	Trp	Tyr	Gln	Lys	His	Thr	
	215					220					225					
cag	ttc	cca	ggc	gct	ggc	cgc	act	gag	aac	aac	gtg	atc	ggg	atc	cga	835
Gln	Phe	Pro	Gly	Ala	Gly	Arg	Thr	Glu	Asn	Asn	Val	Ile	Gly	Ile	Arg	
					235				240						245	
atc	atg	cct	ctg	ttc	gca	gtt	aag	gct	gtt	gct	ttc	ggc	ctc	atc	gtc	883
Ile	Met	Pro	Leu	Phe	Ala	Val	Lys	Ala	Val	Ala	Phe	Gly	Leu	Ile	Val	
				250					255					260		
ttc	ggg	ttc	ctc	gca	ctg	ctt	gct	ggg	gtc	acc	acc	att	aac	gca	att	931
Phe	Gly	Phe	Leu	Ala	Leu	Leu	Ala	Gly	Val	Thr	Thr	Ile	Asn	Ala	Ile	
			265					270					275			
tgg	aat	ctt	gga	ccg	tac	aac	cct	tca	cag	gtg	tct	gct	ggg	tcc	cag	979
Trp	Asn	Leu	Gly	Pro	Tyr	Asn	Pro	Ser	Gln	Val	Ser	Ala	Gly	Ser	Gln	
		280					285					290				
cct	gac	gtt	tac	atg	ctg	tgg	aca	gat	ggg	gct	gct	cgt	gtc	atg	ccg	1027
Pro	Asp	Val	Tyr	Met	Leu	Trp	Thr	Asp	Gly	Ala	Ala	Arg	Val	Met	Pro	
		295				300					305					
gca	tgg	gag	ctc	tac	ctc	ggg	aac	tac	act	att	cca	gca	gtc	ttc	tgg	1075
Ala	Trp	Glu	Leu	Tyr	Leu	Gly	Asn	Tyr	Thr	Ile	Pro	Ala	Val	Phe	Trp	
	310				315					320					325	
gtt	gct	gtg	atg	ctg	ggg	atc	ctc	gtg	gtt	ctg	ctt	gtg	act	tac	cca	1123
Val	Ala	Val	Met	Leu	Gly	Ile	Leu	Val	Val	Leu	Leu	Val	Thr	Tyr	Pro	

330	335	340	
ttc att gag cgt aag ttc acc ggc gac gat gca cac cac aac ttg ctg			1171
Phe Ile Glu Arg Lys Phe Thr Gly Asp Asp Ala His His Asn Leu Leu			
345	350	355	
cag cgt cct cgc gat gtt cca gtc cgc acc tca ctc ggt gtc atg gcg			1219
Gln Arg Pro Arg Asp Val Pro Val Arg Thr Ser Leu Gly Val Met Ala			
360	365	370	
ctt gtc ttc tac atc ctg ctt acc gtt tct ggt ggt aac gat gtt tac			1267
Leu Val Phe Tyr Ile Leu Leu Thr Val Ser Gly Gly Asn Asp Val Tyr			
375	380	385	
gca atg cag ttc cat gtt tca ctg aac gcg atg acc tgg atc ggt cgt			1315
Ala Met Gln Phe His Val Ser Leu Asn Ala Met Thr Trp Ile Gly Arg			
390	395	400	405
atc ggc ctc atc gtt gga cca gct att gca tac ttc atc act tac cga			1363
Ile Gly Leu Ile Val Gly Pro Ala Ile Ala Tyr Phe Ile Thr Tyr Arg			
410	415	420	
ctg tgc atc ggc ttg cag cgc tct gac cgc gag gtc ctg gag cac ggc			1411
Leu Cys Ile Gly Leu Gln Arg Ser Asp Arg Glu Val Leu Glu His Gly			
425	430	435	
atc gag acc ggt atc atc aag cag atg cca aat ggt gcc ttc att gaa			1459
Ile Glu Thr Gly Ile Ile Lys Gln Met Pro Asn Gly Ala Phe Ile Glu			
440	445	450	
gtt cac cag cca ctt ggc cca gtt gat gac cat ggt cac cca atc cca			1507
Val His Gln Pro Leu Gly Pro Val Asp Asp His Gly His Pro Ile Pro			
455	460	465	
ctg cca tac gct ggc gct gcg gtt cca aag cag atg aac cag ctt ggt			1555
Leu Pro Tyr Ala Gly Ala Ala Val Pro Lys Gln Met Asn Gln Leu Gly			
470	475	480	485
tac gct gag gtt gaa acc cgc ggt gga ttc ttc gga cct gat cca gaa			1603
Tyr Ala Glu Val Glu Thr Arg Gly Gly Phe Phe Gly Pro Asp Pro Glu			
490	495	500	
gac atc cgt gcg aag gct aag gaa att gag cac gca aac cac att gag			1651
Asp Ile Arg Ala Lys Ala Lys Glu Ile Glu His Ala Asn His Ile Glu			
505	510	515	
gaa gcg aac act ctt cgt gca ctc aac gag gca aac att gag cgt gac			1699
Glu Ala Asn Thr Leu Arg Ala Leu Asn Glu Ala Asn Ile Glu Arg Asp			
520	525	530	
aag aat gag ggc aag aac tagtttctag gacttcatct ctg			1740
Lys Asn Glu Gly Lys Asn			
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<210> 12

<211> 539

<212> PRT

<213> Corynebacterium glutamicum

<400> 12

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 Ala Ser Gly Ile Arg Arg Gln Ile Asn Lys Val Phe Pro Thr His Trp
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 Ser Phe Met Leu Gly Glu Ile Ala Leu Tyr Ser Phe Ile Val Leu Leu
 35 40 45
 Leu Thr Gly Val Tyr Leu Thr Leu Phe Phe Asp Pro Ser Ile Thr Lys
 50 55 60
 Val Ile Tyr Asp Gly Gly Tyr Leu Pro Leu Asn Gly Val Glu Met Ser
 65 70 75 80
 Arg Ala Tyr Ala Thr Ala Leu Asp Ile Ser Phe Glu Val Arg Gly Gly
 85 90 95
 Leu Phe Ile Arg Gln Met His His Trp Ala Ala Leu Leu Phe Val Val
 100 105 110
 Ser Met Leu Val His Met Leu Arg Ile Phe Phe Thr Gly Ala Phe Arg
 115 120 125
 Arg Pro Arg Glu Ala Asn Trp Ile Ile Gly Val Val Leu Ile Ile Leu
 130 135 140
 Gly Met Ala Glu Gly Phe Met Gly Tyr Ser Leu Pro Asp Asp Leu Leu
 145 150 155 160
 Ser Gly Val Gly Leu Arg Ile Met Ser Ala Ile Ile Val Gly Leu Pro
 165 170 175
 Ile Ile Gly Thr Trp Met His Trp Leu Ile Phe Gly Gly Asp Phe Pro
 180 185 190
 Ser Asp Leu Met Leu Asp Arg Phe Tyr Ile Ala His Val Leu Ile Ile
 195 200 205
 Pro Ala Ile Leu Leu Gly Leu Ile Ala Ala His Leu Ala Leu Val Trp
 210 215 220
 Tyr Gln Lys His Thr Gln Phe Pro Gly Ala Gly Arg Thr Glu Asn Asn
 225 230 235 240
 Val Ile Gly Ile Arg Ile Met Pro Leu Phe Ala Val Lys Ala Val Ala
 245 250 255
 Phe Gly Leu Ile Val Phe Gly Phe Leu Ala Leu Leu Ala Gly Val Thr
 260 265 270
 Thr Ile Asn Ala Ile Trp Asn Leu Gly Pro Tyr Asn Pro Ser Gln Val
 275 280 285
 Ser Ala Gly Ser Gln Pro Asp Val Tyr Met Leu Trp Thr Asp Gly Ala
 290 295 300
 Ala Arg Val Met Pro Ala Trp Glu Leu Tyr Leu Gly Asn Tyr Thr Ile
 305 310 315 320
 Pro Ala Val Phe Trp Val Ala Val Met Leu Gly Ile Leu Val Val Leu

				325				330				335			
Leu	Val	Thr	Tyr	Pro	Phe	Ile	Glu	Arg	Lys	Phe	Thr	Gly	Asp	Asp	Ala
			340				345						350		
His	His	Asn	Leu	Leu	Gln	Arg	Pro	Arg	Asp	Val	Pro	Val	Arg	Thr	Ser
		355					360						365		
Leu	Gly	Val	Met	Ala	Leu	Val	Phe	Tyr	Ile	Leu	Leu	Thr	Val	Ser	Gly
		370			375						380				
Gly	Asn	Asp	Val	Tyr	Ala	Met	Gln	Phe	His	Val	Ser	Leu	Asn	Ala	Met
385				390						395				400	
Thr	Trp	Ile	Gly	Arg	Ile	Gly	Leu	Ile	Val	Gly	Pro	Ala	Ile	Ala	Tyr
			405				410						415		
Phe	Ile	Thr	Tyr	Arg	Leu	Cys	Ile	Gly	Leu	Gln	Arg	Ser	Asp	Arg	Glu
			420				425						430		
Val	Leu	Glu	His	Gly	Ile	Glu	Thr	Gly	Ile	Ile	Lys	Gln	Met	Pro	Asn
		435			440						445				
Gly	Ala	Phe	Ile	Glu	Val	His	Gln	Pro	Leu	Gly	Pro	Val	Asp	Asp	His
450				455						460					
Gly	His	Pro	Ile	Pro	Leu	Pro	Tyr	Ala	Gly	Ala	Ala	Val	Pro	Lys	Gln
465				470				475						480	
Met	Asn	Gln	Leu	Gly	Tyr	Ala	Glu	Val	Glu	Thr	Arg	Gly	Gly	Phe	Phe
			485				490						495		
Gly	Pro	Asp	Pro	Glu	Asp	Ile	Arg	Ala	Lys	Ala	Lys	Glu	Ile	Glu	His
			500				505						510		
Ala	Asn	His	Ile	Glu	Glu	Ala	Asn	Thr	Leu	Arg	Ala	Leu	Asn	Glu	Ala
		515			520						525				
Asn	Ile	Glu	Arg	Asp	Lys	Asn	Glu	Gly	Lys	Asn					
530				535											

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<210> 13
<211> 759
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101) .. (736)
<223> RXA01064
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cttatccact acccagacct ctacaagaaa gttccccaga atg tca cta tct att 115
                                         Met Ser Leu Ser Ile
                                         1                               5
agt ttt cat aaa att gca ctc tct gcc acc acc ttg ctt ggc gct gtc 163
Ser Phe His Lys Ile Ala Leu Ser Ala Thr Thr Leu Leu Gly Ala Val

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	10	15	20	
gca atc tct gcc tgt gcg cta gta act caa gca cct cct att aac gca	25	30	35	211
Ala Ile Ser Ala Cys Ala Leu Val Thr Gln Ala Pro Pro Ile Asn Ala				
gcc ccg gtt act ggc agc agc tca tta agc ttc acc ctc gac ctg ggc	40	45	50	259
Ala Pro Val Thr Gly Ser Ser Ser Leu Ser Phe Thr Leu Asp Leu Gly				
acc acc acc cct acc agc atc gac aca gta aaa ctc act cag caa gca	55	60	65	307
Thr Thr Thr Pro Thr Ser Ile Asp Thr Val Lys Leu Thr Gln Gln Ala				
caa aat caa gcg gca cca cgc gtt gca gcg agc ctg gtg cgc gtg gtt	70	75	80	355
Gln Asn Gln Ala Ala Pro Arg Val Ala Ala Ser Leu Val Arg Val Val				
gac ggc gac acc att gtc gtg aac tat cag ggt gct cag aaa act gtt	90	95	100	403
Asp Gly Asp Thr Ile Val Val Asn Tyr Gln Gly Ala Gln Lys Thr Val				
cgt atg atc ggt att gat tcc ccc gaa acc aaa cac ccc acc aag cct	105	110	115	451
Arg Met Ile Gly Ile Asp Ser Pro Glu Thr Lys His Pro Thr Lys Pro				
gtg ggc ttc tac gga cca gaa tct tca cag aat ctc acc acc atg ctg	120	125	130	499
Val Gly Phe Tyr Gly Pro Glu Ser Ser Gln Asn Leu Thr Thr Met Leu				
cgc ggt gcc acc atc aca cta gaa ttt gat tcc acc caa gcc cgc gaa	135	140	145	547
Arg Gly Ala Thr Ile Thr Leu Glu Phe Asp Ser Thr Gln Ala Arg Glu				
gat caa tac gga cgc ctg ctt gct tat gtc tgg tac acc aag ggc gat	150	155	160	595
Asp Gln Tyr Gly Arg Leu Leu Ala Tyr Val Trp Tyr Thr Lys Gly Asp				
agc ggt ctt aag ctt gcc aat ttg gaa caa att gcc tca ggc tct gct	170	175	180	643
Ser Gly Leu Lys Leu Ala Asn Leu Glu Gln Ile Ala Ser Gly Ser Ala				
gct gaa tac agc ttc gac acc cgc tac aac cac cgc aat att ttc cta	185	190	195	691
Ala Glu Tyr Ser Phe Asp Thr Arg Tyr Asn His Arg Asn Ile Phe Leu				
cgt gca caa acc ctt gcc aag gca agc agt cta ggt atg tgg ggt	200	205	210	736
Arg Ala Gln Thr Leu Ala Lys Ala Ser Ser Leu Gly Met Trp Gly				
taaaagaaac ccacctatac caa				759

<210> 14

<211> 212

<212> PRT

<213> Corynebacterium glutamicum

<400> 14

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 20 25 30
 Pro Pro Ile Asn Ala Ala Pro Val Thr Gly Ser Ser Ser Leu Ser Phe
 35 40 45
 Thr Leu Asp Leu Gly Thr Thr Thr Pro Thr Ser Ile Asp Thr Val Lys
 50 55 60
 Leu Thr Gln Gln Ala Gln Asn Gln Ala Ala Pro Arg Val Ala Ala Ser
 65 70 75 80
 Leu Val Arg Val Val Asp Gly Asp Thr Ile Val Val Asn Tyr Gln Gly
 85 90 95
 Ala Gln Lys Thr Val Arg Met Ile Gly Ile Asp Ser Pro Glu Thr Lys
 100 105 110
 His Pro Thr Lys Pro Val Gly Phe Tyr Gly Pro Glu Ser Ser Gln Asn
 115 120 125
 Leu Thr Thr Met Leu Arg Gly Ala Thr Ile Thr Leu Glu Phe Asp Ser
 130 135 140
 Thr Gln Ala Arg Glu Asp Gln Tyr Gly Arg Leu Leu Ala Tyr Val Trp
 145 150 155 160
 Tyr Thr Lys Gly Asp Ser Gly Leu Lys Leu Ala Asn Leu Glu Gln Ile
 165 170 175
 Ala Ser Gly Ser Ala Ala Glu Tyr Ser Phe Asp Thr Arg Tyr Asn His
 180 185 190
 Arg Asn Ile Phe Leu Arg Ala Gln Thr Leu Ala Lys Ala Ser Ser Leu
 195 200 205
 Gly Met Trp Gly
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<210> 15

<211> 942

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(919)

<223> RXN01594

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cactattttt taaccactca cgaaagaaga acacctccag atg gtt gca cgc aga 115
 Met Val Ala Arg Arg
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aga ctg gac gca gaa ctt gtt cgt cga aag atc gca cga tca agg gaa 163
 Arg Leu Asp Ala Glu Leu Val Arg Arg Lys Ile Ala Arg Ser Arg Glu
 10 15 20

cac gcg gtt gaa atg atc cgc ggt cgg cgc gtc ttt gtt gca gga atg	211
His Ala Val Glu Met Ile Arg Gly Arg Arg Val Phe Val Ala Gly Met	
25 30 35	
ctt gct tta aag ccc gca aca gtc gtg gaa cca gag gtg tct att cgt	259
Leu Ala Leu Lys Pro Ala Thr Val Val Glu Pro Glu Val Ser Ile Arg	
40 45 50	
gtg gaa gaa gat gct agt gaa gat tgg gca tcc cgc ggt gcg cac aag	307
Val Glu Glu Asp Ala Ser Glu Asp Trp Ala Ser Arg Gly Ala His Lys	
55 60 65	
ctt ctt ggt gcg ctg gaa tct ttt gag ccc ttg ggg ctc aag gtc aag	355
Leu Leu Gly Ala Leu Glu Ser Phe Glu Pro Leu Gly Leu Lys Val Lys	
70 75 80 85	
ggc cgt cgc gtg cta gat gcc ggc gct tcg aca ggc gga ttt acg gac	403
Gly Arg Arg Val Leu Asp Ala Gly Ala Ser Thr Gly Gly Phe Thr Asp	
90 95 100	
gtg ttg cta cgt cga gaa gcg tct gaa gta gtg gca gta gac gtg ggc	451
Val Leu Leu Arg Arg Glu Ala Ser Glu Val Val Ala Val Asp Val Gly	
105 110 115	
tac gga cag ctt att tgg cgc ctg caa aac gac gac cgc gtg cgc gtg	499
Tyr Gly Gln Leu Ile Trp Arg Leu Gln Asn Asp Asp Arg Val Arg Val	
120 125 130	
gtg gac cgc acc aac atc aga tac atg acg ctg gaa gac acc ggc gga	547
Val Asp Arg Thr Asn Ile Arg Tyr Met Thr Leu Glu Asp Thr Gly Gly	
135 140 145	
gaa tgc gac atg atg gtg ggc gat ctc tca ttt att tcg ctt aaa ctc	595
Glu Cys Asp Met Met Val Gly Asp Leu Ser Phe Ile Ser Leu Lys Leu	
150 155 160 165	
acg ttg ccg gcg atc gcc aag gtc cta agc gac ggc gct gat cta tta	643
Thr Leu Pro Ala Ile Ala Lys Val Leu Ser Asp Gly Ala Asp Leu Leu	
170 175 180	
ccc atg gtc aag cca caa ttt gaa gtc gga aaa gac cga ttg ggc agt	691
Pro Met Val Lys Pro Gln Phe Glu Val Gly Lys Asp Arg Leu Gly Ser	
185 190 195	
ggc ggc gtg gtg cgc tca cca gag ttg cgc gca gaa gtt acc gcg gat	739
Gly Gly Val Val Arg Ser Pro Glu Leu Arg Ala Glu Val Thr Ala Asp	
200 205 210	
gtc gcg aaa ttt gcg gcc act ttg ggc ctg agc ttg aag cat gtt gtt	787
Val Ala Lys Phe Ala Ala Thr Leu Gly Leu Ser Leu Lys His Val Val	
215 220 225	
gca tcc ccg ctg ccc ggc ccg tca ggc aac gta gaa tac ttc ctg tgg	835
Ala Ser Pro Leu Pro Gly Pro Ser Gly Asn Val Glu Tyr Phe Leu Trp	
230 235 240 245	
ctg gtt aaa gat ggt ggc gct tca atg ccg gat gac cag caa ttg tcg	883
Leu Val Lys Asp Gly Gly Ala Ser Met Pro Asp Asp Gln Gln Leu Ser	
250 255 260	

gca atg att gac acg gct gta aag gaa ggt ccg caa taatgactgc 929
 Ala Met Ile Asp Thr Ala Val Lys Glu Gly Pro Gln
 265 270

acccacgaac gct 942

<210> 16

<211> 273

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 16

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 20 25 30

Phe Val Ala Gly Met Leu Ala Leu Lys Pro Ala Thr Val Val Glu Pro
 35 40 45

Glu Val Ser Ile Arg Val Glu Glu Asp Ala Ser Glu Asp Trp Ala Ser
 50 55 60

Arg Gly Ala His Lys Leu Leu Gly Ala Leu Glu Ser Phe Glu Pro Leu
 65 70 75 80

Gly Leu Lys Val Lys Gly Arg Arg Val Leu Asp Ala Gly Ala Ser Thr
 85 90 95

Gly Gly Phe Thr Asp Val Leu Leu Arg Arg Glu Ala Ser Glu Val Val
 100 105 110

Ala Val Asp Val Gly Tyr Gly Gln Leu Ile Trp Arg Leu Gln Asn Asp
 115 120 125

Asp Arg Val Arg Val Val Asp Arg Thr Asn Ile Arg Tyr Met Thr Leu
 130 135 140

Glu Asp Thr Gly Gly Glu Cys Asp Met Met Val Gly Asp Leu Ser Phe
 145 150 155 160

Ile Ser Leu Lys Leu Thr Leu Pro Ala Ile Ala Lys Val Leu Ser Asp
 165 170 175

Gly Ala Asp Leu Leu Pro Met Val Lys Pro Gln Phe Glu Val Gly Lys
 180 185 190

Asp Arg Leu Gly Ser Gly Gly Val Val Arg Ser Pro Glu Leu Arg Ala
 195 200 205

Glu Val Thr Ala Asp Val Ala Lys Phe Ala Ala Thr Leu Gly Leu Ser
 210 215 220

Leu Lys His Val Val Ala Ser Pro Leu Pro Gly Pro Ser Gly Asn Val
 225 230 235 240

Glu Tyr Phe Leu Trp Leu Val Lys Asp Gly Gly Ala Ser Met Pro Asp
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Asp Gln Gln Leu Ser Ala Met Ile Asp Thr Ala Val Lys Glu Gly Pro
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Gln

<210> 17

<211> 867

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(844)

<223> FRXA01594

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 Met Ile Arg Gly Arg
 1 5

cgc gtc ttt gtt gca gga atg ctt gct tta aag ccc gca aca gtc gtg 163
 Arg Val Phe Val Ala Gly Met Leu Ala Leu Lys Pro Ala Thr Val Val
 10 15 20

gaa cca gag gtg tct att cgt gtg gaa gaa gat gct agt gaa gat tgg 211
 Glu Pro Glu Val Ser Ile Arg Val Glu Glu Asp Ala Ser Glu Asp Trp
 25 30 35

gca tcc cgc ggt gcg cac aag ctt ctt ggt gcg ctg gaa tct ttt gag 259
 Ala Ser Arg Gly Ala His Lys Leu Leu Gly Ala Leu Glu Ser Phe Glu
 40 45 50

ccc ttg ggg ctc aag gtc aag ggc cgt cgc gtg cta gat gcc ggc gct 307
 Pro Leu Gly Leu Lys Val Lys Gly Arg Arg Val Leu Asp Ala Gly Ala
 55 60 65

tcg aca ggc gga ttt acg gac gtg ttg cta cgt cga gaa gcg tct gaa 355
 Ser Thr Gly Gly Phe Thr Asp Val Leu Leu Arg Arg Glu Ala Ser Glu
 70 75 80 85

gta gtg gca gta gac gtg ggc tac gga cag ctt att tgg cgc ctg caa 403
 Val Val Ala Val Asp Val Gly Tyr Gly Gln Leu Ile Trp Arg Leu Gln
 90 95 100

aac gac gac cgc gtg cgc gtg gtg gac cgc acc aac atc aga tac atg 451
 Asn Asp Asp Arg Val Arg Val Val Asp Arg Thr Asn Ile Arg Tyr Met
 105 110 115

acg ctg gaa gac acc ggc gga gaa tgc gac atg atg gtg ggc gat ctc 499
 Thr Leu Glu Asp Thr Gly Gly Glu Cys Asp Met Met Val Gly Asp Leu
 120 125 130

tca ttt att tcg ctt aaa ctc acg ttg ccg gcg atc gcc aag gtc cta 547
 Ser Phe Ile Ser Leu Lys Leu Thr Leu Pro Ala Ile Ala Lys Val Leu
 135 140 145

agc gac ggc gct gat cta tta ccc atg gtc aag cca caa ttt gaa gtc 595

Ser Asp Gly Ala Asp Leu Leu Pro Met Val Lys Pro Gln Phe Glu Val
 150 155 160 165

gga aaa gac cga ttg ggc agt ggc ggc gtg gtg cgc tca cca gag ttg 643
 Gly Lys Asp Arg Leu Gly Ser Gly Gly Val Val Arg Ser Pro Glu Leu
 170 175 180

cgc gca gaa gtt acc gcg gat gtc gcg aaa ttt gcg gcc act ttg ggc 691
 Arg Ala Glu Val Thr Ala Asp Val Ala Lys Phe Ala Ala Thr Leu Gly
 185 190 195

ctg agc ttg aag cat gtt gtt gca tcc ccg ctg ccc ggc ccg tca ggc 739
 Leu Ser Leu Lys His Val Val Ala Ser Pro Leu Pro Gly Pro Ser Gly
 200 205 210

aac gta gaa tac ttc ctg tgg ctg gtt aaa gat ggt ggc gct tca atg 787
 Asn Val Glu Tyr Phe Leu Trp Leu Val Lys Asp Gly Gly Ala Ser Met
 215 220 225

ccg gat gac cag caa ttg tcg gca atg att gac acg gct gta aag gaa 835
 Pro Asp Asp Gln Gln Leu Ser Ala Met Ile Asp Thr Ala Val Lys Glu
 230 235 240 245

ggt ccg caa taatgactgc acccaggaac gct 867
 Gly Pro Gln

<210> 18
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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45

Leu Glu Ser Phe Glu Pro Leu Gly Leu Lys Val Lys Gly Arg Arg Val
 50 55 60

Leu Asp Ala Gly Ala Ser Thr Gly Gly Phe Thr Asp Val Leu Leu Arg
 65 70 75 80

Arg Glu Ala Ser Glu Val Val Ala Val Asp Val Gly Tyr Gly Gln Leu
 85 90 95

Ile Trp Arg Leu Gln Asn Asp Asp Arg Val Arg Val Val Asp Arg Thr
 100 105 110

Asn Ile Arg Tyr Met Thr Leu Glu Asp Thr Gly Gly Glu Cys Asp Met
 115 120 125

Met Val Gly Asp Leu Ser Phe Ile Ser Leu Lys Leu Thr Leu Pro Ala
 130 135 140

Ile Ala Lys Val Leu Ser Asp Gly Ala Asp Leu Leu Pro Met Val Lys
 145 150 155 160

Pro Gln Phe Glu Val Gly Lys Asp Arg Leu Gly Ser Gly Gly Val Val
 165 170 175

Arg Ser Pro Glu Leu Arg Ala Glu Val Thr Ala Asp Val Ala Lys Phe
 180 185 190

Ala Ala Thr Leu Gly Leu Ser Leu Lys His Val Val Ala Ser Pro Leu
 195 200 205

Pro Gly Pro Ser Gly Asn Val Glu Tyr Phe Leu Trp Leu Val Lys Asp
 210 215 220

Gly Gly Ala Ser Met Pro Asp Asp Gln Gln Leu Ser Ala Met Ile Asp
 225 230 235 240

Thr Ala Val Lys Glu Gly Pro Gln
 245

<210> 19
 <211> 609
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(586)
 <223> RXA01718

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 Leu Leu Thr Ala Val
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 10 15 20

aac gga tat ttt gtg gct cag gaa ttt gcc tac atg tcc gtt gat cga 211
 Asn Gly Tyr Phe Val Ala Gln Glu Phe Ala Tyr Met Ser Val Asp Arg
 25 30 35

aat gag ctg cga gct ctc gct gac tct gga gat aag aag gct cgt cgc 259
 Asn Glu Leu Arg Ala Leu Ala Asp Ser Gly Asp Lys Lys Ala Arg Arg
 40 45 50

gct ctc agc atc act aag cgc aca tcc ttt atg ctt tct ggt gcg caa 307
 Ala Leu Ser Ile Thr Lys Arg Thr Ser Phe Met Leu Ser Gly Ala Gln
 55 60 65

ttg ggt atc acc gtc acc gga ctt ttg gtg ggt ttt gtg gcc gaa cct 355
 Leu Gly Ile Thr Val Thr Gly Leu Leu Val Gly Phe Val Ala Glu Pro
 70 75 80 85

ctg gtg ggt aac gcg tta ggt gtt ctg cta gga ggg gtg ggg gtt ccc 403
 Leu Val Gly Asn Ala Leu Gly Val Leu Leu Gly Gly Val Gly Val Pro

	90	95	100	
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Ala Ala Val Ser Ile Ser Val Gly Thr Val Leu Ala Leu Ala Ile Ser				
	105	110	115	
acg gtt gtc caa atg att ttt ggt gaa ctc ttt cct aag aac tac acc				499
Thr Val Val Gln Met Ile Phe Gly Glu Leu Phe Pro Lys Asn Tyr Thr				
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ctt gcc acg ccg ttg aag tct gcg ctg gcg ctt gcg cct tcg acc acg				547
Leu Ala Thr Pro Leu Lys Ser Ala Leu Ala Leu Ala Pro Ser Thr Thr				
	135	140	145	
tgg tat ttg aaa cct cgc tgg ttg gtt gat cac att ctt tgattttgca				596
Trp Tyr Leu Lys Pro Arg Trp Leu Val Asp His Ile Leu				
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<210> 20

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 20

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Met Ser Val Asp Arg Asn Glu Leu Arg Ala Leu Ala Asp Ser Gly Asp				
35	40	45		
Lys Lys Ala Arg Arg Ala Leu Ser Ile Thr Lys Arg Thr Ser Phe Met				
50	55	60		
Leu Ser Gly Ala Gln Leu Gly Ile Thr Val Thr Gly Leu Leu Val Gly				
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Phe Val Ala Glu Pro Leu Val Gly Asn Ala Leu Gly Val Leu Leu Gly				
85	90	95		
Gly Val Gly Val Pro Ala Ala Val Ser Ile Ser Val Gly Thr Val Leu				
100	105	110		
Ala Leu Ala Ile Ser Thr Val Val Gln Met Ile Phe Gly Glu Leu Phe				
115	120	125		
Pro Lys Asn Tyr Thr Leu Ala Thr Pro Leu Lys Ser Ala Leu Ala Leu				
130	135	140		
Ala Pro Ser Thr Thr Trp Tyr Leu Lys Pro Arg Trp Leu Val Asp His				
145	150	155	160	
Ile Leu				

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<211> 489
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(466)  
<223> RXN03148
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Met Val Ile Asn Phe															5
1															
att att tta ttt ttg atg att gca att act tca ttt ttt gta gca agt															163
Ile Ile Leu Phe Leu Met Ile Ala Ile Thr Ser Phe Phe Val Ala Ser															
10 15 20															
gaa ttt gct tta gtg aaa atc aga cga tca aga ttg gaa caa cta gaa															211
Glu Phe Ala Leu Val Lys Ile Arg Arg Ser Arg Leu Glu Gln Leu Glu															
25 30 35															
aag gaa aat gta aag aac gcc aag cta gct ctt cat gtt aca cac cat															259
Lys Glu Asn Val Lys Asn Ala Lys Leu Ala Leu His Val Thr His His															
40 45 50															
tta gat aac tat tta tca gct agt caa tta gga att acg cta acc ggt															307
Leu Asp Asn Tyr Leu Ser Ala Ser Gln Leu Gly Ile Thr Leu Thr Gly															
55 60 65															
ttg atc atc ggg tgg gtc ggt gaa gga tct gtc gcg gct tta cta gaa															355
Leu Ile Ile Gly Trp Val Gly Glu Gly Ser Val Ala Ala Leu Leu Glu															
70 75 80 85															
cca gtg atc ggt aaa cta cct ttt agt tcg gct att agc agt aca atc															403
Pro Val Ile Gly Lys Leu Pro Phe Ser Ser Ala Ile Ser Ser Thr Ile															
90 95 100															
tct gtg gcg ctg gga ttt att tta gtt acc gta tat cga tgt ggt tat															451
Ser Val Ala Leu Gly Phe Ile Leu Val Thr Val Tyr Arg Cys Gly Tyr															
105 110 115															
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Trp Arg Thr Ala Ser															
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<210> 22
<211> 122
<212> PRT
<213> Corynebacterium glutamicum
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<400> 22
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Phe Phe Val Ala Ser Glu Phe Ala Leu Val Lys Ile Arg Arg Ser Arg
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Leu	Glu	Gln	Leu	Glu	Lys	Glu	Asn	Val	Lys	Asn	Ala	Lys	Leu	Ala	Leu	
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50						55						60				
Ile	Thr	Leu	Thr	Gly	Leu	Ile	Ile	Gly	Trp	Val	Gly	Glu	Gly	Ser	Val	
65						70						75			80	
Ala	Ala	Leu	Leu	Glu	Pro	Val	Ile	Gly	Lys	Leu	Pro	Phe	Ser	Ser	Ala	
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Ile	Ser	Ser	Thr	Ile	Ser	Val	Ala	Leu	Gly	Phe	Ile	Leu	Val	Thr	Val	
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<210> 23
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<212> DNA
<213> Corynebacterium glutamicum
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<223> RXN00562
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Met Asp Ala Asp Pro																115
1 5																
ctg att gag gat gac gtt agt gga gca gaa gta aaa gat agt tcg gat																163
Leu Ile Glu Asp Asp Val Ser Gly Ala Glu Val Lys Asp Ser Ser Asp																
10 15 20																
gaa ccg ctt ctc gca ctg aca cgt tac gtt ttt gat cgc ggt gag ccg																211
Glu Pro Leu Leu Ala Leu Thr Arg Tyr Val Phe Asp Arg Gly Glu Arg																
25 30 35																
cca gtt act cgt gga ctg ttc cac cag gtt gcg gcc att ttg agt att																259
Pro Val Thr Arg Gly Leu Phe His Gln Val Ala Ala Ile Leu Ser Ile																
40 45 50																
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Val Ser Gly Ser Val Leu Ser Thr Tyr Ala Trp Met Glu Leu Val Trp																
55 60 65																
tgg cag gcg cta ggt gtc atg gtg tac gcc ttg gcc atg ctg gga ctg																355
Trp Gln Ala Leu Gly Val Met Val Tyr Ala Leu Ala Met Leu Gly Leu																
70 75 80 85																
ttt gct gtc tct gcg gcg tat cac cga gga ccg tgg cgt cga ttg cac																403
Phe Ala Val Ser Ala Ala Tyr His Arg Gly Pro Trp Arg Arg Leu His																
90 95 100																

acc gtg gcg tgg tgg cgc aaa gct gat cac tcc acc atc gcg gtg ttt 451
 Thr Val Ala Trp Trp Arg Lys Ala Asp His Ser Thr Ile Ala Val Phe
 105 110 115

atc gca gca acc tat acg cca ctg tgc ttg atc gtc tta gag ccc ggt 499
 Ile Ala Ala Thr Tyr Thr Pro Leu Cys Leu Ile Val Leu Glu Pro Gly
 120 125 130

acc gca gca tgg atg tta ggt att gcg tgg gtt ggt gcc att gac agc 547
 Thr Ala Ala Trp Met Leu Gly Ile Ala Trp Val Gly Ala Ile Asp Ser
 135 140 145

gtg atc atg aac atg gtg tgg atc aat cac cca cga tgg ctc agc gtg 595
 Val Ile Met Asn Met Val Trp Ile Asn His Pro Arg Trp Leu Ser Val
 150 155 160 165

ctg gtc tac ttg gcc ttg gga tgg ctc att gtg cca ctt gtc cct caa 643
 Leu Val Tyr Leu Ala Leu Gly Trp Leu Ile Val Pro Leu Val Pro Gln
 170 175 180

ttg tgg tct ggt gct ggc ccc aca gtg gtg tgg ctc ctg ctg gcc gga 691
 Leu Trp Ser Gly Ala Gly Pro Thr Val Val Trp Leu Leu Leu Ala Gly
 185 190 195

ggc atc gtc tac agc gtt ggc gcg ttg gtg tac ggc ttt aaa tgg cca 739
 Gly Ile Val Tyr Ser Val Gly Ala Leu Val Tyr Gly Phe Lys Trp Pro
 200 205 210

gga cgc aac gca cga gtg att ggc tac cac gag cac ttc cac atc gcc 787
 Gly Arg Asn Ala Arg Val Ile Gly Tyr His Glu His Phe His Ile Ala
 215 220 225

acg atc gtc gca gcg att gtc cat ctg gtt gca gtg tgaatgggtg 833
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<210> 24

<211> 241

<212> PRT

<213> Corynebacterium glutamicum

<400> 24

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 20 25 30

Asp Arg Gly Glu Arg Pro Val Thr Arg Gly Leu Phe His Gln Val Ala
 35 40 45

Ala Ile Leu Ser Ile Val Ser Gly Ser Val Leu Ser Thr Tyr Ala Trp
 50 55 60

Met Glu Leu Val Trp Trp Gln Ala Leu Gly Val Met Val Tyr Ala Leu
 65 70 75 80

Ala Met Leu Gly Leu Phe Ala Val Ser Ala Ala Tyr His Arg Gly Pro

85

90

95

Trp Arg Arg Leu His Thr Val Ala Trp Trp Arg Lys Ala Asp His Ser
 100 105 110
 Thr Ile Ala Val Phe Ile Ala Ala Thr Tyr Thr Pro Leu Cys Leu Ile
 115 120 125
 Val Leu Glu Pro Gly Thr Ala Ala Trp Met Leu Gly Ile Ala Trp Val
 130 135 140
 Gly Ala Ile Asp Ser Val Ile Met Asn Met Val Trp Ile Asn His Pro
 145 150 155 160
 Arg Trp Leu Ser Val Leu Val Tyr Leu Ala Leu Gly Trp Leu Ile Val
 165 170 175
 Pro Leu Val Pro Gln Leu Trp Ser Gly Ala Gly Pro Thr Val Val Trp
 180 185 190
 Leu Leu Leu Ala Gly Gly Ile Val Tyr Ser Val Gly Ala Leu Val Tyr
 195 200 205
 Gly Phe Lys Trp Pro Gly Arg Asn Ala Arg Val Ile Gly Tyr His Glu
 210 215 220
 His Phe His Ile Ala Thr Ile Val Ala Ala Ile Val His Leu Val Ala
 225 230 235 240
 Val

<210> 25

<211> 730

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(730)

<223> FRXA00562

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 Met Asp Ala Asp Pro
 1 5

ctg att gag gat gac gtt agt gga gca gaa gta aaa gat agt tcg gat 163
 Leu Ile Glu Asp Asp Val Ser Gly Ala Glu Val Lys Asp Ser Ser Asp
 10 15 20

gaa ccg ctt ctc gca ctg aca cgt tac gtt ttt gat cgc ggt gag ccg 211
 Glu Pro Leu Leu Ala Leu Thr Arg Tyr Val Phe Asp Arg Gly Glu Arg
 25 30 35

cca gtt act cgt gga ctg ttc cac cag gtt gcg gcc att ttg agt att 259
 Pro Val Thr Arg Gly Leu Phe His Gln Val Ala Ala Ile Leu Ser Ile
 40 45 50

gtg tca ggt tcg gtg ctc tcc acg tat gca tgg atg gaa ctg gtg tgg 307
 Val Ser Gly Ser Val Leu Ser Thr Tyr Ala Trp Met Glu Leu Val Trp
 55 60 65
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 Trp Gln Ala Leu Gly Val Met Val Tyr Ala Leu Ala Met Leu Gly Leu
 70 75 80 85
 ttt gct gtc tct gcg gcg tat cac cga gga ccg tgg cgt cga ttg cac 403
 Phe Ala Val Ser Ala Ala Tyr His Arg Gly Pro Trp Arg Arg Leu His
 90 95 100
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 Thr Val Ala Trp Trp Arg Lys Ala Asp His Ser Thr Ile Ala Val Phe
 105 110 115
 atc gca gca acc tat acg cca ctg tgc ttg atc gtc tta gag ccc ggt 499
 Ile Ala Ala Thr Tyr Thr Pro Leu Cys Leu Ile Val Leu Glu Pro Gly
 120 125 130
 acc gca gca tgg atg tta ggt att gcg tgg gtt ggt gcc att gac agc 547
 Thr Ala Ala Trp Met Leu Gly Ile Ala Trp Val Gly Ala Ile Asp Ser
 135 140 145
 gtg atc atg aac atg gtg tgg atc aat cac cca cga tgg ctg agc gtg 595
 Val Ile Met Asn Met Val Trp Ile Asn His Pro Arg Trp Leu Ser Val
 150 155 160 165
 ctg gtc tac ttg gcc ttg gga tgg ctg att gtg cca ctt gtc cct caa 643
 Leu Val Tyr Leu Ala Leu Gly Trp Leu Ile Val Pro Leu Val Pro Gln
 170 175 180
 ttg tgg tct ggt gct ggc ccc aca gtg gtg tgg ctg ctg ctg gcc gaa 691
 Leu Trp Ser Gly Ala Gly Pro Thr Val Val Trp Leu Leu Leu Ala Glu
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 Gly Ile Val Tyr Ser Val Gly Ala Leu Val Tyr Gly Phe
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<212> PRT

<213> Corynebacterium glutamicum

<400> 26

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Lys Asp Ser Ser Asp Glu Pro Leu Leu Ala Leu Thr Arg Tyr Val Phe
 20 25 30

Asp Arg Gly Glu Arg Pro Val Thr Arg Gly Leu Phe His Gln Val Ala
 35 40 45

Ala Ile Leu Ser Ile Val Ser Gly Ser Val Leu Ser Thr Tyr Ala Trp
 50 55 60

Met Glu Leu Val Trp Trp Gln Ala Leu Gly Val Met Val Tyr Ala Leu

65		70		75		80
Ala Met Leu Gly Leu Phe Ala Val Ser Ala Ala Tyr His Arg Gly Pro						
	85			90		95
Trp Arg Arg Leu His Thr Val Ala Trp Trp Arg Lys Ala Asp His Ser						
	100			105		110
Thr Ile Ala Val Phe Ile Ala Ala Thr Tyr Thr Pro Leu Cys Leu Ile						
	115			120		125
Val Leu Glu Pro Gly Thr Ala Ala Trp Met Leu Gly Ile Ala Trp Val						
	130			135		140
Gly Ala Ile Asp Ser Val Ile Met Asn Met Val Trp Ile Asn His Pro						
	145			150		155
Arg Trp Leu Ser Val Leu Val Tyr Leu Ala Leu Gly Trp Leu Ile Val						
	165			170		175
Pro Leu Val Pro Gln Leu Trp Ser Gly Ala Gly Pro Thr Val Val Trp						
	180			185		190
Leu Leu Leu Ala Glu Gly Ile Val Tyr Ser Val Gly Ala Leu Val Tyr						
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Gly Phe						
	210					

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1399)

<223> RXN00890

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tgaggcgctt gagtccctagg tggaatcctc agttatatgg ttg agc atc gcc aca	115
Leu Ser Ile Ala Thr	
1 5	

gtc gtt gcg ttg ctc ttc tcc ggt tta tta ggt gcg gtt gaa tct gcg	163
Val Val Ala Leu Leu Phe Ser Gly Leu Leu Gly Ala Val Glu Ser Ala	
10 15 20	

ctt tct tct gtt tcc cgc gcc cgc gtt gaa caa atg ctc aag gat gaa	211
Leu Ser Ser Val Ser Arg Ala Arg Val Glu Gln Met Leu Lys Asp Glu	
25 30 35	

gcc tcc ggg tcc gcg tcc ttg ctg cga gtc atc gac gaa cgc gca ctc	259
Ala Ser Gly Ser Ala Ser Leu Leu Arg Val Ile Asp Glu Arg Ala Leu	
40 45 50	

cac atc aac atg ctc atc atg ttg cgc acc ttg ctg gat gcc tcc gca	307
His Ile Asn Met Leu Ile Met Leu Arg Thr Leu Leu Asp Ala Ser Ala	

55	60	65	
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tgg ggc atc gtc ctg gcc atc gtg gtg gtt tcc ctc ctg acc ttc gca Trp Gly Ile Val Leu Ala Ile Val Val Val Ser Leu Leu Thr Phe Ala 90 95 100			403
gta gtg ggc gtg ttt ggc cgc acc gtt ggc cgc aaa aac cca tat tca Val Val Gly Val Phe Gly Arg Thr Val Gly Arg Lys Asn Pro Tyr Ser 105 110 115			451
gtg atg ctt cgc tcc gca gtc gtg ctg agc ggt tta gct aaa atc ctt Val Met Leu Arg Ser Ala Val Val Leu Ser Gly Leu Ala Lys Ile Leu 120 125 130			499
ggc ccc att gca cgt ggc ctc atc tgg atc ggc aac atc atc gcg ccc Gly Pro Ile Ala Arg Gly Leu Ile Trp Ile Gly Asn Ile Ile Ala Pro 135 140 145			547
ggc cca ggt ttc cgc aat ggc cct tac gcc act gaa gtg gaa ctg cgt Gly Pro Gly Phe Arg Asn Gly Pro Tyr Ala Thr Glu Val Glu Leu Arg 150 155 160 165			595
gag atg gtc gat atc gcc caa gaa cac ggc atc gtg gaa att gaa gag Glu Met Val Asp Ile Ala Gln Glu His Gly Ile Val Glu Ile Glu Glu 170 175 180			643
cgc cgc atg atc cag tcg gtg ttc gac ctg gca tcc acg acg gtt cgc Arg Arg Met Ile Gln Ser Val Phe Asp Leu Ala Ser Thr Thr Val Arg 185 190 195			691
cag gtg atg gtg cca cgt cct gaa atg atc tgg att gaa tct gga aaa Gln Val Met Val Pro Arg Pro Glu Met Ile Trp Ile Glu Ser Gly Lys 200 205 210			739
aca gcc ggg caa gca acc gcg ctg tgc gtg cgc tct ggt cat tcg cgc Thr Ala Gly Gln Ala Thr Ala Leu Cys Val Arg Ser Gly His Ser Arg 215 220 225			787
atc cca gtc atc ggt gaa aac gtc gac gac atc atc ggc atc gtc tac Ile Pro Val Ile Gly Glu Asn Val Asp Asp Ile Ile Gly Ile Val Tyr 230 235 240 245			835
ctc aaa gac ttg gtc caa aaa acc tac tac gcc act gat ggc gga aag Leu Lys Asp Leu Val Gln Lys Thr Tyr Tyr Ala Thr Asp Gly Gly Lys 250 255 260			883
tct gtg ctt gta gac gag gtc atg cgc gaa gct acc ttc gtg cca gac Ser Val Leu Val Asp Glu Val Met Arg Glu Ala Thr Phe Val Pro Asp 265 270 275			931
tcc aag tcc ctt gat gcg ctg ctg cag gaa atg cag gaa gac cac aaa Ser Lys Ser Leu Asp Ala Leu Leu Gln Glu Met Gln Glu Asp His Lys 280 285 290			979
cac atc gca atc ctg gtt gat gaa tac ggc ggc gtg gca ggt ctt att His Ile Ala Ile Leu Val Asp Glu Tyr Gly Gly Val Ala Gly Leu Ile 295 300 305			1027

tcc att gag gat att ttg gaa gaa atc gtc ggt gaa atc gct gat gaa 1075
 Ser Ile Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Ala Asp Glu
 310 315 320 325

tat gac gcc cgc gaa gta gcc ccc atc gag aaa atc ggc gac cgc acc 1123
 Tyr Asp Ala Arg Glu Val Ala Pro Ile Glu Lys Ile Gly Asp Arg Thr
 330 335 340

tac cgc gtg gtc tcc cga ctc tcg ctg gaa gat ctc aaa gac cac atc 1171
 Tyr Arg Val Val Ser Arg Leu Ser Leu Glu Asp Leu Lys Asp His Ile
 345 350 355

gaa gaa gaa ctc gac cta gaa atc gaa ttc ggt gat gaa att gaa gat 1219
 Glu Glu Glu Leu Asp Leu Glu Ile Glu Phe Gly Asp Glu Ile Glu Asp
 360 365 370

cag gtc gac act gtc ggt ggc ctt att gcc ttt gaa ctt ggc cga gtg 1267
 Gln Val Asp Thr Val Gly Gly Leu Ile Ala Phe Glu Leu Gly Arg Val
 375 380 385

cct ctg ccg ggt gcc act gtg gaa acc tgc gga cta aag ctc acc gcc 1315
 Pro Leu Pro Gly Ala Thr Val Glu Thr Cys Gly Leu Lys Leu Thr Ala
 390 395 400 405

gag gga gcc aag aac cgc cgg ggt cgt ttg cgc atg cat tca gca gtc 1363
 Glu Gly Ala Lys Asn Arg Arg Gly Arg Leu Arg Met His Ser Ala Val
 410 415 420

gta gaa gtt ggc gag ccc agc gag gac aac gaa ggt tagtttttta 1409
 Val Glu Val Gly Glu Pro Ser Glu Asp Asn Glu Gly
 425 430

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 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Met Leu Lys Asp Glu Ala Ser Gly Ser Ala Ser Leu Leu Arg Val Ile
 35 40 45
 Asp Glu Arg Ala Leu His Ile Asn Met Leu Ile Met Leu Arg Thr Leu
 50 55 60
 Leu Asp Ala Ser Ala Ala Val Phe Ala Gly Ala Ile Ala Val Asn Val
 65 70 75 80
 Met Asp Ser Trp Ala Trp Gly Ile Val Leu Ala Ile Val Val Val Ser
 85 90 95
 Leu Leu Thr Phe Ala Val Val Gly Val Phe Gly Arg Thr Val Gly Arg

100					105					110					
Lys	Asn	Pro	Tyr	Ser	Val	Met	Leu	Arg	Ser	Ala	Val	Val	Leu	Ser	Gly
	115						120					125			
Leu	Ala	Lys	Ile	Leu	Gly	Pro	Ile	Ala	Arg	Gly	Leu	Ile	Trp	Ile	Gly
	130					135					140				
Asn	Ile	Ile	Ala	Pro	Gly	Pro	Gly	Phe	Arg	Asn	Gly	Pro	Tyr	Ala	Thr
145					150					155					160
Glu	Val	Glu	Leu	Arg	Glu	Met	Val	Asp	Ile	Ala	Gln	Glu	His	Gly	Ile
				165					170					175	
Val	Glu	Ile	Glu	Glu	Arg	Arg	Met	Ile	Gln	Ser	Val	Phe	Asp	Leu	Ala
			180					185					190		
Ser	Thr	Thr	Val	Arg	Gln	Val	Met	Val	Pro	Arg	Pro	Glu	Met	Ile	Trp
	195						200					205			
Ile	Glu	Ser	Gly	Lys	Thr	Ala	Gly	Gln	Ala	Thr	Ala	Leu	Cys	Val	Arg
	210					215					220				
Ser	Gly	His	Ser	Arg	Ile	Pro	Val	Ile	Gly	Glu	Asn	Val	Asp	Asp	Ile
225					230					235					240
Ile	Gly	Ile	Val	Tyr	Leu	Lys	Asp	Leu	Val	Gln	Lys	Thr	Tyr	Tyr	Ala
				245					250					255	
Thr	Asp	Gly	Gly	Lys	Ser	Val	Leu	Val	Asp	Glu	Val	Met	Arg	Glu	Ala
			260					265					270		
Thr	Phe	Val	Pro	Asp	Ser	Lys	Ser	Leu	Asp	Ala	Leu	Leu	Gln	Glu	Met
	275						280					285			
Gln	Glu	Asp	His	Lys	His	Ile	Ala	Ile	Leu	Val	Asp	Glu	Tyr	Gly	Gly
	290					295					300				
Val	Ala	Gly	Leu	Ile	Ser	Ile	Glu	Asp	Ile	Leu	Glu	Glu	Ile	Val	Gly
305					310					315					320
Glu	Ile	Ala	Asp	Glu	Tyr	Asp	Ala	Arg	Glu	Val	Ala	Pro	Ile	Glu	Lys
			325						330				335		
Ile	Gly	Asp	Arg	Thr	Tyr	Arg	Val	Val	Ser	Arg	Leu	Ser	Leu	Glu	Asp
		340						345					350		
Leu	Lys	Asp	His	Ile	Glu	Glu	Glu	Leu	Asp	Leu	Glu	Ile	Glu	Phe	Gly
	355						360					365			
Asp	Glu	Ile	Glu	Asp	Gln	Val	Asp	Thr	Val	Gly	Gly	Leu	Ile	Ala	Phe
	370					375					380				
Glu	Leu	Gly	Arg	Val	Pro	Leu	Pro	Gly	Ala	Thr	Val	Glu	Thr	Cys	Gly
385					390					395					400
Leu	Lys	Leu	Thr	Ala	Glu	Gly	Ala	Lys	Asn	Arg	Arg	Gly	Arg	Leu	Arg
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Met	His	Ser	Ala	Val	Val	Glu	Val	Gly	Glu	Pro	Ser	Glu	Asp	Asn	Glu
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<210> 29

<211> 1398

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1375)

<223> FRXA00890

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				Leu	Ser	Ile	Ala	Thr	
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gtc	ggt	gcg	ttg	ctc	ttc	tcc	ggt	tta	tta	ggt	gcg	ggt	gaa	tct	gcg	163
Val	Val	Ala	Leu	Leu	Phe	Ser	Gly	Leu	Leu	Gly	Ala	Val	Glu	Ser	Ala	
			10					15					20			

ctt	tct	tct	ggt	tcc	cgc	gcc	cgc	ggt	gaa	caa	atg	ctc	aag	gat	gaa	211
Leu	Ser	Ser	Val	Ser	Arg	Ala	Arg	Val	Glu	Gln	Met	Leu	Lys	Asp	Glu	
			25					30					35			

gcc	tcc	ggg	tcc	gcg	tcc	ttg	ctg	cga	gtc	atc	gac	gaa	cgc	gca	ctc	259
Ala	Ser	Gly	Ser	Ala	Ser	Leu	Leu	Arg	Val	Ile	Asp	Glu	Arg	Ala	Leu	
		40					45				50					

cac	atc	aac	atg	ctc	atc	atg	ttg	cgc	acc	ttg	ctg	gat	gcc	tcc	gca	307
His	Ile	Asn	Met	Leu	Ile	Met	Leu	Arg	Thr	Leu	Leu	Asp	Ala	Ser	Ala	
	55					60					65					

gca	gtc	ttc	gcc	ggg	gca	atc	gca	gtc	aat	gtg	atg	gac	agc	tggt	gcg	355
Ala	Val	Phe	Ala	Gly	Ala	Ile	Ala	Val	Asn	Val	Met	Asp	Ser	Trp	Ala	
70				75					80					85		

tggt	ggc	atc	gtc	ctg	gcc	atc	gtg	gtg	ggt	tcc	ctc	ctg	acc	ttc	gca	403
Trp	Gly	Ile	Val	Leu	Ala	Ile	Val	Val	Val	Ser	Leu	Leu	Thr	Phe	Ala	
			90						95					100		

gta	gtg	ggc	gtg	ttt	ggc	cgc	acc	ggt	ggc	cgc	aaa	aac	cca	tat	tca	451
Val	Val	Gly	Val	Phe	Gly	Arg	Thr	Val	Gly	Arg	Lys	Asn	Pro	Tyr	Ser	
		105						110					115			

gtg	atg	ctt	cgc	tcc	gca	gtc	gtg	ctg	agc	ggt	tta	gct	aaa	atc	ctt	499
Val	Met	Leu	Arg	Ser	Ala	Val	Val	Leu	Ser	Gly	Leu	Ala	Lys	Ile	Leu	
		120					125					130				

ggc	ccc	att	gca	cgt	ggc	ctc	atc	tggt	atc	ggc	aac	atc	atc	gcg	ccc	547
Gly	Pro	Ile	Ala	Arg	Gly	Leu	Ile	Trp	Ile	Gly	Asn	Ile	Ile	Ala	Pro	
	135					140					145					

ggc	cca	ggt	ttc	cgc	aat	ggc	cct	tac	gcc	act	gaa	gtg	gaa	ctg	cgt	595
Gly	Pro	Gly	Phe	Arg	Asn	Gly	Pro	Tyr	Ala	Thr	Glu	Val	Glu	Leu	Arg	
150					155					160				165		

gag atg gtc gat atc gcc caa gaa cac ggc atc gtg gaa att gaa gag	643
Glu Met Val Asp Ile Ala Gln Glu His Gly Ile Val Glu Ile Glu Glu	
170 175 180	
cgc cgc atg atc cag tcg gtg ttc gac ctg gca tcc acg acg gtt cgc	691
Arg Arg Met Ile Gln Ser Val Phe Asp Leu Ala Ser Thr Thr Val Arg	
185 190 195	
cag gtg atg gtg cca cgt cct gaa atg atc tgg att gaa tct gga aaa	739
Gln Val Met Val Pro Arg Pro Glu Met Ile Trp Ile Glu Ser Gly Lys	
200 205 210	
aca gcc ggg caa gca acc gcg ctg tgc gtg cgc tct ggt cat tcg cgc	787
Thr Ala Gly Gln Ala Thr Ala Leu Cys Val Arg Ser Gly His Ser Arg	
215 220 225	
atc cca gtc atc ggt gaa aac gtc gac gac atc atc ggc atc gtc tac	835
Ile Pro Val Ile Gly Glu Asn Val Asp Asp Ile Ile Gly Ile Val Tyr	
230 235 240 245	
ctc aaa gac ttg gtc caa aaa acc tac tac gcc act gat ggc gga aag	883
Leu Lys Asp Leu Val Gln Lys Thr Tyr Tyr Ala Thr Asp Gly Gly Lys	
250 255 260	
tct gtg ctt gta gac gag gtc atg cgc gaa gct acc ttc gtg cca gac	931
Ser Val Leu Val Asp Glu Val Met Arg Glu Ala Thr Phe Val Pro Asp	
265 270 275	
tcc aag tcc ctt gat gcg ctg ctg cag gaa atg cag gaa gac cac aaa	979
Ser Lys Ser Leu Asp Ala Leu Leu Gln Glu Met Gln Glu Asp His Lys	
280 285 290	
cac atc gca atc ctg gtt gat gaa tac ggc ggc gtg gca ggt ctt att	1027
His Ile Ala Ile Leu Val Asp Glu Tyr Gly Gly Val Ala Gly Leu Ile	
295 300 305	
tcc att gag gat att ttg gaa gaa atc gtc ggt gaa atc gct gat gaa	1075
Ser Ile Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Ala Asp Glu	
310 315 320 325	
tat gac gcc cgc gaa gta gcc ccc atc gag aaa atc ggc gac cgc acc	1123
Tyr Asp Ala Arg Glu Val Ala Pro Ile Glu Lys Ile Gly Asp Arg Thr	
330 335 340	
tac cgc gtg gtc tcc cga ctc tcg ctg gaa gat ctc aaa gac cac atc	1171
Tyr Arg Val Val Ser Arg Leu Ser Leu Glu Asp Leu Lys Asp His Ile	
345 350 355	
gaa gaa gaa ctc gac cta gaa atc gaa ttc ggt gat gaa att gaa gat	1219
Glu Glu Glu Leu Asp Leu Glu Ile Glu Phe Gly Asp Glu Ile Glu Asp	
360 365 370	
cag gtc gac act gtc ggt ggc ctt att gcc ttt gaa ctt ggc cga gtg	1267
Gln Val Asp Thr Val Gly Gly Leu Ile Ala Phe Glu Leu Gly Arg Val	
375 380 385	
cct ctg ccg ggt gcc act gtg gaa acc tgc gga cta aag ctc acc gcc	1315
Pro Leu Pro Gly Ala Thr Val Glu Thr Cys Gly Leu Lys Leu Thr Ala	
390 395 400 405	

gag gga gcc aag aac cgc cgg ggt cgt ttg cgc atg cat tca gca gtc 1363
 Glu Gly Ala Lys Asn Arg Arg Gly Arg Leu Arg Met His Ser Ala Val
 410 415 420

gta gaa gtt ggc tagcccagcg aggacaacga agg 1398
 Val Glu Val Gly
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<210> 30

<211> 425

<212> PRT

<213> Corynebacterium glutamicum

<400> 30

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Ala Val Glu Ser Ala Leu Ser Ser Val Ser Arg Ala Arg Val Glu Gln
 20 25 30

Met Leu Lys Asp Glu Ala Ser Gly Ser Ala Ser Leu Leu Arg Val Ile
 35 40 45

Asp Glu Arg Ala Leu His Ile Asn Met Leu Ile Met Leu Arg Thr Leu
 50 55 60

Leu Asp Ala Ser Ala Ala Val Phe Ala Gly Ala Ile Ala Val Asn Val
 65 70 75 80

Met Asp Ser Trp Ala Trp Gly Ile Val Leu Ala Ile Val Val Val Ser
 85 90 95

Leu Leu Thr Phe Ala Val Val Gly Val Phe Gly Arg Thr Val Gly Arg
 100 105 110

Lys Asn Pro Tyr Ser Val Met Leu Arg Ser Ala Val Val Leu Ser Gly
 115 120 125

Leu Ala Lys Ile Leu Gly Pro Ile Ala Arg Gly Leu Ile Trp Ile Gly
 130 135 140

Asn Ile Ile Ala Pro Gly Pro Gly Phe Arg Asn Gly Pro Tyr Ala Thr
 145 150 155 160

Glu Val Glu Leu Arg Glu Met Val Asp Ile Ala Gln Glu His Gly Ile
 165 170 175

Val Glu Ile Glu Glu Arg Arg Met Ile Gln Ser Val Phe Asp Leu Ala
 180 185 190

Ser Thr Thr Val Arg Gln Val Met Val Pro Arg Pro Glu Met Ile Trp
 195 200 205

Ile Glu Ser Gly Lys Thr Ala Gly Gln Ala Thr Ala Leu Cys Val Arg
 210 215 220

Ser Gly His Ser Arg Ile Pro Val Ile Gly Glu Asn Val Asp Asp Ile
 225 230 235 240

Ile Gly Ile Val Tyr Leu Lys Asp Leu Val Gln Lys Thr Tyr Tyr Ala

245										250					255						
Thr	Asp	Gly	Gly	Lys	Ser	Val	Leu	Val	Asp	Glu	Val	Met	Arg	Glu	Ala						
			260						265					270							
Thr	Phe	Val	Pro	Asp	Ser	Lys	Ser	Leu	Asp	Ala	Leu	Leu	Gln	Glu	Met						
		275					280						285								
Gln	Glu	Asp	His	Lys	His	Ile	Ala	Ile	Leu	Val	Asp	Glu	Tyr	Gly	Gly						
		290				295					300										
Val	Ala	Gly	Leu	Ile	Ser	Ile	Glu	Asp	Ile	Leu	Glu	Glu	Ile	Val	Gly						
		305			310					315					320						
Glu	Ile	Ala	Asp	Glu	Tyr	Asp	Ala	Arg	Glu	Val	Ala	Pro	Ile	Glu	Lys						
			325						330					335							
Ile	Gly	Asp	Arg	Thr	Tyr	Arg	Val	Val	Ser	Arg	Leu	Ser	Leu	Glu	Asp						
			340					345					350								
Leu	Lys	Asp	His	Ile	Glu	Glu	Glu	Leu	Asp	Leu	Glu	Ile	Glu	Phe	Gly						
		355					360					365									
Asp	Glu	Ile	Glu	Asp	Gln	Val	Asp	Thr	Val	Gly	Gly	Leu	Ile	Ala	Phe						
		370				375					380										
Glu	Leu	Gly	Arg	Val	Pro	Leu	Pro	Gly	Ala	Thr	Val	Glu	Thr	Cys	Gly						
		385			390					395				400							
Leu	Lys	Leu	Thr	Ala	Glu	Gly	Ala	Lys	Asn	Arg	Arg	Gly	Arg	Leu	Arg						
			405					410						415							
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 <212> DNA
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 <221> CDS
 <222> (101)..(5038)
 <223> RXN01772

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 Met Glu Cys Met Ser
 1 5
 acg att act gat gct gta tcc gcc ctg cgc aca ctg cct tcc cag tct 163
 Thr Ile Thr Asp Ala Val Ser Ala Leu Arg Thr Leu Pro Ser Gln Ser
 10 15 20
 gcg cag ggt ttg gct ttt gaa aaa ctc atg gtc aac ttc att aag tct 211
 Ala Gln Gly Leu Ala Phe Glu Lys Leu Met Val Asn Phe Ile Lys Ser
 25 30 35

gac	ccc	act	ctc	tcc	act	gag	ttt	gat	gaa	gtc	cat	cgt	tgg	gtc	gat	259
Asp	Pro	Thr	Leu	Ser	Thr	Glu	Phe	Asp	Glu	Val	His	Arg	Trp	Val	Asp	
		40					45					50				
tgg	cca	tat	aac	ggt	ggc	acc	atg	gat	act	ggc	atc	gac	tta	gtg	gct	307
Trp	Pro	Tyr	Asn	Gly	Gly	Thr	Met	Asp	Thr	Gly	Ile	Asp	Leu	Val	Ala	
	55					60					65					
tat	aac	aag	gac	gat	gat	gct	tat	acg	gcg	atc	cag	tgc	aag	ttt	tat	355
Tyr	Asn	Lys	Asp	Asp	Asp	Ala	Tyr	Thr	Ala	Ile	Gln	Cys	Lys	Phe	Tyr	
	70					75				80					85	
ctt	ccc	act	act	tcc	ctg	gca	aaa	gga	cag	cta	gat	tcc	ttc	ttt	gaa	403
Leu	Pro	Thr	Thr	Ser	Leu	Ala	Lys	Gly	Gln	Leu	Asp	Ser	Phe	Phe	Glu	
				90					95					100		
gcc	tcg	gga	cgc	act	ttt	gaa	acc	cct	gaa	gga	aca	cgc	tcc	ttt	agc	451
Ala	Ser	Gly	Arg	Thr	Phe	Glu	Thr	Pro	Glu	Gly	Thr	Arg	Ser	Phe	Ser	
			105					110					115			
aat	aga	ctc	gtt	att	tcc	act	act	gat	aag	tgg	agt	tca	aat	gcg	gaa	499
Asn	Arg	Leu	Val	Ile	Ser	Thr	Thr	Asp	Lys	Trp	Ser	Ser	Asn	Ala	Glu	
		120					125					130				
aag	atg	ttg	gag	aac	caa	acc	att	cca	act	aac	cgc	att	ggt	cta	tct	547
Lys	Met	Leu	Glu	Asn	Gln	Thr	Ile	Pro	Thr	Asn	Arg	Ile	Gly	Leu	Ser	
	135					140					145					
gca	att	gcg	gaa	tcc	ccg	att	gac	tgg	gat	att	gcc	tat	cca	ggt	tct	595
Ala	Ile	Ala	Glu	Ser	Pro	Ile	Asp	Trp	Asp	Ile	Ala	Tyr	Pro	Gly	Ser	
	150				155					160					165	
gaa	tta	act	att	aac	ctg	cag	ctt	aaa	gag	ccg	tat	agc	cct	cgt	cct	643
Glu	Leu	Thr	Ile	Asn	Leu	Gln	Leu	Lys	Glu	Pro	Tyr	Ser	Pro	Arg	Pro	
				170				175						180		
cac	cag	caa	act	gct	att	gaa	aaa	gca	att	gaa	ggc	ttc	caa	act	cat	691
His	Gln	Gln	Thr	Ala	Ile	Glu	Lys	Ala	Ile	Glu	Gly	Phe	Gln	Thr	His	
			185					190					195			
gac	cgt	ggc	aag	ctc	atc	atg	gct	tgc	ggg	acc	gga	aaa	acc	ttt	act	739
Asp	Arg	Gly	Lys	Leu	Ile	Met	Ala	Cys	Gly	Thr	Gly	Lys	Thr	Phe	Thr	
		200				205						210				
gcc	ctg	cgt	ctt	tct	gaa	gag	gtt	gcg	cga	ctc	aat	ggc	aat	aaa	gct	787
Ala	Leu	Arg	Leu	Ser	Glu	Glu	Val	Ala	Arg	Leu	Asn	Gly	Asn	Lys	Ala	
	215					220					225					
cgc	att	ctt	ttt	cta	gtc	cct	tcc	atc	agc	ttg	ctt	tcg	caa	aca	ctc	835
Arg	Ile	Leu	Phe	Leu	Val	Pro	Ser	Ile	Ser	Leu	Leu	Ser	Gln	Thr	Leu	
	230				235					240					245	
aaa	gag	tgg	act	gca	caa	aag	aca	atg	gat	ctt	cgt	cct	gtc	gcc	gta	883
Lys	Glu	Trp	Thr	Ala	Gln	Lys	Thr	Met	Asp	Leu	Arg	Pro	Val	Ala	Val	
				250				255						260		
tgt	tct	gac	tcc	aag	gtc	tcc	aag	gct	gca	gaa	gat	att	gct	gct	tat	931
Cys	Ser	Asp	Ser	Lys	Val	Ser	Lys	Ala	Ala	Glu	Asp	Ile	Ala	Ala	Tyr	
			265				270						275			
gat	ctt	gaa	gtt	ccg	gta	agt	act	gat	ggg	gca	ttg	att	gcg	gaa	aaa	979

Asp	Leu	Glu	Val	Pro	Val	Ser	Thr	Asp	Gly	Ala	Leu	Ile	Ala	Glu	Lys	
		280					285					290				
ctg	gag	cat	cgt	aag	cga	gca	gca	gga	ttg	acc	gtg	gtg	ttc	tct	act	1027
Leu	Glu	His	Arg	Lys	Arg	Ala	Ala	Gly	Leu	Thr	Val	Val	Phe	Ser	Thr	
		295				300					305					
tac	cag	tcc	ctt	cct	gct	gtt	cac	gcg	gct	caa	gaa	gct	ggg	gct	gag	1075
Tyr	Gln	Ser	Leu	Pro	Ala	Val	His	Ala	Ala	Gln	Glu	Ala	Gly	Ala	Glu	
310					315					320					325	
ccc	ttt	gat	ctt	gtc	atc	tgc	gat	gaa	gcc	cac	cgc	acc	aca	ggc	atc	1123
Pro	Phe	Asp	Leu	Val	Ile	Cys	Asp	Glu	Ala	His	Arg	Thr	Thr	Gly	Ile	
				330					335					340		
acc	ttg	gct	gga	gaa	gac	cct	tca	aac	ttc	acc	cgc	att	cat	gac	gct	1171
Thr	Leu	Ala	Gly	Glu	Asp	Pro	Ser	Asn	Phe	Thr	Arg	Ile	His	Asp	Ala	
			345					350					355			
tct	tat	atc	aag	gca	gca	aag	cgg	ctg	tac	atg	acg	gca	acc	cca	agg	1219
Ser	Tyr	Ile	Lys	Ala	Ala	Lys	Arg	Leu	Tyr	Met	Thr	Ala	Thr	Pro	Arg	
		360					365					370				
ctt	ttc	gac	gac	tcc	gtg	aag	ggc	aag	gct	gca	gat	cat	tca	gct	gaa	1267
Leu	Phe	Asp	Asp	Ser	Val	Lys	Gly	Lys	Ala	Ala	Asp	His	Ser	Ala	Glu	
		375				380					385					
gtt	tct	tcc	atg	gat	gat	gaa	gca	atc	tac	gga	ccc	gaa	ttt	cac	cgg	1315
Val	Ser	Ser	Met	Asp	Asp	Glu	Ala	Ile	Tyr	Gly	Pro	Glu	Phe	His	Arg	
390					395					400					405	
ctg	ggt	ttt	ggg	gaa	gca	gta	gaa	aaa	ggc	ctg	ctt	act	gac	tac	aaa	1363
Leu	Gly	Phe	Gly	Glu	Ala	Val	Glu	Lys	Gly	Leu	Leu	Thr	Asp	Tyr	Lys	
				410					415					420		
gtt	gta	gtg	atg	aca	gtt	gat	gag	caa	gtt	gca	gcc	agt	gcc	tta	act	1411
Val	Val	Val	Met	Thr	Val	Asp	Glu	Gln	Val	Ala	Ala	Ser	Ala	Leu	Thr	
			425					430					435			
gtt	ttg	ggt	tca	aca	cct	ggt	gaa	gaa	ctc	act	ctg	gac	atg	act	tcc	1459
Val	Leu	Gly	Ser	Thr	Pro	Gly	Glu	Glu	Leu	Thr	Leu	Asp	Met	Thr	Ser	
		440				445						450				
gca	att	att	ggc	gcg	tgg	aat	ggc	ttg	gca	aag	cgt	tcg	ggt	aaa	gag	1507
Ala	Ile	Ile	Gly	Ala	Trp	Asn	Gly	Leu	Ala	Lys	Arg	Ser	Gly	Lys	Glu	
		455				460					465					
caa	gac	acc	aag	act	ggt	ttc	tca	agc	tct	gac	gca	gca	atg	gaa	cga	1555
Gln	Asp	Thr	Lys	Thr	Gly	Phe	Ser	Ser	Ser	Asp	Ala	Ala	Met	Glu	Arg	
470					475					480					485	
gct	gtt	gca	ttt	gcg	cga	gac	att	aag	act	tct	cag	caa	atc	gcg	gag	1603
Ala	Val	Ala	Phe	Ala	Arg	Asp	Ile	Lys	Thr	Ser	Gln	Gln	Ile	Ala	Glu	
				490					495						500	
tct	ttt	cca	cga	gtt	gtc	aat	gct	tat	acg	act	gag	ctt	gag	gtt	aaa	1651
Ser	Phe	Pro	Arg	Val	Val	Asn	Ala	Tyr	Thr	Thr	Glu	Leu	Glu	Val	Lys	
			505					510					515			
aac	gat	gac	gta	gat	gag	cac	aac	ctc	aat	ttg	agc	gtg	gca	tgc	cag	1699
Asn	Asp	Asp	Val	Asp	Glu	His	Asn	Leu	Asn	Leu	Ser	Val	Ala	Cys	Gln	

520	525	530	
cat gtc gat gga tca atg aat gcg ctg gaa cga aac tct cgt tta act			1747
His Val Asp Gly Ser Met Asn Ala Leu Glu Arg Asn Ser Arg Leu Thr			
535	540	545	
tgg ctt aaa gct cct acc cag tca atg gaa acc aag att ctt act aac			1795
Trp Leu Lys Ala Pro Thr Gln Ser Met Glu Thr Lys Ile Leu Thr Asn			
550	555	560	565
gcg cgc tgc ctt tct gag ggt gtc gat gta ccg gct ttg gat tcc gta			1843
Ala Arg Cys Leu Ser Glu Gly Val Asp Val Pro Ala Leu Asp Ser Val			
	570	575	580
atc ttc ttt aat ccc cgt aat tcc atg gtg gat gtg gtt cag tcg gtt			1891
Ile Phe Phe Asn Pro Arg Asn Ser Met Val Asp Val Val Gln Ser Val			
	585	590	595
ggc cga gtt atg cgt aaa tct cca ggt aag aat tac gga tat atc atc			1939
Gly Arg Val Met Arg Lys Ser Pro Gly Lys Asn Tyr Gly Tyr Ile Ile			
	600	605	610
ttg cca gtt gct gtt ccc cca ggt gtt gca cca tca gct gcg tta aat			1987
Leu Pro Val Ala Val Pro Pro Gly Val Ala Pro Ser Ala Ala Leu Asn			
	615	620	625
gat tca cgc cgc ttc aag gtt gta tgg cag gtt ctt aac gcc ctt cgt			2035
Asp Ser Arg Arg Phe Lys Val Val Trp Gln Val Leu Asn Ala Leu Arg			
	630	635	640
gct cac gat gac cgt ttt aac gca atg gtg aac tcc att gcg ctc aat			2083
Ala His Asp Asp Arg Phe Asn Ala Met Val Asn Ser Ile Ala Leu Asn			
	650	655	660
gag gga aat att aag gat cta cct gtt gag act gag cat act ggc cct			2131
Glu Gly Asn Ile Lys Asp Leu Pro Val Glu Thr Glu His Thr Gly Pro			
	665	670	675
aca agt aaa gat aga gat aac gca ccc tat gac agt gct gaa tcc gct			2179
Thr Ser Lys Asp Arg Asp Asn Ala Pro Tyr Asp Ser Ala Glu Ser Ala			
	680	685	690
aca caa tac gta ctg ttc tct tta gaa cag tgg caa gaa gcg atc tac			2227
Thr Gln Tyr Val Leu Phe Ser Leu Glu Gln Trp Gln Glu Ala Ile Tyr			
	695	700	705
acc aag ctt gta gat aaa gtt ggt acc cga acc tac tgg gaa gat tgg			2275
Thr Lys Leu Val Asp Lys Val Gly Thr Arg Thr Tyr Trp Glu Asp Trp			
	710	715	720
gca gat gat gtt gct gac atc gcc caa gca caa ata acc cgt att aaa			2323
Ala Asp Asp Val Ala Asp Ile Ala Gln Ala Gln Ile Thr Arg Ile Lys			
	730	735	740
gcg ctc tta gac aat gct tca cca acg atc aaa gaa gag ttc gag cga			2371
Ala Leu Leu Asp Asn Ala Ser Pro Thr Ile Lys Glu Glu Phe Glu Arg			
	745	750	755
ttt gtt gaa ggt cta cgt ggc aac ctc aat gag tcc atc tct gac gac			2419
Phe Val Glu Gly Leu Arg Gly Asn Leu Asn Glu Ser Ile Ser Asp Asp			
	760	765	770

gag gca atc agc atg ttg tca cag cat ctg atc acc gca cca gtg ttt	2467
Glu Ala Ile Ser Met Leu Ser Gln His Leu Ile Thr Ala Pro Val Phe	
775 780 785	
gac gct cta ttt gct gaa tca agc ttc gct aag caa aac cct gtt tcc	2515
Asp Ala Leu Phe Ala Glu Ser Ser Phe Ala Lys Gln Asn Pro Val Ser	
790 795 800 805	
cag gtt atg caa cgc atg gca gat gct ctt aat agt gct gaa ctt aac	2563
Gln Val Met Gln Arg Met Ala Asp Ala Leu Asn Ser Ala Glu Leu Asn	
810 815 820	
tct gaa acg gaa aaa ctt gag aag ttc tat gac tct gtt cgt atc cgt	2611
Ser Glu Thr Glu Lys Leu Glu Lys Phe Tyr Asp Ser Val Arg Ile Arg	
825 830 835	
gct gct gaa gta agc tcc gca gct ggt aaa caa gca gta att aaa gac	2659
Ala Ala Glu Val Ser Ser Ala Ala Gly Lys Gln Ala Val Ile Lys Asp	
840 845 850	
ctc tac gaa cga ttc ttt aaa aag gcc ttt aaa aag caa tct gaa gct	2707
Leu Tyr Glu Arg Phe Phe Lys Lys Ala Phe Lys Lys Gln Ser Glu Ala	
855 860 865	
cta ggt att gtc tat acc cct gtt gag atc gtg gac ttt att ctg cga	2755
Leu Gly Ile Val Tyr Thr Pro Val Glu Ile Val Asp Phe Ile Leu Arg	
870 875 880 885	
gct gcc gat gat gtg tcc aag aag cat ttt ggt cgt gcc tta agc gat	2803
Ala Ala Asp Asp Val Ser Lys Lys His Phe Gly Arg Gly Leu Ser Asp	
890 895 900	
aaa gat gtc cat gtt ctt gat cct ttc acc ggt acg ggt act ttt atg	2851
Lys Asp Val His Val Leu Asp Pro Phe Thr Gly Thr Gly Thr Phe Met	
905 910 915	
gtg cgt tta ttg cag tca ggt cta att aag cct gaa gat ttg gcc cgt	2899
Val Arg Leu Leu Gln Ser Gly Leu Ile Lys Pro Glu Asp Leu Ala Arg	
920 925 930	
aaa tat gcc aat gag ctg cac gct act gag atc atg ttg ctt gcc tat	2947
Lys Tyr Ala Asn Glu Leu His Ala Thr Glu Ile Met Leu Leu Ala Tyr	
935 940 945	
tat gtt gcg gcc gtt aac att gag acc act tat ttt ggt ctc gag gga	2995
Tyr Val Ala Ala Val Asn Ile Glu Thr Thr Tyr Phe Gly Leu Glu Gly	
950 955 960 965	
gag cgt gct ctg cgt aat ggt gaa gat gcg ccg gtc tat gag ccg ttt	3043
Glu Arg Ala Leu Arg Asn Gly Glu Asp Ala Pro Val Tyr Glu Pro Phe	
970 975 980	
gat gcc att gtg ttg ggt gat acc ttc cag atg tat gaa gac gat gac	3091
Asp Gly Ile Val Leu Gly Asp Thr Phe Gln Met Tyr Glu Asp Asp Asp	
985 990 995	
aaa ctc gat cta gat gtt ttt act gct aac aat gac cgt atg gag cgt	3139
Lys Leu Asp Leu Asp Val Phe Thr Ala Asn Asn Asp Arg Met Glu Arg	
1000 1005 1010	

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Ser Trp Val Val Asp Asn Gly Val Thr Ser Pro Lys Glu Ala Asp Val	
1270	1275 1280 1285
aat caa ttc ctt aag cag aac cct gat tta gcg gat agc aag aaa ata	4003
Asn Gln Phe Leu Lys Gln Asn Pro Asp Leu Ala Asp Ser Lys Lys Ile	
	1290 1295 1300
tcc tgg gat tcc aat cta aaa atg tcc ttg tca cgc ggt gat act ttt	4051
Ser Trp Asp Ser Asn Leu Lys Met Ser Leu Ser Arg Gly Asp Thr Phe	
	1305 1310 1315
tct ttt gat cca agc agc atc caa atg tcc ttg tat cgt cca ttt ttc	4099
Ser Phe Asp Pro Ser Ser Ile Gln Met Ser Leu Tyr Arg Pro Phe Phe	
	1320 1325 1330
cct caa cag aca tac ttc cat gtt tca ttg aac cag cgt cga tac cag	4147
Pro Gln Gln Thr Tyr Phe His Val Ser Leu Asn Gln Arg Arg Tyr Gln	
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Leu Pro Ser Met Phe Pro Thr Pro Glu His Asp Asn Gln Gly Phe Tyr	
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Ile Val Asn Pro Gly Ser Ala Lys Pro Phe Ser Thr Leu Ala Thr Asn	
	1370 1375 1380
cta ctt cca gat ctt gct atg tgg ggt tct aac gcc gga cag ttc ttt	4291
Leu Leu Pro Asp Leu Ala Met Trp Gly Ser Asn Ala Gly Gln Phe Phe	
	1385 1390 1395
acc cga tgg act tgg gaa ccc atc gaa act cga gaa ggc gaa tta gac	4339
Thr Arg Trp Thr Glu Pro Ile Glu Thr Arg Glu Gly Glu Leu Asp	
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Phe Gly Asn Gly Leu Phe Ser Thr Thr Pro Lys Lys Gly Val Glu Gly	
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Glu Ile Leu Asp Gly Tyr Arg Arg Val Asp Asn Ile Thr Asp Glu Ile	
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Leu Lys Leu Tyr Gln Ser Ser Leu Gly Glu Asp Val Thr Lys Asp Asp	
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Ile Phe Tyr Phe Val Tyr Ala Gln Leu His Asp Pro Ala Tyr Arg Glu	
	1465 1470 1475
gcc tat gcg gct gat cta aag aag atg ctg cca cat att gaa acc cct	4579
Ala Tyr Ala Ala Asp Leu Lys Lys Met Leu Pro His Ile Glu Thr Pro	
	1480 1485 1490
act gat cgc gca cgc ttt gat cac ttt gtg aca gcc ggc aag gaa ttg	4627
Thr Asp Arg Ala Arg Phe Asp His Phe Val Thr Ala Gly Lys Glu Leu	

1495	1500	1505	
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Met Asp Leu His Ile Asn Tyr Glu Asp Val Glu Pro Trp Asp Val Glu			
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gta aag gtc aaa gaa aaa gct gat ccc acg gat cgt gag acc tgg cgt			4723
Val Lys Val Lys Glu Lys Ala Asp Pro Thr Asp Arg Glu Thr Trp Arg			
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Val Thr Lys Met Lys Trp Ala Lys Val Arg Asp Pro Glu Thr Lys Lys			
	1545	1550	1555
ttg gtg gag gac cat acc acc ttg att tac aac agc tca atc acc atc			4819
Leu Val Glu Asp His Thr Thr Leu Ile Tyr Asn Ser Ser Ile Thr Ile			
	1560	1565	1570
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Ser Gly Ile Pro Glu Glu Ala Glu Asn Tyr Gln Leu Gly Ser Arg Ser			
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Ala Ile Ala Trp Leu Ile Asp Arg Tyr Gln Val Lys Lys Asp Lys Ala			
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Ser Gly Ile Val Asn Asp Pro Asn Asp Trp Ala Asp Glu Val Gly Asn			
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Pro Arg Tyr Ile Val Glu Leu Ile Ala Lys Val Thr Arg Val Ala Val			
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Asn Phe Ile Lys Ser Asp Pro Thr Leu Ser Thr Glu Phe Asp Glu Val			
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His Arg Trp Val Asp Trp Pro Tyr Asn Gly Gly Thr Met Asp Thr Gly			
	50	55	60
Ile Asp Leu Val Ala Tyr Asn Lys Asp Asp Ala Tyr Thr Ala Ile			
	65	70	75
			80

Gln Cys Lys Phe Tyr Leu Pro Thr Thr Ser Leu Ala Lys Gly Gln Leu
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 Asp Ser Phe Phe Glu Ala Ser Gly Arg Thr Phe Glu Thr Pro Glu Gly
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 Thr Arg Ser Phe Ser Asn Arg Leu Val Ile Ser Thr Thr Asp Lys Trp
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 Ser Ser Asn Ala Glu Lys Met Leu Glu Asn Gln Thr Ile Pro Thr Asn
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 Arg Ile Gly Leu Ser Ala Ile Ala Glu Ser Pro Ile Asp Trp Asp Ile
 145 150 155 160
 Ala Tyr Pro Gly Ser Glu Leu Thr Ile Asn Leu Gln Leu Lys Glu Pro
 165 170 175
 Tyr Ser Pro Arg Pro His Gln Gln Thr Ala Ile Glu Lys Ala Ile Glu
 180 185 190
 Gly Phe Gln Thr His Asp Arg Gly Lys Leu Ile Met Ala Cys Gly Thr
 195 200 205
 Gly Lys Thr Phe Thr Ala Leu Arg Leu Ser Glu Glu Val Ala Arg Leu
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 Asn Gly Asn Lys Ala Arg Ile Leu Phe Leu Val Pro Ser Ile Ser Leu
 225 230 235 240
 Leu Ser Gln Thr Leu Lys Glu Trp Thr Ala Gln Lys Thr Met Asp Leu
 245 250 255
 Arg Pro Val Ala Val Cys Ser Asp Ser Lys Val Ser Lys Ala Ala Glu
 260 265 270
 Asp Ile Ala Ala Tyr Asp Leu Glu Val Pro Val Ser Thr Asp Gly Ala
 275 280 285
 Leu Ile Ala Glu Lys Leu Glu His Arg Lys Arg Ala Ala Gly Leu Thr
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 Val Val Phe Ser Thr Tyr Gln Ser Leu Pro Ala Val His Ala Ala Gln
 305 310 315 320
 Glu Ala Gly Ala Glu Pro Phe Asp Leu Val Ile Cys Asp Glu Ala His
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 Arg Thr Thr Gly Ile Thr Leu Ala Gly Glu Asp Pro Ser Asn Phe Thr
 340 345 350
 Arg Ile His Asp Ala Ser Tyr Ile Lys Ala Ala Lys Arg Leu Tyr Met
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 Thr Ala Thr Pro Arg Leu Phe Asp Asp Ser Val Lys Gly Lys Ala Ala
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 Asp His Ser Ala Glu Val Ser Ser Met Asp Asp Glu Ala Ile Tyr Gly
 385 390 395 400

Pro Glu Phe His Arg Leu Gly Phe Gly Glu Ala Val Glu Lys Gly Leu
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 Leu Thr Asp Tyr Lys Val Val Val Met Thr Val Asp Glu Gln Val Ala
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 Ala Ser Ala Leu Thr Val Leu Gly Ser Thr Pro Gly Glu Glu Leu Thr
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 Leu Asp Met Thr Ser Ala Ile Ile Gly Ala Trp Asn Gly Leu Ala Lys
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 Arg Ser Gly Lys Glu Gln Asp Thr Lys Thr Gly Phe Ser Ser Ser Asp
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 Ala Ala Met Glu Arg Ala Val Ala Phe Ala Arg Asp Ile Lys Thr Ser
 485 490 495
 Gln Gln Ile Ala Glu Ser Phe Pro Arg Val Val Asn Ala Tyr Thr Thr
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 Glu Leu Glu Val Lys Asn Asp Asp Val Asp Glu His Asn Leu Asn Leu
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 Ser Val Ala Cys Gln His Val Asp Gly Ser Met Asn Ala Leu Glu Arg
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 Asn Ser Arg Leu Thr Trp Leu Lys Ala Pro Thr Gln Ser Met Glu Thr
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 Lys Ile Leu Thr Asn Ala Arg Cys Leu Ser Glu Gly Val Asp Val Pro
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 Tyr Gly Tyr Ile Ile Leu Pro Val Ala Val Pro Pro Gly Val Ala Pro
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 Ser Ala Glu Ser Ala Thr Gln Tyr Val Leu Phe Ser Leu Glu Gln Trp
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 Gln Glu Ala Ile Tyr Thr Lys Leu Val Asp Lys Val Gly Thr Arg Thr
 705 710 715 720
 Tyr Trp Glu Asp Trp Ala Asp Asp Val Ala Asp Ile Ala Gln Ala Gln

725										730					735				
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Glu	Glu	Phe	Glu	Arg	Phe	Val	Glu	Gly	Leu	Arg	Gly	Asn	Leu	Asn	Glu				
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Thr	Ala	Pro	Val	Phe	Asp	Ala	Leu	Phe	Ala	Glu	Ser	Ser	Phe	Ala	Lys				
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Gln	Asn	Pro	Val	Ser	Gln	Val	Met	Gln	Arg	Met	Ala	Asp	Ala	Leu	Asn				
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Ser	Val	Arg	Ile	Arg	Ala	Ala	Glu	Val	Ser	Ser	Ala	Ala	Gly	Lys	Gln				
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Ala	Val	Ile	Lys	Asp	Leu	Tyr	Glu	Arg	Phe	Phe	Lys	Lys	Ala	Phe	Lys				
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Lys	Gln	Ser	Glu	Ala	Leu	Gly	Ile	Val	Tyr	Thr	Pro	Val	Glu	Ile	Val				
865					870					875					880				
Asp	Phe	Ile	Leu	Arg	Ala	Ala	Asp	Asp	Val	Ser	Lys	Lys	His	Phe	Gly				
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Arg	Gly	Leu	Ser	Asp	Lys	Asp	Val	His	Val	Leu	Asp	Pro	Phe	Thr	Gly				
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Thr	Gly	Thr	Phe	Met	Val	Arg	Leu	Gln	Ser	Gly	Leu	Ile	Lys	Pro					
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Glu	Asp	Leu	Ala	Arg	Lys	Tyr	Ala	Asn	Glu	Leu	His	Ala	Thr	Glu	Ile				
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Met	Leu	Leu	Ala	Tyr	Tyr	Val	Ala	Ala	Val	Asn	Ile	Glu	Thr	Thr	Tyr				
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Phe	Gly	Leu	Glu	Gly	Glu	Arg	Ala	Leu	Arg	Asn	Gly	Glu	Asp	Ala	Pro				
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Val	Tyr	Glu	Pro	Phe	Asp	Gly	Ile	Val	Leu	Gly	Asp	Thr	Phe	Gln	Met				
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Tyr	Glu	Asp	Asp	Asp	Lys	Leu	Asp	Leu	Asp	Val	Phe	Thr	Ala	Asn	Asn				
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 Tyr Arg Pro Phe Phe Pro Gln Gln Thr Tyr Phe His Val Ser Leu Asn
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 Lys Gly Val Glu Gly Glu Ile Leu Asp Gly Tyr Arg Arg Val Asp Asn
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tcc Ser	aag Lys	aag Lys 35	cat His	ttt Phe	ggg Gly	cgt Arg	ggc Gly 40	tta Leu	agc Ser	gat Asp	aaa Lys	gat Asp 45	gtc Val	cat His	gtt Val	144
ctt Leu	gat Asp 50	cct Pro	ttc Phe	acc Thr	ggg Gly	acg Thr 55	ggg Gly	act Thr	ttt Phe	atg Met	gtg Val 60	cgt Arg	tta Leu	ttg Leu	cag Gln	192
tca Ser 65	ggg Gly	cta Leu	att Ile	aag Lys	cct Pro 70	gaa Glu	gat Asp	ttg Leu	gcc Ala	cgt Arg 75	aaa Lys	tat Tyr	gcc Ala	aat Asn	gag Glu 80	240
ctg Leu	cac His	gct Ala	act Thr	gag Glu 85	atc Ile	atg Met	ttg Leu	ctt Leu	gcc Ala 90	tat Tyr	tat Tyr	ggt Val	gcg Ala 95	gcc Ala	gtt Val	288
aac Asn	att Ile	gag Glu	acc Thr 100	act Thr	tat Tyr	ttt Phe	ggg Gly	ctc Leu 105	gag Glu	gga Gly	gag Glu	cgt Arg	gct Ala 110	ctg Leu	cgt Arg	336
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ggg Gly	gat Asp 130	acc Thr	ttc Phe	cag Gln	atg Met	tat Tyr 135	gaa Glu	gac Asp	gat Asp	gac Asp	aaa Lys 140	ctc Leu	gat Asp	cta Leu	gat Asp	432
gtt Val 145	ttt Phe	act Thr	gct Ala	aac Asn	aat Asn 150	gac Asp	cgt Arg	atg Met	gag Glu	cgt Arg 155	cag Gln	aga Arg	ctt Leu	act Thr	cct Pro 160	480
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cac His 225	aca Thr	caa Gln	ggg Gly	gtt Val	gtt Val 230	gct Ala	ttt Phe	gtt Val	tct Ser	aac Asn 235	aac Asn	ggg Gly	tgg Trp	gtt Val	gac Asp 240	720

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Glu Ile Tyr Val Phe Asn Leu Arg Gly Asn Ser Arg Thr Gly Gly Asp	
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Leu Ala Lys Arg Glu Gly Gly Asn Val Phe Asn Val Arg Val Gly Thr	
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Gln Ile Ile Val Ala Val Lys Asn Pro Gln Leu Ser Gly Cys Arg Ile	
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Thr Trp Pro Val Leu Gly Asp Lys Lys Asn Lys Ser Ala Leu Lys Val	
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Tyr Gly Pro Thr Ser Ala Gln Val Lys Thr Asn Ile Thr Arg Leu Leu	
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Glu Thr Tyr Glu Gln Ala Gln Gln Arg Phe Asn Ser Trp Val Val Asp	
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Gln Asn Pro Asp Leu Ala Asp Ser Lys Lys Ile Ser Trp Asp Ser Asn	
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Leu Lys Met Ser Leu Ser Arg Gly Asp Thr Phe Ser Phe Asp Pro Ser	
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Pro Thr Pro Glu His Asp Asn Gln Gly Phe Tyr Ile Val Asn Pro Gly	
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agt gcc aag cca ttc tct acc ctt gca aca aat cta ctt cca gat ctt	1584
Ser Ala Lys Pro Phe Ser Thr Leu Ala Thr Asn Leu Leu Pro Asp Leu	
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Ser Ser Leu Gly Glu Asp Val Thr Lys Asp Asp Ile Phe Tyr Phe Val	
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Tyr Ala Gln Leu His Asp Pro Ala Tyr Arg Glu Ala Tyr Ala Ala Asp	
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Leu Lys Lys Met Leu Pro His Ile Glu Thr Pro Thr Asp Arg Ala Arg	
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675 680 685	
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 Ser Gly Leu Ile Lys Pro Glu Asp Leu Ala Arg Lys Tyr Ala Asn Glu
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 Val Gln Val Ile Val Gly Asn Pro Pro Tyr Ser Val Gly Gln Ser Ser
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Ile Glu Asp Ser Tyr Ala Lys Tyr Ser Thr Ala Thr Asn Lys Asn Ser
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 His Thr Gln Gly Val Val Ala Phe Val Ser Asn Asn Gly Trp Val Asp
 225 230 235 240
 Gly Asn Thr Ala Asp Gly Val Arg Leu Ser Leu Ala Gln Asp Phe Ser
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 Leu Ala Lys Arg Glu Gly Gly Asn Val Phe Asn Val Arg Val Gly Thr
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 Ser Arg Leu Asp Ala Ala Leu Pro Lys Asp Arg Pro Leu Tyr Gln His
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tcc cag caa tca agc act cga gtt gaa gac atc ggc aag ggt ctt tgg Ser Gln Gln Ser Ser Thr Arg Val Glu Asp Ile Gly Lys Gly Leu Trp 425 430 435			1411
cca aat gtt act gat aaa gca tca atg cac cgc aca cat atg ctg gtg Pro Asn Val Thr Asp Lys Ala Ser Met His Arg Thr His Met Leu Val 440 445 450			1459

aat tta ggc agt ggc gtt cta tcc cat gat gga gta cca gct ctg tcc	1507
Asn Leu Gly Ser Gly Val Leu Ser His Asp Gly Val Pro Ala Leu Ser	
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Ala Arg Tyr His Met Phe Val Arg Ala Val Glu Gly Ala Phe Leu Gly	
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Tyr Thr Glu Gln Gly Lys Pro Ile Val Ser Leu Asp Arg Gln Val Thr	
490 495 500	
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Leu Gly Asp Thr Ala Arg Pro Met Tyr Glu Met Gly Ala Cys Ile Lys	
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Cys Gly Thr Val His Ile Ser Ala His Asn Asp Ser Gly Phe Leu Val	
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cct cca gag aat tcc tca aat ttc gac gaa caa cag ctc aaa tgg gta	1747
Pro Pro Glu Asn Ser Ser Asn Phe Asp Glu Gln Gln Leu Lys Trp Val	
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Val Leu Thr Asp Asp Phe Glu Thr Ala Asp Ile Asp Glu Asp Asp Leu	
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Glu Thr Asp Ala Asp Glu Asn Val Lys Val Leu Glu Leu Gln Lys Leu	
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Cys Thr Ala Cys Gly Lys Leu Asn Gly Lys Asn Ser Leu Leu Cys Ser	
585 590 595	
gga tgc tca tca cat cat gac cag ttt att gat gta aag atc ttg gaa	1939
Gly Cys Ser Ser His His Asp Gln Phe Ile Asp Val Lys Ile Leu Glu	
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ccc cgg aat ggt agc caa tta aca tgc act cga tgc ggt ggc cga gaa	1987
Pro Arg Asn Gly Ser Gln Leu Thr Cys Thr Arg Cys Gly Gly Arg Glu	
615 620 625	
aag aac ctg att cga cga ctc cga acc gat tca aat gct gca cct tct	2035
Lys Asn Leu Ile Arg Arg Leu Arg Thr Asp Ser Asn Ala Ala Pro Ser	
630 635 640 645	
gtc ctc acc aca tca ttg ttc caa ctg ttg cca gaa tca gct gat caa	2083
Val Leu Thr Thr Ser Leu Phe Gln Leu Leu Pro Glu Ser Ala Asp Gln	
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Asp Thr Ser Arg Lys Ile Gly Ala Gly Arg Lys Leu Leu Thr Phe Ser	
665 670 675	
gac tcc cgc cag gct gcc gct tac gca gca cca tat ttg caa gca agt	2179
Asp Ser Arg Gln Ala Ala Ala Tyr Ala Ala Pro Tyr Leu Gln Ala Ser	
680 685 690	

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Tyr Thr Arg Leu Leu Glu Arg Arg Ile Leu Ile Glu Thr Leu Arg Asp	
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Glu Glu Phe Thr Glu Gly Ala Ser Ile Glu Arg Trp Ile Ser Arg Ala	
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Ser Glu Val Ala Lys Asn Asn Arg Val Leu Ala Asn Asn Leu Asn Pro	
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cgc gaa aca cta gaa cag aca ggt aac tgg gta ttc gca gat ctt gct	2371
Arg Glu Thr Leu Glu Gln Thr Gly Asn Trp Val Phe Ala Asp Leu Ala	
745 750 755	
tcg aca gtc cga agt agt tcg act gaa ggg ctt gga cta gcc aaa att	2419
Ser Thr Val Arg Ser Ser Ser Thr Glu Gly Leu Gly Leu Ala Lys Ile	
760 765 770	
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Glu Leu Thr Pro Glu Ala Leu Ser Gln Leu Ser Phe Arg Lys Pro Leu	
775 780 785	
ggc gag atg ttt ggg gat ccg gat gcc gcc gac gcc ttt ttt aat ctc	2515
Gly Glu Met Phe Gly Asp Pro Asp Ala Ala Asp Ala Phe Phe Asn Leu	
790 795 800 805	
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Phe Ala Gln Glu Phe Arg His Lys Gly Ala Ile Asn Cys Pro Asp Tyr	
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Val Asn Leu Glu Asp Glu Arg Phe Gly Pro Arg Arg Gly Gln His Phe	
825 830 835	
ttc acc aaa gat ggt gga aga aaa tca aca cga cgc ctc tac tca tgg	2659
Phe Thr Lys Asp Gly Gly Arg Lys Ser Thr Arg Arg Leu Tyr Ser Trp	
840 845 850	
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Ile Pro Gln Arg Gly Thr Asn Asn Arg Lys Asp Phe Ile Thr Lys Val	
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Val Pro Gly Glu Lys Ala Glu Gly Tyr Thr Leu Asn Tyr Asn Ser Leu	
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caa gta agc cct gga aaa caa cat tcc tgg tat gaa tgt gac act tgt	2899
Gln Val Ser Pro Gly Lys Gln His Ser Trp Tyr Glu Cys Asp Thr Cys	
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aga aat aca acg cca ttt aat gtt ctc ggg ctg tgt cca cat ggg ttc	2947

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Cys	Lys	Gly	Lys	Leu	Lys	Glu	Ile	Asp	Thr	Phe	Leu	Pro	Glu	Tyr	Ala	
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acc	aat	cat	tat	cgg	aag	ttg	gca	aca	tcg	ctt	gaa	att	ctt	ccg	ctt	3043
Thr	Asn	His	Tyr	Arg	Lys	Leu	Ala	Thr	Ser	Leu	Glu	Ile	Leu	Pro	Leu	
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tca	gcc	aaa	gag	cac	act	gct	caa	tgg	acg	cca	acg	gag	gct	gca	gag	3091
Ser	Ala	Lys	Glu	His	Thr	Ala	Gln	Trp	Thr	Pro	Thr	Glu	Ala	Ala	Glu	
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Val	Gln	Lys	Glu	Phe	Ile	Glu	Gly	Lys	Ile	Asn	Val	Leu	Ser	Cys	Ser	
		1000					1005					1010				
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Thr	Thr	Phe	Glu	Leu	Gly	Val	Asp	Val	Gly	Asp	Leu	Gln	Ser	Val	Met	
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Met	Arg	Asn	Val	Pro	Pro	Arg	Thr	Ala	Asn	Tyr	Val	Gln	Arg	Ala	Gly	
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Arg	Ala	Gly	Arg	Arg	Ser	Gly	Ser	Ala	Ala	Phe	Val	Leu	Thr	Phe	Ala	
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Lys	Arg	Ser	Ser	His	Asp	Leu	Ala	Val	Phe	Lys	Asn	Pro	Thr	Gln	Met	
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Ile	Asp	Gly	Glu	Met	Thr	Val	Pro	Phe	Leu	His	Ile	Asn	Asn	Ala	Arg	
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atc	gcc	cgt	cgt	cac	acc	tat	tca	atc	gct	ctc	gcc	gca	ttt	ttc	cga	3427
Ile	Ala	Arg	Arg	His	Thr	Tyr	Ser	Ile	Ala	Leu	Ala	Ala	Phe	Phe	Arg	
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Glu	Gln	Ala	Ala	Gln	Asn	Arg	Phe	Trp	Lys	Lys	Ala	Gly	Glu	Phe	Phe	
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ctt	ggc	act	gat	gca	gct	cca	tac	ctt	agg	cct	gct	gtc	gca	gag	caa	3523
Leu	Gly	Thr	Asp	Ala	Ala	Pro	Tyr	Leu	Arg	Pro	Ala	Val	Ala	Glu	Gln	
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Ile	Thr	Glu	Ala	Leu	Arg	Arg	Val	Phe	Pro	Glu	Ser	Leu	His	Glu	Asp	
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Leu	Asp	Ile	Glu	Asn	Gln	Gly	Trp	Val	Lys	Gln	Phe	Leu	Glu	Ile	Phe	

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Phe Lys Arg Thr Ile Thr Thr Leu Met Asp Gln Asp Leu Leu Gly Tyr			
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Val Asp Leu Gln Thr Asn Phe Ser Glu Ala Gly Asn Lys Val Ser Leu			
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tca cga gat ctt cag cta gcg att acc gac tat gct cct ggt gcg gag			3955
Ser Arg Asp Leu Gln Leu Ala Ile Thr Asp Tyr Ala Pro Gly Ala Glu			
1270	1275	1280	1285
tta gta gca ggc gga aaa ttg tgg aaa tcc gct ggc att cga cac cta			4003
Leu Val Ala Gly Lys Leu Trp Lys Ser Ala Gly Ile Arg His Leu			
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gcc ggt aaa aag gtg gaa act ttt tat tgg aca acg tgt act gag tgt			4051
Ala Gly Lys Lys Val Glu Thr Phe Tyr Trp Thr Thr Cys Thr Glu Cys			
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Lys His Thr Glu Thr Ser Arg Phe Gly Phe Thr Ser Glu Asp Val Cys			
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Ile Pro Arg Phe Gly Phe Val Ala Asp Pro Asn Pro Thr Glu Val Gly			
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Thr Ala Pro Pro Val Arg Ser Ser Asn Arg Leu Glu Phe Val Lys Gln			
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Phe Gly Val Lys Asp Asp Ser Glu Glu Phe Ser Asn Ser Asp Gly Thr			
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Ala Thr Ala Gln Val Leu Thr Ser Ser Trp Ser Arg Thr Glu Met Gly			
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Ala Leu Glu Thr Gly Pro Asn Lys Asn Gly Phe Trp Tyr Cys Gln Thr			
	1415	1420	1425

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 Cys Gly Phe Gly Thr Pro Asn Gly Ala Glu Ile Pro Lys Ser His Arg
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 Asn Pro Arg Thr Lys Gln Gln Cys Gly Thr Tyr Tyr Leu Glu Pro His
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 Gln Arg Phe His Leu Asp Leu Arg Arg Asp Ile Ala Leu Asp Leu Leu
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 cag 4923

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<400> 36

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 20 25 30

Lys Val Asn Ala Lys Thr Glu Val Thr Arg Asn Ile Asp Pro Val Glu

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Ile	Ser	Pro	Ser	Asn	Lys	Thr	Ile	Ala	Ala	Glu	Phe	Asn	Arg	Glu	Ile
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Asp	Glu	Ser	Glu	Asn	Leu	Val	Tyr	Gly	Pro	Ile	Leu	Gln	Leu	Thr	Pro
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Pro	Tyr	Ala	Pro	Gly	Lys	Ser	Pro	Ala	Gln	Leu	Ile	Asp	Glu	Gly	Val
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Leu	Ser	Pro	Asn	Phe	Ser	Arg	Leu	Asp	Ala	Ala	Leu	Pro	Lys	Asp	Arg
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Pro	Leu	Tyr	Gln	His	Gln	Glu	Asp	Ala	Leu	Arg	Lys	Ile	Ala	Ser	Gly
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Phe	Leu	Ile	Pro	Ile	Phe	Asp	Gln	Leu	Leu	Arg	Gln	Gln	Gln	Ala	Gly
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Glu	Leu	Asn	Pro	Gly	Val	Arg	Ala	Leu	Leu	Leu	Tyr	Pro	Met	Asn	Ala
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Pro	Glu	Ile	Thr	Phe	Gly	Arg	Tyr	Thr	Gly	Asp	Thr	Lys	Gln	Thr	Arg
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Pro	Leu	Pro	Asn	Glu	Leu	Ile	Ser	Arg	Asp	Glu	Met	Gln	Glu	Asn	Pro
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Pro	His	Ile	Leu	Leu	Thr	Asn	Tyr	Ala	Met	Leu	Glu	Tyr	Leu	Leu	Leu
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Arg	Pro	Ala	Asp	Asn	Ala	Phe	Phe	Asp	Asp	Ala	Tyr	Ser	Asn	Asn	Trp
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Lys	Phe	Leu	Val	Leu	Asp	Glu	Ala	His	Val	Tyr	Ala	Gly	Ala	Gln	Gly
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Thr	Glu	Val	Gly	Met	Leu	Met	Arg	Arg	Leu	Lys	Asp	Arg	Val	Gln	Arg
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Gly	Asn	Pro	Leu	Gln	Cys	Ile	Ala	Thr	Ser	Ala	Ser	Leu	Glu	Gly	Thr
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 Phe Asp Gln Pro Leu Glu Ser Asp Gly Leu Phe Gln Ala Leu Gln Glu
 385 390 395 400
 Arg Gly Gly Asp Gln Tyr Glu Glu Leu Ser Lys Glu Glu His Ile Val
 405 410 415
 Lys Leu Arg Glu Leu Ser Gln Gln Ser Ser Thr Arg Val Glu Asp Ile
 420 425 430
 Gly Lys Gly Leu Trp Pro Asn Val Thr Asp Lys Ala Ser Met His Arg
 435 440 445
 Thr His Met Leu Val Asn Leu Gly Ser Gly Val Leu Ser His Asp Gly
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 Val Pro Ala Leu Ser Ala Arg Tyr His Met Phe Val Arg Ala Val Glu
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 Asp Arg Gln Val Thr Leu Gly Asp Thr Ala Arg Pro Met Tyr Glu Met
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 Ser Leu Leu Cys Ser Gly Cys Ser Ser His His Asp Gln Phe Ile Asp
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 Val Lys Ile Leu Glu Pro Arg Asn Gly Ser Gln Leu Thr Cys Thr Arg
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 Cys Gly Gly Arg Glu Lys Asn Leu Ile Arg Arg Leu Arg Thr Asp Ser
 625 630 635 640
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Tyr Leu Gln Ala Ser Tyr Thr Arg Leu Leu Glu Arg Arg Ile Leu Ile
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 Gly Leu Ala Lys Ile Glu Leu Thr Pro Glu Ala Leu Ser Gln Leu Ser
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Val Gln Arg Ala Gly Arg Ala Gly Arg Arg Ser Gly Ser Ala Ala Phe			
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Val Leu Thr Phe Ala Lys Arg Ser Ser His Asp Leu Ala Val Phe Lys			
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Asn Pro Thr Gln Met Ile Asp Gly Glu Met Thr Val Pro Phe Leu His			
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Ile Asn Asn Ala Arg Ile Ala Arg Arg His Thr Tyr Ser Ile Ala Leu			
	1090	1095	1100
Ala Ala Phe Phe Arg Glu Gln Ala Ala Gln Asn Arg Phe Trp Lys Lys			
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Ala Gly Glu Phe Phe Leu Gly Thr Asp Ala Ala Pro Tyr Leu Arg Pro			
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Ala Val Ala Glu Gln Glu Ala Thr Glu Ile Leu Glu Glu Phe Leu Ser			
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Pro Val Pro Asn Tyr Ile Thr Glu Ala Leu Arg Arg Val Phe Pro Glu			
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Ser Leu His Glu Asp Leu Asp Ile Glu Asn Gln Gly Trp Val Lys Gln			
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Phe Leu Glu Ile Phe Asp Thr Thr Arg Gln Glu Ile Ser Glu Asp Phe			
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Gln Thr Leu Lys Lys Met Gln Gly Arg Ala Leu Gly Ser Glu Gln Gly			
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Lys Lys Ala Asp Ala Phe Lys Arg Thr Ile Thr Thr Leu Met Asp Gln			
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Asp Leu Leu Gly Tyr Leu Ala Lys Lys Asn Met Leu Pro Lys Tyr Ser			
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Phe Pro Val Asp Thr Val Asp Leu Gln Thr Asn Phe Ser Glu Ala Gly			
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Asn Lys Val Ser Leu Ser Arg Asp Leu Gln Leu Ala Ile Thr Asp Tyr			
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Ala Pro Gly Ala Glu Leu Val Ala Gly Gly Lys Leu Trp Lys Ser Ala			
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Gly Ile Arg His Leu Ala Gly Lys Lys Val Glu Thr Phe Tyr Trp Thr			
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Thr Cys Thr Glu Cys Lys His Thr Glu Thr Ser Arg Phe Gly Phe Thr			
	1315	1320	1325
Ser Glu Asp Val Cys Ser Gln Cys Ser Ala Pro Ile Ser Leu Gly Lys			
	1330	1335	1340

Glu Asn Lys Phe Leu Ile Pro Arg Phe Gly Phe Val Ala Asp Pro Asn
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 Pro Thr Glu Val Gly Thr Ala Pro Pro Val Arg Ser Ser Asn Arg Leu
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 Asn Ser Asp Gly Thr Ala Thr Ala Gln Val Leu Thr Ser Ser Trp Ser
 1395 1400 1405
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 1410 1415 1420
 Trp Tyr Cys Gln Thr Cys Gly Phe Gly Thr Pro Asn Gly Ala Glu Ile
 1425 1430 1435 1440
 Pro Lys Ser His Arg Asn Pro Arg Thr Lys Gln Gln Cys Gly Thr Tyr
 1445 1450 1455
 Tyr Leu Glu Pro His Ser Leu Gly His Thr Tyr Gln Thr Asp Ile Ala
 1460 1465 1470
 Thr Val Ala Val Pro Ser Tyr Thr Asn Leu Asp Phe Glu Gly Trp Arg
 1475 1480 1485
 Ser Gly Met Tyr Ala Ile Ile Glu Ala Ala Ala Glu Cys Leu Glu Ile
 1490 1495 1500
 Asn Arg Asp Asp Leu Asn Gly Thr Met Ala Lys His Asp Asn Arg Pro
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 1525 1530 1535
 Lys Val Arg Glu Asn Phe Pro Gln Val Leu Glu Ala Ala Ile Arg Arg
 1540 1545 1550
 Val Glu Thr Cys Ser Cys Gly Ile Asp Thr Ser Cys Tyr Ala Cys Leu
 1555 1560 1565
 Arg Ser Phe Ser Asn Gln Arg Phe His Leu Asp Leu Arg Arg Asp Ile
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<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2776)

<223> RXN01606

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                                   1           5

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Ala Met Asp Arg Ala Gln Ile Ser Ala Leu Leu Asp Arg Ala Gln His
                        10                15                20

aca atc aac ctt gcc gaa caa gca aac aac gtg ctc cga ctg ttg aaa 211
Thr Ile Asn Leu Ala Glu Gln Ala Asn Asn Val Leu Arg Leu Leu Lys
                        25                30                35

aca ccc gga acg gcc aca gta ggg gac aac ggg aca ctc ggc acc gat 259
Thr Pro Gly Thr Ala Thr Val Gly Asp Asn Gly Thr Leu Gly Thr Asp
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acc tat ctg atc cca tcc cgc aac atc acc tgg cct gac aac ctg tat 307
Thr Tyr Leu Ile Pro Ser Arg Asn Ile Thr Trp Pro Asp Asn Leu Tyr
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gtc aac gtc ttt cta gac ggc atg aat gca gaa gcc acc ctt acc gat 355
Val Asn Val Phe Leu Asp Gly Met Asn Ala Glu Ala Thr Leu Thr Asp
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tac gtc gca tca gtc gct tcg atc cca cgc cta tgc cag atc atc aac 403
Tyr Val Ala Ser Val Ala Ser Ile Pro Arg Leu Cys Gln Ile Ile Asn
                        90                95                100

gag ggc caa ggc ggc atg ttc cgc aga cta ttc aac ccc acc aag gtc 451
Glu Gly Gln Gly Gly Met Phe Arg Arg Leu Phe Asn Pro Thr Lys Val
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caa gcc ggc gac caa gct gtc ttc gac ctc atg gtc aaa ctc gac gag 499
Gln Ala Gly Asp Gln Ala Val Phe Asp Leu Met Val Lys Leu Asp Glu
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att tca tct acc acc cac gaa gtc tcc cgc atg ctc gag ggc gtc cac 547
Ile Ser Ser Thr Thr His Glu Val Ser Arg Met Leu Glu Gly Val His
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Ala Ala Arg Thr Arg Gln Gln Gln Gly Val Ala Leu Phe Pro Gly Ile
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cat gga gtg gga gag cgc tac atc gaa cgc gca caa cag gta ctc gcc 643
His Gly Val Gly Glu Arg Tyr Ile Glu Arg Ala Gln Gln Val Leu Ala
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Ser Ala Leu Gly Ile Ala Gly Phe Gly Ala Glu Pro Trp Asp Gly His
                        185                190                195

acc ctt gcc caa gcg cgc cgg gta gtc caa cgc tac gcc caa gat cct 739
Thr Leu Ala Gln Ala Arg Arg Val Val Gln Arg Tyr Ala Gln Asp Pro
                        200                205                210

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Asn Ser Glu Tyr Arg Leu Lys Ser Glu Ala Glu Lys His Leu Thr Ser	
215 220 225	
atc aac gag ctc cgc gta cag ata ctc ctc gaa caa ctc ccc gtt gat	835
Ile Asn Glu Leu Arg Val Gln Ile Leu Leu Glu Gln Leu Pro Val Asp	
230 235 240 245	
gcc cta cgc atg gct acc gac cac cgc ctg cgc ttt gga tcc ctc gat	883
Ala Leu Arg Met Ala Thr Asp His Arg Leu Arg Phe Gly Ser Leu Asp	
250 255 260	
tcc atc cac gtc gca acc gtc gcc gac gtc cta aaa aca cac acc tcc	931
Ser Ile His Val Ala Thr Val Ala Asp Val Leu Lys Thr His Thr Ser	
265 270 275	
atc ctc acc acc gtg caa ggt atc ggc gcc caa acc gcg ggg cgg atg	979
Ile Leu Thr Thr Val Gln Gly Ile Gly Ala Gln Thr Ala Gly Arg Met	
280 285 290	
aaa gcc gca gca gaa aca ctc aaa caa gaa gca cta cgc cgc caa aac	1027
Lys Ala Ala Ala Glu Thr Leu Lys Gln Glu Ala Leu Arg Arg Gln Asn	
295 300 305	
acc tcc atc ggc gac gaa cct acc caa ccc gcc atg cgt cta atc aac	1075
Thr Ser Ile Gly Asp Glu Pro Thr Gln Pro Ala Met Arg Leu Ile Asn	
310 315 320 325	
gtg ctg gcc cgc ttc gac caa acc gaa acc atc acg ccc gaa gaa cgc	1123
Val Leu Ala Arg Phe Asp Gln Thr Glu Thr Ile Thr Pro Glu Glu Arg	
330 335 340	
gcc cgc cgc acc cgc gtc atc gac tac gta gaa cac ata ccc cca agc	1171
Ala Arg Arg Thr Arg Val Ile Asp Tyr Val Glu His Ile Pro Pro Ser	
345 350 355	
ctc gac ccc tac atc gtc atc aac cca gca acg cct gag ttc aac aac	1219
Leu Asp Pro Tyr Ile Val Ile Asn Pro Ala Thr Pro Glu Phe Asn Asn	
360 365 370	
ttc acc gac gac ctc cgc tgg atc gac gca aac ccc aac ctc ttc cac	1267
Phe Thr Asp Asp Leu Arg Trp Ile Asp Ala Asn Pro Asn Leu Phe His	
375 380 385	
cca caa aca atc acc acc cca ccc gcc gac atc tgg gac gac tac atc	1315
Pro Gln Thr Ile Thr Thr Pro Pro Ala Asp Ile Trp Asp Asp Tyr Ile	
390 395 400 405	
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Ser Arg Pro Ala His Tyr Gln Gly Leu Leu Ala Thr Leu Leu Gly Arg	
410 415 420	
gac atc gaa ggc gca gac gaa ctc ctc gac gcc acc acc ctc caa aaa	1411
Asp Ile Glu Gly Ala Asp Glu Leu Leu Asp Ala Thr Thr Leu Gln Lys	
425 430 435	
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Ile Arg Asp Leu Thr Leu Asp Lys Thr His Leu Thr Asp Leu His Leu	
440 445 450	
cgc gga tac caa tca ttc ggc gcc cgc ttc gcc atc atc caa aag aaa	1507

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455						460					465					
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Thr	Leu	Leu	Gly	Asp	Asp	Met	Gly	Leu	Gly	Lys	Thr	Val	Gln	Ala	Leu	
470				475						480					485	
tcc	gca	gct	gca	cac	ctt	gcc	gcc	acc	gaa	aaa	gac	ttc	cgc	acc	ctc	1603
Ser	Ala	Ala	Ala	His	Leu	Ala	Ala	Thr	Glu	Lys	Asp	Phe	Arg	Thr	Leu	
				490					495					500		
gtc	gtc	gta	ccc	gca	tcc	gtc	att	gtt	aac	tgg	acc	cgc	gaa	tgc	aaa	1651
Val	Val	Val	Pro	Ala	Ser	Val	Ile	Val	Asn	Trp	Thr	Arg	Glu	Cys	Lys	
			505					510					515			
cgc	ttc	ctc	aac	ctc	ccc	gta	ttc	atc	gcc	cac	gga	gac	aac	aaa	caa	1699
Arg	Phe	Leu	Asn	Leu	Pro	Val	Phe	Ile	Ala	His	Gly	Asp	Asn	Lys	Gln	
		520					525					530				
gac	gcc	atc	aac	gcc	tgg	tct	aac	acc	aac	gga	atc	gca	atc	tgc	acc	1747
Asp	Ala	Ile	Asn	Ala	Trp	Ser	Asn	Thr	Asn	Gly	Ile	Ala	Ile	Cys	Thr	
	535					540					545					
tac	gac	ggc	gtc	cgc	acc	atg	gac	atc	ccc	gcg	ccg	ggt	ctg	gtc	att	1795
Tyr	Asp	Gly	Val	Arg	Thr	Met	Asp	Ile	Pro	Ala	Pro	Gly	Leu	Val	Ile	
550					555					560					565	
gcc	gat	gaa	gcc	cac	ctg	atc	aaa	aac	ccc	tcc	acc	aaa	cgc	acc	caa	1843
Ala	Asp	Glu	Ala	His	Leu	Ile	Lys	Asn	Pro	Ser	Thr	Lys	Arg	Thr	Gln	
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gca	ctg	cgc	aaa	ctt	atc	gac	gcc	gcc	cca	tac	acc	ctt	ctg	atg	acc	1891
Ala	Leu	Arg	Lys	Leu	Ile	Asp	Ala	Ala	Pro	Tyr	Thr	Leu	Leu	Met	Thr	
			585					590					595			
ggc	aca	cca	cta	gaa	aac	aaa	gtg	gaa	gag	ttt	gta	aat	ctc	gtg	cgc	1939
Gly	Thr	Pro	Leu	Glu	Asn	Lys	Val	Glu	Glu	Phe	Val	Asn	Leu	Val	Arg	
		600					605					610				
tac	atc	caa	ccg	gag	ctg	atc	acc	cgt	ggc	atg	tcc	aaa	atg	cag	gcc	1987
Tyr	Ile	Gln	Pro	Glu	Leu	Ile	Thr	Arg	Gly	Met	Ser	Lys	Met	Gln	Ala	
	615					620					625					
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Glu	Asn	Phe	Arg	Glu	Arg	Ile	Ala	Pro	Ala	Tyr	Leu	Arg	Arg	Asn	Gln	
630					635					640					645	
gct	gat	gtg	ctt	gac	gaa	ctc	cca	gag	cgc	acc	gac	tcc	atc	gac	tgg	2083
Ala	Asp	Val	Leu	Asp	Glu	Leu	Pro	Glu	Arg	Thr	Asp	Ser	Ile	Asp	Trp	
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atc	gac	ctc	acc	cca	gaa	gac	cgc	agc	gcc	tac	gac	gac	caa	gtc	cgc	2131
Ile	Asp	Leu	Thr	Pro	Glu	Asp	Arg	Ser	Ala	Tyr	Asp	Asp	Gln	Val	Arg	
			665					670					675			
caa	ggc	agc	tgg	atg	ggc	atg	cgc	cgc	tcc	gcc	atg	ctc	tca	cca	aca	2179
Gln	Gly	Ser	Trp	Met	Gly	Met	Arg	Arg	Ser	Ala	Met	Leu	Ser	Pro	Thr	
		680					685					690				
cca	cgc	cta	act	tcc	gca	aaa	atg	caa	cgc	atc	cta	gaa	ctc	ttc	gaa	2227
Pro	Arg	Leu	Thr	Ser	Ala	Lys	Met	Gln	Arg	Ile	Leu	Glu	Leu	Phe	Glu	

695	700	705	
gaa gca gaa gaa cac ggc cgc aaa gcc ctc atc ttc acc tac ttc ctc			2275
Glu Ala Glu Glu His Gly Arg Lys Ala Leu Ile Phe Thr Tyr Phe Leu			
710	715	720	725
gac gtc ctc gac gaa ctg gaa aag cat cta ggc gag cgc gtc atc ggc			2323
Asp Val Leu Asp Glu Leu Glu Lys His Leu Gly Glu Arg Val Ile Gly			
	730	735	740
cgc att tcc ggc gac gtg cca gcc acc aag cgc caa ttg ctt gtc gac			2371
Arg Ile Ser Gly Asp Val Pro Ala Thr Lys Arg Gln Leu Leu Val Asp			
	745	750	755
gcc ctg tcc cac tcc aaa ccc gga tcc gcc ctc att gcc caa atc acc			2419
Ala Leu Ser His Ser Lys Pro Gly Ser Ala Leu Ile Ala Gln Ile Thr			
	760	765	770
gcc ggg gga gta ggc cta aac atc caa tcc gcg agc cta tgc att att			2467
Ala Gly Gly Val Gly Leu Asn Ile Gln Ser Ala Ser Leu Cys Ile Ile			
	775	780	785
tgt gaa cct caa gta aag cca acc atc gaa cag cag gcc gtc gcc cga			2515
Cys Glu Pro Gln Val Lys Pro Thr Ile Glu Gln Gln Ala Val Ala Arg			
	795	800	805
gtc cac cgc atg ggc caa acc gcc acc gtc caa gtc cac cga ctc atc			2563
Val His Arg Met Gly Gln Thr Ala Thr Val Gln Val His Arg Leu Ile			
	810	815	820
ggc gac gaa acc gca gac gaa cgc atg cta gaa atc ctg gca ggc aaa			2611
Gly Asp Glu Thr Ala Asp Glu Arg Met Leu Glu Ile Leu Ala Gly Lys			
	825	830	835
act cac gtc ttc gac gtc tac gcc cgg cta tct gaa acc gca gag att			2659
Thr His Val Phe Asp Val Tyr Ala Arg Leu Ser Glu Thr Ala Glu Ile			
	840	845	850
cca gat gct gtg gat atc act gaa tca cag ctg gca gca cgg gtt att			2707
Pro Asp Ala Val Asp Ile Thr Glu Ser Gln Leu Ala Ala Arg Val Ile			
	855	860	865
gat gag gag cgt gca cgg tta ggg ctt act gaa tcc act ggc cct aaa			2755
Asp Glu Glu Arg Ala Arg Leu Gly Leu Thr Glu Ser Thr Gly Pro Lys			
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<210> 38

<211> 892

<212> PRT

<213> Corynebacterium glutamicum

<400> 38

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Leu	Arg	Leu	Leu	Lys	Thr	Pro	Gly	Thr	Ala	Thr	Val	Gly	Asp	Asn	Gly		
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Thr	Leu	Gly	Thr	Asp	Thr	Tyr	Leu	Ile	Pro	Ser	Arg	Asn	Ile	Thr	Trp		
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Pro	Asp	Asn	Leu	Tyr	Val	Asn	Val	Phe	Leu	Asp	Gly	Met	Asn	Ala	Glu		
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Ala	Thr	Leu	Thr	Asp	Tyr	Val	Ala	Ser	Val	Ala	Ser	Ile	Pro	Arg	Leu		
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Cys	Gln	Ile	Ile	Asn	Glu	Gly	Gln	Gly	Gly	Met	Phe	Arg	Arg	Leu	Phe		
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Asn	Pro	Thr	Lys	Val	Gln	Ala	Gly	Asp	Gln	Ala	Val	Phe	Asp	Leu	Met		
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Val	Lys	Leu	Asp	Glu	Ile	Ser	Ser	Thr	Thr	His	Glu	Val	Ser	Arg	Met		
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145					150					155					160		
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Gln	Gln	Val	Leu	Ala	Ser	Ala	Leu	Gly	Ile	Ala	Gly	Phe	Gly	Ala	Glu		
			180					185					190				
Pro	Trp	Asp	Gly	His	Thr	Leu	Ala	Gln	Ala	Arg	Arg	Val	Val	Gln	Arg		
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Tyr	Ala	Gln	Asp	Pro	Asn	Ser	Glu	Tyr	Arg	Leu	Lys	Ser	Glu	Ala	Glu		
210						215					220						
Lys	His	Leu	Thr	Ser	Ile	Asn	Glu	Leu	Arg	Val	Gln	Ile	Leu	Leu	Glu		
225					230					235					240		
Gln	Leu	Pro	Val	Asp	Ala	Leu	Arg	Met	Ala	Thr	Asp	His	Arg	Leu	Arg		
			245					250					255				
Phe	Gly	Ser	Leu	Asp	Ser	Ile	His	Val	Ala	Thr	Val	Ala	Asp	Val	Leu		
			260					265					270				
Lys	Thr	His	Thr	Ser	Ile	Leu	Thr	Thr	Val	Gln	Gly	Ile	Gly	Ala	Gln		
		275					280					285					
Thr	Ala	Gly	Arg	Met	Lys	Ala	Ala	Ala	Glu	Thr	Leu	Lys	Gln	Glu	Ala		
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Leu	Arg	Arg	Gln	Asn	Thr	Ser	Ile	Gly	Asp	Glu	Pro	Thr	Gln	Pro	Ala		
305					310					315					320		
Met	Arg	Leu	Ile	Asn	Val	Leu	Ala	Arg	Phe	Asp	Gln	Thr	Glu	Thr	Ile		
				325					330					335			
Thr	Pro	Glu	Glu	Arg	Ala	Arg	Arg	Thr	Arg	Val	Ile	Asp	Tyr	Val	Glu		
			340					345					350				

His Ile Pro Pro Ser Leu Asp Pro Tyr Ile Val Ile Asn Pro Ala Thr
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 Pro Glu Phe Asn Asn Phe Thr Asp Asp Leu Arg Trp Ile Asp Ala Asn
 370 375 380
 Pro Asn Leu Phe His Pro Gln Thr Ile Thr Thr Pro Pro Ala Asp Ile
 385 390 395 400
 Trp Asp Asp Tyr Ile Ser Arg Pro Ala His Tyr Gln Gly Leu Leu Ala
 405 410 415
 Thr Leu Leu Gly Arg Asp Ile Glu Gly Ala Asp Glu Leu Leu Asp Ala
 420 425 430
 Thr Thr Leu Gln Lys Ile Arg Asp Leu Thr Leu Asp Lys Thr His Leu
 435 440 445
 Thr Asp Leu His Leu Arg Gly Tyr Gln Ser Phe Gly Ala Arg Phe Ala
 450 455 460
 Ile Ile Gln Lys Lys Thr Leu Leu Gly Asp Asp Met Gly Leu Gly Lys
 465 470 475 480
 Thr Val Gln Ala Leu Ser Ala Ala Ala His Leu Ala Ala Thr Glu Lys
 485 490 495
 Asp Phe Arg Thr Leu Val Val Val Pro Ala Ser Val Ile Val Asn Trp
 500 505 510
 Thr Arg Glu Cys Lys Arg Phe Leu Asn Leu Pro Val Phe Ile Ala His
 515 520 525
 Gly Asp Asn Lys Gln Asp Ala Ile Asn Ala Trp Ser Asn Thr Asn Gly
 530 535 540
 Ile Ala Ile Cys Thr Tyr Asp Gly Val Arg Thr Met Asp Ile Pro Ala
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 Pro Gly Leu Val Ile Ala Asp Glu Ala His Leu Ile Lys Asn Pro Ser
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 Thr Lys Arg Thr Gln Ala Leu Arg Lys Leu Ile Asp Ala Ala Pro Tyr
 580 585 590
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 Val Asn Leu Val Arg Tyr Ile Gln Pro Glu Leu Ile Thr Arg Gly Met
 610 615 620
 Ser Lys Met Gln Ala Glu Asn Phe Arg Glu Arg Ile Ala Pro Ala Tyr
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 645 650 655
 Asp Ser Ile Asp Trp Ile Asp Leu Thr Pro Glu Asp Arg Ser Ala Tyr
 660 665 670

Asp Asp Gln Val Arg Gln Gly Ser Trp Met Gly Met Arg Arg Ser Ala
 675 680 685
 Met Leu Ser Pro Thr Pro Arg Leu Thr Ser Ala Lys Met Gln Arg Ile
 690 695 700
 Leu Glu Leu Phe Glu Glu Ala Glu Glu His Gly Arg Lys Ala Leu Ile
 705 710 715 720
 Phe Thr Tyr Phe Leu Asp Val Leu Asp Glu Leu Glu Lys His Leu Gly
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 Glu Arg Val Ile Gly Arg Ile Ser Gly Asp Val Pro Ala Thr Lys Arg
 740 745 750
 Gln Leu Leu Val Asp Ala Leu Ser His Ser Lys Pro Gly Ser Ala Leu
 755 760 765
 Ile Ala Gln Ile Thr Ala Gly Gly Val Gly Leu Asn Ile Gln Ser Ala
 770 775 780
 Ser Leu Cys Ile Ile Cys Glu Pro Gln Val Lys Pro Thr Ile Glu Gln
 785 790 795 800
 Gln Ala Val Ala Arg Val His Arg Met Gly Gln Thr Ala Thr Val Gln
 805 810 815
 Val His Arg Leu Ile Gly Asp Glu Thr Ala Asp Glu Arg Met Leu Glu
 820 825 830
 Ile Leu Ala Gly Lys Thr His Val Phe Asp Val Tyr Ala Arg Leu Ser
 835 840 845
 Glu Thr Ala Glu Ile Pro Asp Ala Val Asp Ile Thr Glu Ser Gln Leu
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<211> 731

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(708)

<223> FRXA01797

<400> 39

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Met Leu Ser Pro Thr Pro Arg Leu Thr Ser Ala Lys Met Gln Arg Ile
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Leu Glu Leu Phe Glu Glu Ala Glu Glu His Gly Arg Lys Ala Leu Ile
      50              55              60

ttc acc tac ttc ctc gac gtc ctc gac gaa ctg gaa aag cat cta ggc 240
Phe Thr Tyr Phe Leu Asp Val Leu Asp Glu Leu Glu Lys His Leu Gly
      65              70              75              80

gag cgc gtc atc ggc cgc att tcc ggc gac gtg cca gcc acc aag cgc 288
Glu Arg Val Ile Gly Arg Ile Ser Gly Asp Val Pro Ala Thr Lys Arg
      85              90              95

caa ttg ctt gtc gac gcc ctg tcc cac tcc aaa ccc gga tcc gcc ctc 336
Gln Leu Leu Val Asp Ala Leu Ser His Ser Lys Pro Gly Ser Ala Leu
      100              105              110

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Ile Ala Gln Ile Thr Ala Gly Gly Val Gly Leu Asn Ile Gln Ser Ala
      115              120              125

agc cta tgc att att tgt gaa cct caa gta aag cca acc atc gaa cag 432
Ser Leu Cys Ile Ile Cys Glu Pro Gln Val Lys Pro Thr Ile Glu Gln
      130              135              140

cag gcc gtc gcc cga gtc cac cgc atg ggc caa acc gcc acc gtc caa 480
Gln Ala Val Ala Arg Val His Arg Met Gly Gln Thr Ala Thr Val Gln
      145              150              155              160

gtc cac cga ctc atc ggc gac gaa acc gca gac gaa cgc atg cta gaa 528
Val His Arg Leu Ile Gly Asp Glu Thr Ala Asp Glu Arg Met Leu Glu
      165              170              175

atc ctg gca ggc aaa act cac gtc ttc gac gtc tac gcc cgg cta tct 576
Ile Leu Ala Gly Lys Thr His Val Phe Asp Val Tyr Ala Arg Leu Ser
      180              185              190

gaa acc gca gag att cca gat gct gtg gat atc act gaa tca cag ctg 624
Glu Thr Ala Glu Ile Pro Asp Ala Val Asp Ile Thr Glu Ser Gln Leu
      195              200              205

gca gca cgg gtt att gat gag gag cgt gca cgg tta ggg ctt act gaa 672
Ala Ala Arg Val Ile Asp Glu Glu Arg Ala Arg Leu Gly Leu Thr Glu
      210              215              220

tcc act ggc cct aaa gat gaa gaa acg gcc tta agc tagttgccta 718
Ser Thr Gly Pro Lys Asp Glu Glu Thr Ala Leu Ser
      225              230              235

aggccggaat taa 731

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<210> 40

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 40

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Asp Asp Gln Val Arg Gln Gly Ser Trp Met Gly Met Arg Arg Ser Ala
 20 25 30

Met Leu Ser Pro Thr Pro Arg Leu Thr Ser Ala Lys Met Gln Arg Ile
 35 40 45

Leu Glu Leu Phe Glu Glu Ala Glu Glu His Gly Arg Lys Ala Leu Ile
 50 55 60

Phe Thr Tyr Phe Leu Asp Val Leu Asp Glu Leu Glu Lys His Leu Gly
 65 70 75 80

Glu Arg Val Ile Gly Arg Ile Ser Gly Asp Val Pro Ala Thr Lys Arg
 85 90 95

Gln Leu Leu Val Asp Ala Leu Ser His Ser Lys Pro Gly Ser Ala Leu
 100 105 110

Ile Ala Gln Ile Thr Ala Gly Gly Val Gly Leu Asn Ile Gln Ser Ala
 115 120 125

Ser Leu Cys Ile Ile Cys Glu Pro Gln Val Lys Pro Thr Ile Glu Gln
 130 135 140

Gln Ala Val Ala Arg Val His Arg Met Gly Gln Thr Ala Thr Val Gln
 145 150 155 160

Val His Arg Leu Ile Gly Asp Glu Thr Ala Asp Glu Arg Met Leu Glu
 165 170 175

Ile Leu Ala Gly Lys Thr His Val Phe Asp Val Tyr Ala Arg Leu Ser
 180 185 190

Glu Thr Ala Glu Ile Pro Asp Ala Val Asp Ile Thr Glu Ser Gln Leu
 195 200 205

Ala Ala Arg Val Ile Asp Glu Glu Arg Ala Arg Leu Gly Leu Thr Glu
 210 215 220

Ser Thr Gly Pro Lys Asp Glu Glu Thr Ala Leu Ser
 225 230 235

<210> 41

<211> 1299

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1276)

<223> RXN01030

<400> 41

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	Met 1	Thr	Ser	Thr	Thr 5	
caa cct ggc aca aca cct gag ctc agc gca gac act cat tct gag ccc 163						
Gln Pro Gly Thr Thr Pro Glu Leu Ser Ala Asp Thr His Ser Glu Pro						
10 15 20						
tgg gat gtc gtc atc gaa aac acc ctt gaa cct ttt caa aaa gtc gtt 211						
Trp Asp Val Val Ile Glu Asn Thr Leu Glu Pro Phe Gln Lys Val Val						
25 30 35						
cgt caa ttt att att gac cgc ccc tat tcc ggc att ttc ctc acc atg 259						
Arg Gln Phe Ile Ile Asp Arg Pro Tyr Ser Gly Ile Phe Leu Thr Met						
40 45 50						
ggc ggc ggc aaa aca ctc act acc ctc tcc gca ttg acc tat atc cag 307						
Gly Gly Gly Lys Thr Leu Thr Thr Leu Ser Ala Leu Thr Tyr Ile Gln						
55 60 65						
cca cct gga cac att ctg gtt gtc gcg cct cta aat atc tct cga ctc 355						
Pro Pro Gly His Ile Leu Val Val Ala Pro Leu Asn Ile Ser Arg Leu						
70 75 80 85						
acc tgg ccc gaa gag gtt cgc aag tgg aat atc cct gtt aac gca atc 403						
Thr Trp Pro Glu Glu Val Arg Lys Trp Asn Ile Pro Val Asn Ala Ile						
90 95 100						
tgc ctg atc acc aat gag cgc ggc acc aaa ctc acc cgc gcc aaa cgc 451						
Ser Leu Ile Thr Asn Glu Arg Gly Thr Lys Leu Thr Arg Ala Lys Arg						
105 110 115						
ctc aaa ctc tat gag gaa aca gcg acc aca cca cca acg ctg tat tac 499						
Leu Lys Leu Tyr Glu Glu Thr Ala Thr Thr Pro Pro Thr Leu Tyr Tyr						
120 125 130						
atc acc att aat ctg ctc gaa gat att gtc aat tac ttt ggt gat agg 547						
Ile Thr Ile Asn Leu Leu Glu Asp Ile Val Asn Tyr Phe Gly Asp Arg						
135 140 145						
tgg ccg ttt tgg aca gtc att att gat gag tca cag aca atc tct gat 595						
Trp Pro Phe Trp Thr Val Ile Ile Asp Glu Ser Gln Thr Ile Ser Asp						
150 155 160 165						
ata tcc tcc aag cgc act aga gcg ctc ttt tct gtg cga ccc tat atc 643						
Ile Ser Ser Lys Arg Thr Arg Ala Leu Phe Ser Val Arg Pro Tyr Ile						
170 175 180						
ggc aga cta att ctg ctc acc gga acc ccc agc gcc aac aag ttc gac 691						
Gly Arg Leu Ile Leu Leu Thr Gly Thr Pro Ser Ala Asn Lys Phe Asp						
185 190 195						
tcc att tac gcc caa gtc gca gtg cta gat tat ggt gcc agc ctg ggt 739						
Ser Ile Tyr Ala Gln Val Ala Val Leu Asp Tyr Gly Ala Ser Leu Gly						
200 205 210						
gac aac atc gac gta ttc cga gcc aga tgg tgt gcg ccc gac att att 787						
Asp Asn Ile Asp Val Phe Arg Ala Arg Trp Cys Ala Pro Asp Ile Ile						
215 220 225						
acc gat aaa caa gtg cgt cgc tgg aag ccg gct aac aag cag gct gaa 835						
Thr Asp Lys Gln Val Arg Arg Trp Lys Pro Ala Asn Lys Gln Ala Glu						

230	235	240	245	
gca gag gtg tac cgc act att agc cac ctg gtc atg tct gcc gtc aac				883
Ala Glu Val Tyr Arg Thr Ile Ser His Leu Val Met Ser Ala Val Asn	250	255	260	
acg gat att aag ctg cca ccg ctg cat ttt gtt gat cac gag gta cac				931
Thr Asp Ile Lys Leu Pro Pro Leu His Phe Val Asp His Glu Val His	265	270	275	
atg agc gac gat gag cac cgc gac tac gag ctc ttc aaa aag gac gcg				979
Met Ser Asp Asp Glu His Arg Asp Tyr Glu Leu Phe Lys Lys Asp Ala	280	285	290	
gtg ctt gct gca ttg ctc gat atg gct gaa gag aat gag ggt ggc gaa				1027
Val Leu Ala Ala Leu Leu Asp Met Ala Glu Glu Asn Glu Gly Gly Glu	295	300	305	
ggc gct gat gac act gac gct gct gat tca gcg aca acg acc cca cct				1075
Gly Ala Asp Asp Thr Asp Ala Ala Asp Ser Ala Thr Thr Thr Pro Pro	310	315	320	325
gcg tca tca cag cca aca aac cct gcc atc ccc gct gga ctg ctt cag				1123
Ala Ser Ser Gln Pro Thr Asn Pro Ala Ile Pro Ala Gly Leu Leu Gln	330	335	340	
gca ata caa caa acc cag gac acc aat ggt cgc gcc atc gcg cct gtg				1171
Ala Ile Gln Gln Thr Gln Asp Thr Asn Gly Arg Ala Ile Ala Pro Val	345	350	355	
acc aca gct gaa ctt gat cat ttt gat gat ctg cca gta cag cgc caa				1219
Thr Thr Ala Glu Leu Asp His Phe Asp Asp Leu Pro Val Gln Arg Gln	360	365	370	
gaa gat ctt ggc acc tta gtt gtt atc tct gct gtt cac gca agc gac				1267
Glu Asp Leu Gly Thr Leu Val Val Ile Ser Ala Val His Ala Ser Asp	375	380	385	
tct gcg gca tgaaactgct gcaatacgca ggt				1299
Ser Ala Ala				
390				

<210> 42

<211> 392

<212> PRT

<213> Corynebacterium glutamicum

<400> 42

Met	Thr	Ser	Thr	Thr	Gln	Pro	Gly	Thr	Thr	Pro	Glu	Leu	Ser	Ala	Asp
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			20					25					30		

Phe	Gln	Lys	Val	Val	Arg	Gln	Phe	Ile	Ile	Asp	Arg	Pro	Tyr	Ser	Gly
		35					40					45			

Ile	Phe	Leu	Thr	Met	Gly	Gly	Gly	Lys	Thr	Leu	Thr	Leu	Ser	Ala
	50					55				60				

Leu Thr Tyr Ile Gln Pro Pro Gly His Ile Leu Val Val Ala Pro Leu
 65 70 75 80
 Asn Ile Ser Arg Leu Thr Trp Pro Glu Glu Val Arg Lys Trp Asn Ile
 85 90 95
 Pro Val Asn Ala Ile Ser Leu Ile Thr Asn Glu Arg Gly Thr Lys Leu
 100 105 110
 Thr Arg Ala Lys Arg Leu Lys Leu Tyr Glu Glu Thr Ala Thr Thr Pro
 115 120 125
 Pro Thr Leu Tyr Tyr Ile Thr Ile Asn Leu Leu Glu Asp Ile Val Asn
 130 135 140
 Tyr Phe Gly Asp Arg Trp Pro Phe Trp Thr Val Ile Ile Asp Glu Ser
 145 150 155 160
 Gln Thr Ile Ser Asp Ile Ser Ser Lys Arg Thr Arg Ala Leu Phe Ser
 165 170 175
 Val Arg Pro Tyr Ile Gly Arg Leu Ile Leu Leu Thr Gly Thr Pro Ser
 180 185 190
 Ala Asn Lys Phe Asp Ser Ile Tyr Ala Gln Val Ala Val Leu Asp Tyr
 195 200 205
 Gly Ala Ser Leu Gly Asp Asn Ile Asp Val Phe Arg Ala Arg Trp Cys
 210 215 220
 Ala Pro Asp Ile Ile Thr Asp Lys Gln Val Arg Arg Trp Lys Pro Ala
 225 230 235 240
 Asn Lys Gln Ala Glu Ala Glu Val Tyr Arg Thr Ile Ser His Leu Val
 245 250 255
 Met Ser Ala Val Asn Thr Asp Ile Lys Leu Pro Pro Leu His Phe Val
 260 265 270
 Asp His Glu Val His Met Ser Asp Asp Glu His Arg Asp Tyr Glu Leu
 275 280 285
 Phe Lys Lys Asp Ala Val Leu Ala Ala Leu Leu Asp Met Ala Glu Glu
 290 295 300
 Asn Glu Gly Gly Glu Gly Ala Asp Asp Thr Asp Ala Ala Asp Ser Ala
 305 310 315 320
 Thr Thr Thr Pro Pro Ala Ser Ser Gln Pro Thr Asn Pro Ala Ile Pro
 325 330 335
 Ala Gly Leu Leu Gln Ala Ile Gln Gln Thr Gln Asp Thr Asn Gly Arg
 340 345 350
 Ala Ile Ala Pro Val Thr Thr Ala Glu Leu Asp His Phe Asp Asp Leu
 355 360 365
 Pro Val Gln Arg Gln Glu Asp Leu Gly Thr Leu Val Val Ile Ser Ala
 370 375 380
 Val His Ala Ser Asp Ser Ala Ala

385

390

<210> 43
 <211> 1299
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1276)
 <223> FRXA01030

<400> 43

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gtattaatcc cctctttgtg cagcatagga gactactgct atg acc tca aca acc 115
               Met Thr Ser Thr Thr
               1               5

caa cct ggc aca aca cct gag ctc agc gca gac act cat tct gag ccc 163
Gln Pro Gly Thr Thr Pro Glu Leu Ser Ala Asp Thr His Ser Glu Pro
               10               15               20

tgg gat gtc gtc atc gaa aac acc ctt gaa cct ttt caa aaa gtc gtt 211
Trp Asp Val Val Ile Glu Asn Thr Leu Glu Pro Phe Gln Lys Val Val
               25               30               35

cgt caa ttt att att gac cgc ccc tat tcc ggc att ttc ctc acc atg 259
Arg Gln Phe Ile Ile Asp Arg Pro Tyr Ser Gly Ile Phe Leu Thr Met
               40               45               50

ggg ggc ggc aaa aca ctc act acc ctc tcc gca ttg acc tat atc cag 307
Gly Gly Gly Lys Thr Leu Thr Thr Leu Ser Ala Leu Thr Tyr Ile Gln
               55               60               65

cca cct gga cac att ctg gtt gtc gcg cct cta aat atc tct cga ctc 355
Pro Pro Gly His Ile Leu Val Val Ala Pro Leu Asn Ile Ser Arg Leu
               70               75               80               85

acc tgg ccc gaa gag gtt cgc aag tgg aat atc cct gtt aac gca atc 403
Thr Trp Pro Glu Glu Val Arg Lys Trp Asn Ile Pro Val Asn Ala Ile
               90               95               100

tcg ctg atc acc aat gag cgc ggc acc aaa ctc acc cgc gcc aaa cgc 451
Ser Leu Ile Thr Asn Glu Arg Gly Thr Lys Leu Thr Arg Ala Lys Arg
               105               110               115

ctc aaa ctc tat gag gaa aca gcg acc aca cca cca acg ctg tat tac 499
Leu Lys Leu Tyr Glu Glu Thr Ala Thr Thr Pro Pro Thr Leu Tyr Tyr
               120               125               130

atc acc att aat ctg ctc gaa gat att gtc aat tac ttt ggt gat agg 547
Ile Thr Ile Asn Leu Leu Glu Asp Ile Val Asn Tyr Phe Gly Asp Arg
               135               140               145

tgg ccg ttt tgg aca gtc att att gat gag tca cag aca atc tct gat 595
Trp Pro Phe Trp Thr Val Ile Ile Asp Glu Ser Gln Thr Ile Ser Asp
               150               155               160               165

ata tcc tcc aag cgc act aga gcg ctc ttt tct gtg cga ccc tat atc 643

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				170					175					180		
ggc	aga	cta	att	ctg	ctc	acc	gga	acc	ccc	agc	gcc	aac	aag	ttc	gac	691
Gly	Arg	Leu	Ile	Leu	Leu	Thr	Gly	Thr	Pro	Ser	Ala	Asn	Lys	Phe	Asp	
			185					190					195			
tcc	att	tac	gcc	caa	gtc	gca	gtg	cta	gat	tat	ggg	gcc	agc	ctg	ggg	739
Ser	Ile	Tyr	Ala	Gln	Val	Ala	Val	Leu	Asp	Tyr	Gly	Ala	Ser	Leu	Gly	
		200					205					210				
gac	aac	atc	gac	gta	ttc	cga	gcc	aga	tgg	tgt	gcg	ccc	gac	att	att	787
Asp	Asn	Ile	Asp	Val	Phe	Arg	Ala	Arg	Trp	Cys	Ala	Pro	Asp	Ile	Ile	
	215					220					225					
acc	gat	aaa	caa	gtg	cgt	cgc	tgg	aag	ccg	gct	aac	aag	cag	gct	gaa	835
Thr	Asp	Lys	Gln	Val	Arg	Arg	Trp	Lys	Pro	Ala	Asn	Lys	Gln	Ala	Glu	
230					235					240					245	
gca	gag	gtg	tac	cgc	act	att	agc	cac	ctg	gtc	atg	tct	gcc	gtc	aac	883
Ala	Glu	Val	Tyr	Arg	Thr	Ile	Ser	His	Leu	Val	Met	Ser	Ala	Val	Asn	
			250						255					260		
acg	gat	att	aag	ctg	cca	ccg	ctg	cat	ttt	gtt	gat	cac	gag	gta	cac	931
Thr	Asp	Ile	Lys	Leu	Pro	Pro	Leu	His	Phe	Val	Asp	His	Glu	Val	His	
			265					270					275			
atg	agc	gac	gat	gag	cac	cgc	gac	tac	gag	ctc	ttc	aaa	aag	gac	gcg	979
Met	Ser	Asp	Asp	Glu	His	Arg	Asp	Tyr	Glu	Leu	Phe	Lys	Lys	Asp	Ala	
		280					285					290				
gtg	ctt	gct	gca	ttg	ctc	gat	atg	gct	gaa	gag	aat	gag	ggg	ggc	gaa	1027
Val	Leu	Ala	Ala	Leu	Leu	Asp	Met	Ala	Glu	Glu	Asn	Glu	Gly	Gly	Glu	
	295					300					305					
ggc	gct	gat	gac	act	gac	gct	gct	gat	tca	gcg	aca	acg	acc	cca	cct	1075
Gly	Ala	Asp	Asp	Thr	Asp	Ala	Ala	Asp	Ser	Ala	Thr	Thr	Thr	Pro	Pro	
310					315					320					325	
gcg	tca	tca	cag	cca	aca	aac	cct	gcc	atc	ccc	gct	gga	ctg	ctt	cag	1123
Ala	Ser	Ser	Gln	Pro	Thr	Asn	Pro	Ala	Ile	Pro	Ala	Gly	Leu	Leu	Gln	
			330					335						340		
gca	ata	caa	caa	acc	cag	gac	acc	aat	ggg	cgc	gcc	atc	gcg	cct	gtg	1171
Ala	Ile	Gln	Gln	Thr	Gln	Asp	Thr	Asn	Gly	Arg	Ala	Ile	Ala	Pro	Val	
			345					350					355			
acc	aca	gct	gaa	ctt	gat	cat	ttt	gat	gat	ctg	cca	gta	cag	cgc	caa	1219
Thr	Thr	Ala	Glu	Leu	Asp	His	Phe	Asp	Asp	Leu	Pro	Val	Gln	Arg	Gln	
		360					365					370				
gaa	gat	ctt	ggc	acc	tta	gtt	gtt	atc	tct	gct	gtt	cac	gca	agc	gac	1267
Glu	Asp	Leu	Gly	Thr	Leu	Val	Val	Ile	Ser	Ala	Val	His	Ala	Ser	Asp	
	375					380					385					
tct	gcg	gca	tgaaactgct	gcaatacgca	ggg											1299
Ser	Ala	Ala														
390																

<210> 44

<211> 392

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 44

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Met Thr Ser Thr Thr Gln Pro Gly Thr Thr Pro Glu Leu Ser Ala Asp
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Thr His Ser Glu Pro Trp Asp Val Val Ile Glu Asn Thr Leu Glu Pro
      20              25              30

Phe Gln Lys Val Val Arg Gln Phe Ile Ile Asp Arg Pro Tyr Ser Gly
      35              40              45

Ile Phe Leu Thr Met Gly Gly Gly Lys Thr Leu Thr Thr Leu Ser Ala
 50              55              60

Leu Thr Tyr Ile Gln Pro Pro Gly His Ile Leu Val Val Ala Pro Leu
 65              70              75              80

Asn Ile Ser Arg Leu Thr Trp Pro Glu Glu Val Arg Lys Trp Asn Ile
      85              90              95

Pro Val Asn Ala Ile Ser Leu Ile Thr Asn Glu Arg Gly Thr Lys Leu
      100              105              110

Thr Arg Ala Lys Arg Leu Lys Leu Tyr Glu Glu Thr Ala Thr Thr Pro
      115              120              125

Pro Thr Leu Tyr Tyr Ile Thr Ile Asn Leu Leu Glu Asp Ile Val Asn
      130              135              140

Tyr Phe Gly Asp Arg Trp Pro Phe Trp Thr Val Ile Ile Asp Glu Ser
      145              150              155              160

Gln Thr Ile Ser Asp Ile Ser Ser Lys Arg Thr Arg Ala Leu Phe Ser
      165              170              175

Val Arg Pro Tyr Ile Gly Arg Leu Ile Leu Leu Thr Gly Thr Pro Ser
      180              185              190

Ala Asn Lys Phe Asp Ser Ile Tyr Ala Gln Val Ala Val Leu Asp Tyr
      195              200              205

Gly Ala Ser Leu Gly Asp Asn Ile Asp Val Phe Arg Ala Arg Trp Cys
      210              215              220

Ala Pro Asp Ile Ile Thr Asp Lys Gln Val Arg Arg Trp Lys Pro Ala
      225              230              235              240

Asn Lys Gln Ala Glu Ala Glu Val Tyr Arg Thr Ile Ser His Leu Val
      245              250              255

Met Ser Ala Val Asn Thr Asp Ile Lys Leu Pro Pro Leu His Phe Val
      260              265              270

Asp His Glu Val His Met Ser Asp Asp Glu His Arg Asp Tyr Glu Leu
      275              280              285

Phe Lys Lys Asp Ala Val Leu Ala Ala Leu Leu Asp Met Ala Glu Glu
      290              295              300

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Asn Glu Gly Gly Glu Gly Ala Asp Asp Thr Asp Ala Ala Asp Ser Ala
 305 310 315 320
 Thr Thr Thr Pro Pro Ala Ser Ser Gln Pro Thr Asn Pro Ala Ile Pro
 325 330 335
 Ala Gly Leu Leu Gln Ala Ile Gln Gln Thr Gln Asp Thr Asn Gly Arg
 340 345 350
 Ala Ile Ala Pro Val Thr Thr Ala Glu Leu Asp His Phe Asp Asp Leu
 355 360 365
 Pro Val Gln Arg Gln Glu Asp Leu Gly Thr Leu Val Val Ile Ser Ala
 370 375 380
 Val His Ala Ser Asp Ser Ala Ala
 385 390

<210> 45
 <211> 720
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(697)
 <223> RXA01739

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 Val Ile Asn Leu Gln
 1 5
 gac ctc gac gag gat caa cgc atc gct gct tct gcg cct cgc gga cca 163
 Asp Leu Asp Glu Asp Gln Arg Ile Ala Ala Ser Ala Pro Arg Gly Pro
 10 15 20
 gtg tgc att ctc gcc gga gcc ggc acg ggt aaa act cga acg att act 211
 Val Cys Ile Leu Ala Gly Ala Gly Thr Gly Lys Thr Arg Thr Ile Thr
 25 30 35
 tat cgc atc gcg cat ctg att gat cag ggt ttt gtg agc ccg aat cgt 259
 Tyr Arg Ile Ala His Leu Ile Asp Gln Gly Phe Val Ser Pro Asn Arg
 40 45 50
 gtt ctt gct gtg acg ttt aca tcc cgc gcg gca ggg gag atg cgt cat 307
 Val Leu Ala Val Thr Phe Thr Ser Arg Ala Ala Gly Glu Met Arg His
 55 60 65
 cgc ttg aat ctc atg ggg atc ggt ggc gtg cag gca agg aca ttc cac 355
 Arg Leu Asn Leu Met Gly Ile Gly Gly Val Gln Ala Arg Thr Phe His
 70 75 80 85
 gca gca gcg agg aag cag ttg ttg tat ttc tgg cct cag gtg gcg ggt 403
 Ala Ala Ala Arg Lys Gln Leu Leu Tyr Phe Trp Pro Gln Val Ala Gly
 90 95 100

aat ctg ccg tgg cgc ctg ttg gat aat aag ttt caa ctt gtg ggt cgt 451
 Asn Leu Pro Trp Arg Leu Leu Asp Asn Lys Phe Gln Leu Val Gly Arg
 105 110 115
 gcg gtt cgt ggt gcg cgg ttg gaa tcg cag act gaa aaa gtt cgc gat 499
 Ala Val Arg Gly Ala Arg Leu Glu Ser Gln Thr Glu Lys Val Arg Asp
 120 125 130
 att ttg ggt gaa att gag tgg gcg aag gcg tcg ttg att aca cct gag 547
 Ile Leu Gly Glu Ile Glu Trp Ala Lys Ala Ser Leu Ile Thr Pro Glu
 135 140 145
 cag tat ccg gat cgt ttg ggt acg agg acc cct ccg gcg ccc gcg gag 595
 Gln Tyr Pro Asp Arg Leu Gly Thr Arg Thr Pro Pro Ala Pro Ala Glu
 150 155 160 165
 aaa atc gct gag gtg tat cag cga tac gaa aac atg aag gca acc cct 643
 Lys Ile Ala Glu Val Tyr Gln Arg Tyr Glu Asn Met Lys Ala Thr Pro
 170 175 180
 gag ggg atg ttg ctt gat ttc gac gat ctg ttg ctt cac acc gcc ggg 691
 Glu Gly Met Leu Leu Asp Phe Asp Asp Leu Leu Leu His Thr Ala Gly
 185 190 195
 gcg ttg tagaattccc cggcgggtggc gga 720
 Ala Leu

<210> 46

<211> 199

<212> PRT

<213> Corynebacterium glutamicum

<400> 46

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 20 25 30
 Thr Arg Thr Ile Thr Tyr Arg Ile Ala His Leu Ile Asp Gln Gly Phe
 35 40 45
 Val Ser Pro Asn Arg Val Leu Ala Val Thr Phe Thr Ser Arg Ala Ala
 50 55 60
 Gly Glu Met Arg His Arg Leu Asn Leu Met Gly Ile Gly Gly Val Gln
 65 70 75 80
 Ala Arg Thr Phe His Ala Ala Ala Arg Lys Gln Leu Leu Tyr Phe Trp
 85 90 95
 Pro Gln Val Ala Gly Asn Leu Pro Trp Arg Leu Leu Asp Asn Lys Phe
 100 105 110
 Gln Leu Val Gly Arg Ala Val Arg Gly Ala Arg Leu Glu Ser Gln Thr
 115 120 125
 Glu Lys Val Arg Asp Ile Leu Gly Glu Ile Glu Trp Ala Lys Ala Ser
 130 135 140

Leu Ile Thr Pro Glu Gln Tyr Pro Asp Arg Leu Gly Thr Arg Thr Pro
 145 150 155 160
 Pro Ala Pro Ala Glu Lys Ile Ala Glu Val Tyr Gln Arg Tyr Glu Asn
 165 170 175
 Met Lys Ala Thr Pro Glu Gly Met Leu Leu Asp Phe Asp Asp Leu Leu
 180 185 190
 Leu His Thr Ala Gly Ala Leu
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<210> 47
 <211> 1992
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1969)
 <223> RXA02359

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 Val Glu Leu Pro Ser
 1 5
 cct ggt gag gcg ctc gca cat gca ggg cac acc cca gaa gtc ctg gaa 163
 Pro Gly Glu Ala Leu Ala His Ala Gly His Thr Pro Glu Val Leu Glu
 10 15 20
 gcc gag ctc ggc att gac ccg gct gcc acc cgt att gtg ttg gaa ctt 211
 Ala Glu Leu Gly Ile Asp Pro Ala Ala Thr Arg Ile Val Leu Glu Leu
 25 30 35
 gcc tca gag gat gac atc gca gca gcg ctt cct agc agc ccg acg tgg 259
 Ala Ser Glu Asp Asp Ile Ala Ala Ala Leu Pro Ser Ser Pro Thr Trp
 40 45 50
 gaa aaa gac gca ctt atc ggc ctt gtc gcc ggt ttg agc att gaa gat 307
 Glu Lys Asp Ala Leu Ile Gly Leu Val Ala Gly Leu Ser Ile Glu Asp
 55 60 65
 atc cgc gaa tcg ctc gct atc ccc gca cct tcc aca gag ccg gat acc 355
 Ile Arg Glu Ser Leu Ala Ile Pro Ala Pro Ser Thr Glu Pro Asp Thr
 70 75 80 85
 cgc agc gaa gat acc agg ctc att gct ggg ctt aaa acc cca gca gcg 403
 Arg Ser Glu Asp Thr Arg Leu Ile Ala Gly Leu Lys Thr Pro Ala Ala
 90 95 100
 caa atg gac ttt gcc tat ttg gat acc cca aat agc aat gac ctg cgc 451
 Gln Met Asp Phe Ala Tyr Leu Asp Thr Pro Asn Ser Asn Asp Leu Arg
 105 110 115
 cgc gtt att gaa act gaa ggt ttt gat agc tgg cgc gtg tat atc gac 499
 Arg Val Ile Glu Thr Glu Gly Phe Asp Ser Trp Arg Val Tyr Ile Asp

120	125	130	
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gtt ttt ggt gga gct ggc acc ggc aaa acc gtg gtg gta gtc cac cgt Val Phe Gly Gly Ala Gly Thr Gly Lys Thr Val Val Val Val His Arg 150 155 160 165			595
gcc aac cgc ctg gtc act tct gat gga cac ctt gag acc gac gat aag Ala Asn Arg Leu Val Thr Ser Asp Gly His Leu Glu Thr Asp Asp Lys 170 175 180			643
acg cct cga gtc ctg ctc acc acc tat acc cgc ggt ttg gcc gat gcg Thr Pro Arg Val Leu Leu Thr Thr Tyr Thr Arg Gly Leu Ala Asp Ala 185 190 195			691
ttg aaa tcc tcc atg aac gcg ctt aat ccc act ttc ccc gag gca gaa Leu Lys Ser Ser Met Asn Ala Leu Asn Pro Thr Phe Pro Glu Ala Glu 200 205 210			739
aaa ccc ggt agt cct ggc ttg tgg atc agc gga att gat gcc ttg gca Lys Pro Gly Ser Pro Gly Leu Trp Ile Ser Gly Ile Asp Ala Leu Ala 215 220 225			787
aat aag gtg gtt gcg cta gca aac acc gcc gaa cgt gag gca gca acc Asn Lys Val Val Ala Leu Ala Asn Thr Ala Glu Arg Glu Ala Ala Thr 230 235 240 245			835
act gct atc ttg ggg cgt gca gcc ggc aga atc acc cca ttc atc ggc Thr Ala Ile Leu Gly Arg Ala Ala Gly Arg Ile Thr Pro Phe Ile Gly 250 255 260			883
aac ggc gaa caa gaa ttt tgg atc gac gcg atc att tcc gca gat ccc Asn Gly Glu Gln Glu Phe Trp Ile Asp Ala Ile Ile Ser Ala Asp Pro 265 270 275			931
ggc gat cta tca gaa gaa atc agc aat act gaa ttc ctc gcc caa gag Gly Asp Leu Ser Glu Glu Ile Ser Asn Thr Glu Phe Leu Ala Gln Glu 280 285 290			979
ttt gaa acc gta atc cta gcc cgc gga atc acc caa gaa aag gac tat Phe Glu Thr Val Ile Leu Ala Arg Gly Ile Thr Gln Glu Lys Asp Tyr 295 300 305			1027
ctg cgt gca cct cgt ccc ggc cgt ggt acc cca cta aac cgc gta caa Leu Arg Ala Pro Arg Pro Gly Arg Gly Thr Pro Leu Asn Arg Val Gln 310 315 320 325			1075
cgc aaa aaa gtg tgg gcg att att cag caa ttc atg act tcc tgt gcg Arg Lys Lys Val Trp Ala Ile Ile Gln Gln Phe Met Thr Ser Cys Ala 330 335 340			1123
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atc ctg gag cag cgc gcc gcc gcc ggc cag ggc cgg cta ttt gac cat Ile Leu Glu Gln Arg Ala Ala Ala Gly Gln Gly Arg Leu Phe Asp His 360 365 370			1219

gtg ctt atc gac gag gcc cag gac ttc cac gcc gga cat tgg ctc tta	1267
Val Leu Ile Asp Glu Ala Gln Asp Phe His Ala Gly His Trp Leu Leu	
375 380 385	
ctc agg gct gcg gta gcc gaa ggt ccc aat gac atc ttc ttg gct gag	1315
Leu Arg Ala Ala Val Ala Glu Gly Pro Asn Asp Ile Phe Leu Ala Glu	
390 395 400 405	
gat tca cac cag cgc atc tac ggc caa cat cat gtg cta agc cgt ttt	1363
Asp Ser His Gln Arg Ile Tyr Gly Gln His Val Leu Ser Arg Phe	
410 415 420	
ggg att tcc acc cgc ggt cgg gcg tct aag cga ctc acc ctt aac tac	1411
Gly Ile Ser Thr Arg Gly Arg Ala Ser Lys Arg Leu Thr Leu Asn Tyr	
425 430 435	
cgc acc acc gcc gaa aac ctc agt tac gca ctt ggc atg ctc acc ggt	1459
Arg Thr Thr Ala Glu Asn Leu Ser Tyr Ala Leu Gly Met Leu Thr Gly	
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Glu Trp Thr Asp Ala Glu Gly Glu Thr Asp Thr Ile Glu His Tyr Arg	
455 460 465	
tca gcg cgt aag ggc ccc aag cca cac ctc tac caa ttt gaa tct gag	1555
Ser Ala Arg Lys Gly Pro Lys Pro His Leu Tyr Gln Phe Glu Ser Glu	
470 475 480 485	
acc gac gag ttc gaa gca atc gct gag ctc atc aag gtg tgg cag gac	1603
Thr Asp Glu Phe Glu Ala Ile Ala Glu Leu Ile Lys Val Trp Gln Asp	
490 495 500	
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Arg Thr Thr Asp Val Arg Ile Gly Ile Leu Ala Arg Thr Arg Pro Leu	
505 510 515	
atc aac cgc gtg gtt aat gcg ctc tct gag cag ggc atc gat gcc gtc	1699
Ile Asn Arg Val Val Asn Ala Leu Ser Glu Gln Gly Ile Asp Ala Val	
520 525 530	
aag acg caa aat gcc gaa ctt gca gcc cac gaa act gtc agt gta atg	1747
Lys Thr Gln Asn Ala Glu Leu Ala Ala His Glu Thr Val Ser Val Met	
535 540 545	
aca atg cac gga gct aaa ggc atg gag ttt acc cat gtc atc ttg atc	1795
Thr Met His Gly Ala Lys Gly Met Glu Phe Thr His Val Ile Leu Ile	
550 555 560 565	
gga atg ggc cgt gac ctc att cct ttg caa tac acc atg caa ggt tta	1843
Gly Met Gly Arg Asp Leu Ile Pro Leu Gln Tyr Thr Met Gln Gly Leu	
570 575 580	
ggc gag gcc gag cgt aac gac gcc caa cag cgc gaa cgc tcc ttg ctc	1891
Gly Glu Ala Glu Arg Asn Asp Ala Gln Gln Arg Glu Arg Ser Leu Leu	
585 590 595	
tac gtt gca gct tct cgt gca cgt gat gcc ctt gtt ctc acc acg cat	1939
Tyr Val Ala Ala Ser Arg Ala Arg Asp Ala Leu Val Leu Thr Thr His	
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gtt 1992

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 35 40 45

Ser Ser Pro Thr Trp Glu Lys Asp Ala Leu Ile Gly Leu Val Ala Gly
 50 55 60

Leu Ser Ile Glu Asp Ile Arg Glu Ser Leu Ala Ile Pro Ala Pro Ser
 65 70 75 80

Thr Glu Pro Asp Thr Arg Ser Glu Asp Thr Arg Leu Ile Ala Gly Leu
 85 90 95

Lys Thr Pro Ala Ala Gln Met Asp Phe Ala Tyr Leu Asp Thr Pro Asn
 100 105 110

Ser Asn Asp Leu Arg Arg Val Ile Glu Thr Glu Gly Phe Asp Ser Trp
 115 120 125

Arg Val Tyr Ile Asp Pro Ser Gln Arg Ser Leu Val Thr Arg Asn Phe
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Ser Gly Ser Gly Arg Val Phe Gly Gly Ala Gly Thr Gly Lys Thr Val
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Val Val Val His Arg Ala Asn Arg Leu Val Thr Ser Asp Gly His Leu
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Glu Thr Asp Asp Lys Thr Pro Arg Val Leu Leu Thr Thr Tyr Thr Arg
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Gly Leu Ala Asp Ala Leu Lys Ser Ser Met Asn Ala Leu Asn Pro Thr
 195 200 205

Phe Pro Glu Ala Glu Lys Pro Gly Ser Pro Gly Leu Trp Ile Ser Gly
 210 215 220

Ile Asp Ala Leu Ala Asn Lys Val Val Ala Leu Ala Asn Thr Ala Glu
 225 230 235 240

Arg Glu Ala Ala Thr Thr Ala Ile Leu Gly Arg Ala Ala Gly Arg Ile
 245 250 255

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Thr Pro Phe Ile Gly Asn Gly Glu Gln Glu Phe Trp Ile Asp Ala Ile
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 Ile Ser Ala Asp Pro Gly Asp Leu Ser Glu Glu Ile Ser Asn Thr Glu
 275 280 285
 Phe Leu Ala Gln Glu Phe Glu Thr Val Ile Leu Ala Arg Gly Ile Thr
 290 295 300
 Gln Glu Lys Asp Tyr Leu Arg Ala Pro Arg Pro Gly Arg Gly Thr Pro
 305 310 315 320
 Leu Asn Arg Val Gln Arg Lys Lys Val Trp Ala Ile Ile Gln Gln Phe
 325 330 335
 Met Thr Ser Cys Ala Arg Glu Gly Lys Met Ser Trp Pro Ala Leu Ser
 340 345 350
 Ser Ile Ala Ala Asn Ile Leu Glu Gln Arg Ala Ala Ala Gly Gln Gly
 355 360 365
 Arg Leu Phe Asp His Val Leu Ile Asp Glu Ala Gln Asp Phe His Ala
 370 375 380
 Gly His Trp Leu Leu Leu Arg Ala Ala Val Ala Glu Gly Pro Asn Asp
 385 390 395 400
 Ile Phe Leu Ala Glu Asp Ser His Gln Arg Ile Tyr Gly Gln His His
 405 410 415
 Val Leu Ser Arg Phe Gly Ile Ser Thr Arg Gly Arg Ala Ser Lys Arg
 420 425 430
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 Gly Met Leu Thr Gly Glu Trp Thr Asp Ala Glu Gly Glu Thr Asp Thr
 450 455 460
 Ile Glu His Tyr Arg Ser Ala Arg Lys Gly Pro Lys Pro His Leu Tyr
 465 470 475 480
 Gln Phe Glu Ser Glu Thr Asp Glu Phe Glu Ala Ile Ala Glu Leu Ile
 485 490 495
 Lys Val Trp Gln Asp Arg Thr Thr Asp Val Arg Ile Gly Ile Leu Ala
 500 505 510
 Arg Thr Arg Pro Leu Ile Asn Arg Val Val Asn Ala Leu Ser Glu Gln
 515 520 525
 Gly Ile Asp Ala Val Lys Thr Gln Asn Ala Glu Leu Ala Ala His Glu
 530 535 540
 Thr Val Ser Val Met Thr Met His Gly Ala Lys Gly Met Glu Phe Thr
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 His Val Ile Leu Ile Gly Met Gly Arg Asp Leu Ile Pro Leu Gln Tyr
 565 570 575
 Thr Met Gln Gly Leu Gly Glu Ala Glu Arg Asn Asp Ala Gln Gln Arg

580

585

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Glu Arg Ser Leu Leu Tyr Val Ala Ala Ser Arg Ala Arg Asp Ala Leu
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 Met Ser Glu Tyr Lys
 1 5

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 Pro Pro Ile Pro Ser Asp Pro Gln Val Arg Leu Ile Lys Pro Thr Ser
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aag ctt cgt cct cgt tcg tgg gag ggc gaa gtt tcg cat tta gtt aaa 211
 Lys Leu Arg Pro Arg Ser Trp Glu Gly Glu Val Ser His Leu Val Lys
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caa ggc acc ggt ttg tgg cgg gtg act ggt gag gcg ggc tcg ggg gtg 259
 Gln Gly Thr Gly Leu Trp Arg Val Thr Gly Glu Ala Gly Ser Gly Val
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agc tcc gct gtt gtc gat act gtc ctt gaa cgc att cgc caa ggg tgg 307
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 Glu Pro Ser Ser Met Leu Val Val Ala Thr Ser Lys Glu Ala Ala Ser
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 Ser Glu Gly Pro Leu Val Arg Ser Val His Ser Val Ala Phe Ala Leu
 105 110 115

att cgt gat gcg tcg gat gat gat gtg cgg ttg att acg ggc gct gag 499
 Ile Arg Asp Ala Ser Asp Asp Asp Val Arg Leu Ile Thr Gly Ala Glu
 120 125 130

caa gat gcg gtg att cgg gag ttg ctg cgt ggt cat gct gat gat ggt 547
 Gln Asp Ala Val Ile Arg Glu Leu Leu Arg Gly His Ala Asp Asp Gly
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cgt ggg ggg tgg ccg cag gag cag cgt gag ggt ttg cgg atg gtg ggg	595
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Phe Ala Arg Gln Leu Arg Asp Phe Leu Leu Arg Ala Val Glu Arg Gly	
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Val Gly Pro Asp Glu Leu Val Glu Leu Gly Glu Arg Phe Glu Arg Ala	
185 190 195	
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Asn Trp Val Ala Ala Gly Glu Phe Leu Arg Glu Tyr Lys Gln Val Met	
200 205 210	
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Lys Leu Ser Gly Ala His Ser Phe Ser Ala Ser Glu Leu Val Thr Glu	
215 220 225	
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Ala Leu Arg Gly Pro Glu Pro Ser Val Lys Tyr Arg Gly Val Phe Ile	
230 235 240 245	
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Asp Asp Ala Gln His Leu Asp Pro Lys Ser Ala Glu Leu Val Ser Arg	
250 255 260	
ttt ttc cct gag gcg gag ttg gct gtg gtg gcg ggt gat ccg cag cag	931
Phe Phe Pro Glu Ala Glu Leu Ala Val Val Ala Gly Asp Pro Gln Gln	
265 270 275	
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Ser Val Phe Arg Phe Arg Gly Ala Asn Pro Asp Phe Leu Thr Lys Leu	
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Ser Val Asp His Glu Val Val Leu Lys Gly Arg Arg Lys Ala Ser Thr	
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Ile Ala Val Ile Val Arg Ser Ala Gly Met Ile Ala Pro Ile Trp Arg	
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Thr Leu Leu Ala Ala Gly Val Val His Ile Ser Pro Thr Asp Val	
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Val Leu Ala Glu Gln Arg Ile Val Ala Ala Met Ile Leu Gly Leu Arg	
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ttt ttg acc gat cgt gag ctg aat ttg ctc gag cgg gtg cga tct gtg	1507
Phe Leu Thr Asp Arg Glu Leu Asn Leu Leu Glu Arg Val Arg Ser Val	
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Leu Glu Ala Gly Arg Glu Ala Leu Ala Glu His Gly Ser Ile Glu Glu	
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gtg ttg tgg gcg ctg tgg tcg gcg acc gat ctg tcg aac tcg ttg tcc	1603
Val Leu Trp Ala Leu Trp Ser Ala Thr Asp Leu Ser Asn Ser Leu Ser	
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Ala Ile Ser Leu Arg Gly Gly Ala Ser Gly Ser Gln Ala Asp Arg Asp	
505 510 515	
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Leu Asp Ala Met Met Ala Leu Phe Asp Ala Ala Gly Asp Tyr Val Glu	
520 525 530	
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Arg Tyr Pro Ser Ala Gly Val Arg Ser Phe Ile Leu His Ile Ser Glu	
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Gln Glu Leu Pro Thr Gly Met Arg Glu Arg Arg Gly Ala Ile Pro Glu	
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Arg Val Ile Val Ala Glu Val Gln Glu Gly Ser Trp Pro Ser Leu Gly	
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Glu Thr Gly Thr Leu Leu Gly Gln Glu Glu Phe Val Asp Leu Val Asp	
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Ala Glu Glu Arg Arg Leu Phe Tyr Leu Ala Thr Thr Arg Ser Thr Glu 630 635 640 645	
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gac tcc gta tcg atc cgt ggt cgc atg gac cgt ttg gag cga aac aaa Asp Ser Val Ser Ile Arg Gly Arg Met Asp Arg Leu Glu Arg Asn Lys	2755

870	875	880	885	
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Ser Gly Glu Leu	Val Val Val Asp	Phe Lys Thr Gly	Lys Thr Gln Ile	
	890	895	900	
gct gca aaa gac	atg ggc gat cac	cca cag ttg ttt	gcg tat caa ttg	2851
Ala Ala Lys Asp	Met Gly Asp His	Pro Gln Leu Phe	Ala Tyr Gln Leu	
	905	910	915	
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<212> PRT

<213> Corynebacterium glutamicum

<400> 50

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Ser His Leu Val	Lys Gln Gly Thr	Gly Leu Trp Arg	Val Thr Gly Glu
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Ala Gly Ser Gly	Val Ser Ser Ala	Val Val Asp Thr	Val Leu Glu Arg
	50	55	60
Ile Arg Gln Gly	Trp Glu Pro Ser	Ser Met Leu Val	Val Ala Thr Ser
	65	70	75
Lys Glu Ala Ala	Ser Arg Leu Arg	Gln Glu Ile Ser	Glu Ser Val Ala
	85	90	95
Gln Met Asp Tyr	Val Ser Glu Gly	Pro Leu Val Arg	Ser Val His Ser
	100	105	110
Val Ala Phe Ala	Leu Ile Arg Asp	Ala Ser Asp Asp	Asp Val Arg Leu
	115	120	125
Ile Thr Gly Ala	Glu Gln Asp Ala	Val Ile Arg Glu	Leu Leu Arg Gly
	130	135	140
His Ala Asp Asp	Gly Arg Gly Gly	Trp Pro Gln Glu	Gln Arg Glu Gly
	145	150	155
Leu Arg Met Val	Gly Phe Ala Arg	Gln Leu Arg Asp	Phe Leu Leu Arg
	165	170	175
Ala Val Glu Arg	Gly Val Gly Pro	Asp Glu Leu Val	Glu Leu Gly Glu
	180	185	190
Arg Phe Glu Arg	Ala Asn Trp Val	Ala Ala Gly Glu	Phe Leu Arg Glu
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Tyr Lys Gln Val	Met Lys Leu Ser	Gly Ala His Ser	Phe Ser Ala Ser

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225					230					235					240
Arg	Gly	Val	Phe	Ile	Asp	Asp	Ala	Gln	His	Leu	Asp	Pro	Lys	Ser	Ala
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Glu	Leu	Val	Ser	Arg	Phe	Phe	Pro	Glu	Ala	Glu	Leu	Ala	Val	Val	Ala
			260					265					270		
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		275					280					285			
Phe	Leu	Thr	Lys	Leu	Ser	Val	Asp	His	Glu	Val	Val	Leu	Lys	Gly	Arg
	290						295					300			
Arg	Lys	Ala	Ser	Thr	Ser	Ile	Val	Val	Ala	Glu	Thr	Glu	Ser	Ala	His
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Ala	Pro	Ile	Trp	Arg	Thr	Leu	Leu	Ala	Ala	Gly	Val	Pro	Val	His	Ile
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Glu	Asp	Leu	Leu	Leu	Gly	Pro	Ile	Gly	Gly	Ala	Asp	Pro	Val	Thr	Leu
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Gln	Ala	Asp	Arg	Asp	Leu	Asp	Ala	Met	Met	Ala	Leu	Phe	Asp	Ala	Ala
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Gly	Asp	Tyr	Val	Glu	Arg	Tyr	Pro	Ser	Ala	Gly	Val	Arg	Ser	Phe	Ile
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Leu His Ile Ser Glu Gln Glu Leu Pro Thr Gly Met Arg Glu Arg Arg
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 Gly Ala Ile Pro Glu Ala Val Glu Val Leu Thr Ala His Ala Thr Thr
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 Gly Arg Glu Trp Lys Arg Val Ile Val Ala Glu Val Gln Glu Gly Ser
 580 585 590
 Trp Pro Ser Leu Gly Glu Thr Gly Thr Leu Leu Gly Gln Glu Glu Phe
 595 600 605
 Val Asp Leu Val Asp Glu Gly Ile Asp Pro Asp Ile Ile Ile Ser Arg
 610 615 620
 Ser Ala Glu Arg Leu Ala Glu Glu Arg Arg Leu Phe Tyr Leu Ala Thr
 625 630 635 640
 Thr Arg Ser Thr Glu Ser Leu Leu Val Thr Ala Val Asn Ser Pro Asp
 645 650 655
 Ser Asp Glu Val Arg Glu Pro Ser Arg Phe Leu Glu Leu Leu Ser Gln
 660 665 670
 Pro Ile Val Val Leu Glu Gly Glu Glu Ala Ser Ala Ile Ala Glu Pro
 675 680 685
 Glu Glu Ile Gly His Arg Leu Leu Ser Ile Pro Ala Met Val Ala Glu
 690 695 700
 Leu Arg Arg Val Val Asn Asp Pro Arg Asp Pro Arg Arg Lys Gln Ala
 705 710 715 720
 Ala Arg Gln Leu Ser Arg Leu Ala Glu Ala Gly Ile Pro Gly Ala Asn
 725 730 735
 Pro Ala Glu Trp Thr Asn Leu Arg Thr Pro Ser Thr Asp Glu Glu Leu
 740 745 750
 Ile Lys Gly Ala Val Ser Leu Ser Pro Ser Arg Ile Glu Gln Leu Leu
 755 760 765
 Asn Cys Pro Leu Arg Ala Val Leu Asp Arg Leu Asp Ser Glu Glu Glu
 770 775 780
 Thr Pro Ile Ala Met Leu Lys Gly Thr Leu Val His Ala Phe Ala Glu
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 Ala Val Ala Gly Gly Val Asp Ala Ala Leu Ala Glu Glu Lys Val Thr
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 Ser Ala Tyr Met Gln Leu Ala Asn Val Pro Ser Trp Ser Arg Glu Ser
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 Thr Glu Ile Ala Phe Arg Arg Ile Leu Ser Arg Thr Asp Thr Trp Leu
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 Lys Thr Ser Arg Ala Asp Phe Thr Glu Val Gly Thr Glu Met Asp Val
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Ser Val Thr Ile Asp Asp Ser Val Ser Ile Arg Gly Arg Met Asp Arg
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Leu Glu Arg Asn Lys Ser Gly Glu Leu Val Val Val Asp Phe Lys Thr
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 Met Ser Glu Tyr Lys
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 Pro Pro Ile Pro Ser Asp Pro Gln Val Arg Leu Ile Lys Pro Thr Ser
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aag ctt cgt cct cgt tcg tgg gag ggc gaa gtt tcg cat tta gtt aaa 211
 Lys Leu Arg Pro Arg Ser Trp Glu Gly Glu Val Ser His Leu Val Lys
 25 30 35

caa ggc acc ggt ttg tgg cgg gtg act ggt gag gcg ggc tcg ggg gtg 259
 Gln Gly Thr Gly Leu Trp Arg Val Thr Gly Glu Ala Gly Ser Gly Val
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agc tcc gct gtt gtc gat act gtc ctt gaa cgc att cgc caa ggg tgg 307
 Ser Ser Ala Val Val Asp Thr Val Leu Glu Arg Ile Arg Gln Gly Trp
 55 60 65

gag ccg tca tcg atg ttg gtt gtc gcc acg tcg aaa gag gcg gcg agt 355
 Glu Pro Ser Ser Met Leu Val Val Ala Thr Ser Lys Glu Ala Ala Ser
 70 75 80 85

cgc ttg agg caa gag atc tcg gaa tcc gta gcc cag atg gat tat gtg 403
 Arg Leu Arg Gln Glu Ile Ser Glu Ser Val Ala Gln Met Asp Tyr Val
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tcg gag ggg ccg ttg gtg cga tcg gtg cac tcg gtg gct ttc gcg ctg 451
 Ser Glu Gly Pro Leu Val Arg Ser Val His Ser Val Ala Phe Ala Leu
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Ile Arg Asp Ala Ser Asp Asp Val Arg Leu Ile Thr Gly Ala Glu	
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caa gat gcg gtg att cgg gag ttg ctg cgt ggt cat gct gat gat ggt	547
Gln Asp Ala Val Ile Arg Glu Leu Leu Arg Gly His Ala Asp Asp Gly	
135 140 145	
cgt ggg ggg tgg ccg cag gag cag cgt gag ggt ttg cgg atg gtg ggg	595
Arg Gly Gly Trp Pro Gln Glu Gln Arg Glu Gly Leu Arg Met Val Gly	
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Phe Ala Arg Gln Leu Arg Asp Phe Leu Leu Arg Ala Val Glu Arg Gly	
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Val Gly Pro Asp Glu Leu Val Glu Leu Gly Glu Arg Phe Glu Arg Ala	
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Asn Trp Val Ala Ala Gly Glu Phe Leu Arg Glu Tyr Lys Gln Val Met	
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Lys Leu Ser Gly Ala His Ser Phe Ser Ala Ser Glu Leu Val Thr Glu	
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gcg ctg cgt ggt cct gag ccg tcg gtg aag tat cgc ggt gtg ttt att	835
Ala Leu Arg Gly Pro Glu Pro Ser Val Lys Tyr Arg Gly Val Phe Ile	
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gat gat gcg cag cat ttg gat ccg aag tcg gcg gaa ctt gtg tcg cgg	883
Asp Asp Ala Gln His Leu Asp Pro Lys Ser Ala Glu Leu Val Ser Arg	
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Phe Phe Pro Glu Ala Glu Leu Ala Val Val Ala Gly Asp Pro Gln Gln	
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Ser Val Phe Arg Phe Arg Gly Ala Asn Pro Asp Phe Leu Thr Lys Leu	
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agt gtg gat cac gag gtg gtg ttg aag ggg agg agg aaa gcg tcg aca	1027
Ser Val Asp His Glu Val Val Leu Lys Gly Arg Arg Lys Ala Ser Thr	
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Asp Thr Val Arg Arg Ala His Leu Ile Asp Gly Arg Ser Trp Ser Glu	
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Ile Ala Val Ile Val Arg Ser Ala Gly Met Ile Ala Pro Ile Trp Arg	
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Ala	Leu	Thr	Glu	Ser	Leu	Asn	Ala	Ile	Glu	Leu	Glu	Asp	Leu	Leu	Leu		
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Glu	Val	Leu	Arg	Ser	Leu	Leu	Ala	Glu	Ser	Asp	Ala	Glu	Met	Leu	Gly		
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Phe	Leu	Thr	Asp	Arg	Glu	Leu	Asn	Leu	Leu	Glu	Arg	Val	Arg	Ser	Val		
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Leu	Glu	Ala	Gly	Arg	Glu	Ala	Leu	Ala	Glu	His	Gly	Ser	Ile	Glu	Glu		
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gtg	ttg	tgg	gcg	ctg	tgg	tcg	gcg	acc	gat	ctg	tcg	aac	tcg	ttg	tcc	1603	
Val	Leu	Trp	Ala	Leu	Trp	Ser	Ala	Thr	Asp	Leu	Ser	Asn	Ser	Leu	Ser		
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gcg	atc	agc	ctt	cga	ggc	ggc	gca	tcg	ggg	tcc	cag	gcc	gat	cgc	gat	1651	
Ala	Ile	Ser	Leu	Arg	Gly	Gly	Ala	Ser	Gly	Ser	Gln	Ala	Asp	Arg	Asp		
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Leu	Asp	Ala	Met	Met	Ala	Leu	Phe	Asp	Ala	Ala	Gly	Asp	Tyr	Val	Glu		
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cgc	tac	ccg	tca	gcg	ggc	gtg	cgg	agt	ttc	att	ctg	cat	att	tct	gag	1747	
Arg	Tyr	Pro	Ser	Ala	Gly	Val	Arg	Ser	Phe	Ile	Leu	His	Ile	Ser	Glu		
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cag	gaa	ctt	ccg	acc	ggc	atg	cgt	gag	cga	cgc	ggc	gcg	atc	ccg	gag	1795	
Gln	Glu	Leu	Pro	Thr	Gly	Met	Arg	Glu	Arg	Arg	Gly	Ala	Ile	Pro	Glu		
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gcc	gtc	gag	gtg	ctg	acg	gcg	cac	gcg	acg	acg	ggt	cgt	gag	tgg	aag	1843	
Ala	Val	Glu	Val	Leu	Thr	Ala	His	Ala	Thr	Thr	Gly	Arg	Glu	Trp	Lys		
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cgc	gtg	atc	gtt	gct	gag	gtg	cag	gag	ggc	agt	tgg	ccg	tcg	ctc	ggt	1891	
Arg	Val	Ile	Val	Ala	Glu	Val	Gln	Glu	Gly	Ser	Trp	Pro	Ser	Leu	Gly		
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gaa	act	ggc	acg	ctg	ctt	ggt	cag	gaa	gag	ttc	gtc	gat	ttg	gtg	gat	1939	
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gaa ccc tcc cgg ttt ttg gaa ttg ctg agt caa ccg atc gtt gtt ctc Glu Pro Ser Arg Phe Leu Glu Leu Leu Ser Gln Pro Ile Val Val Leu 665 670 675			2131
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aat ctg cgc act ccg tcg act gat gag gag ttg atc aag ggg gcg gtg Asn Leu Arg Thr Pro Ser Thr Asp Glu Glu Leu Ile Lys Gly Ala Val 745 750 755			2371
tcg ttg tcg ccg tcg cgg att gag cag ttg ttg aat tgt ccg ctg cgc Ser Leu Ser Pro Ser Arg Ile Glu Gln Leu Leu Asn Cys Pro Leu Arg 760 765 770			2419
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855 860 865

gac tcc gta tcg atc cgt ggt cgc atg gac cgt ttg gag cga aac aaa 2755
Asp Ser Val Ser Ile Arg Gly Arg Met Asp Arg Leu Glu Arg Asn Lys
870 875 880 885

tcc ggc gag ttg gtg gtt gtt gat ttc aaa acg ggc aaa act caa atc 2803
Ser Gly Glu Leu Val Val Val Asp Phe Lys Thr Gly Lys Thr Gln Ile
890 895 900

gct gca aaa gac atg ggc gat cac cca cag ttg ttt gcg tat caa ttg 2851
Ala Ala Lys Asp Met Gly Asp His Pro Gln Leu Phe Ala Tyr Gln Leu
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Ala Gly Ser Gly Val Ser Ser Ala Val Val Asp Thr Val Leu Glu Arg
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Ile Arg Gln Gly Trp Glu Pro Ser Ser Met Leu Val Val Ala Thr Ser
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Lys Glu Ala Ala Ser Arg Leu Arg Gln Glu Ile Ser Glu Ser Val Ala
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Gln Met Asp Tyr Val Ser Glu Gly Pro Leu Val Arg Ser Val His Ser
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Val Ala Phe Ala Leu Ile Arg Asp Ala Ser Asp Asp Asp Val Arg Leu
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Ile Thr Gly Ala Glu Gln Asp Ala Val Ile Arg Glu Leu Leu Arg Gly
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His Ala Asp Asp Gly Arg Gly Gly Trp Pro Gln Glu Gln Arg Glu Gly
145 150 155 160

Leu Arg Met Val Gly Phe Ala Arg Gln Leu Arg Asp Phe Leu Leu Arg
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Ala Val Glu Arg Gly Val Gly Pro Asp Glu Leu Val Glu Leu Gly Glu
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 Arg Phe Glu Arg Ala Asn Trp Val Ala Ala Gly Glu Phe Leu Arg Glu
 195 200 205
 Tyr Lys Gln Val Met Lys Leu Ser Gly Ala His Ser Phe Ser Ala Ser
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 Glu Leu Val Thr Glu Ala Leu Arg Gly Pro Glu Pro Ser Val Lys Tyr
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 Ala Asp Leu Leu Ala Asp Thr Val Arg Arg Ala His Leu Ile Asp Gly
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 Arg Ser Trp Ser Glu Ile Ala Val Ile Val Arg Ser Ala Gly Met Ile
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 Ser Pro Thr Asp Val Val Leu Ala Glu Gln Arg Ile Val Ala Ala Met
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 Ile Leu Gly Leu Arg Ala Leu Thr Glu Ser Leu Asn Ala Ile Glu Leu
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 Glu Asp Leu Leu Leu Gly Pro Ile Gly Gly Ala Asp Pro Val Thr Leu
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 Arg Arg Leu Leu Arg Gly Leu Arg Gln Ala Glu Met Lys Met Gly Gly
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 Gln Arg Arg Ala Ile Glu Val Leu Arg Ser Leu Leu Ala Glu Ser Asp
 435 440 445
 Ala Glu Met Leu Gly Phe Leu Thr Asp Arg Glu Leu Asn Leu Leu Glu
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 Arg Val Arg Ser Val Leu Glu Ala Gly Arg Glu Ala Leu Ala Glu His
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 Gly Ser Ile Glu Glu Val Leu Trp Ala Leu Trp Ser Ala Thr Asp Leu
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 Ser Asn Ser Leu Ser Ala Ile Ser Leu Arg Gly Gly Ala Ser Gly Ser

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Gly	Ala	Ile	Pro	Glu	Ala	Val	Glu	Val	Leu	Thr	Ala	His	Ala	Thr	Thr
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Pro	Ala	Glu	Trp	Thr	Asn	Leu	Arg	Thr	Pro	Ser	Thr	Asp	Glu	Glu	Leu
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		755					760					765			
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Lys Thr Ser Arg Ala Asp Phe Thr Glu Val Gly Thr Glu Met Asp Val
850 855 860

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Leu Glu Arg Asn Lys Ser Gly Glu Leu Val Val Asp Phe Lys Thr
885 890 895

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<223> RXA01736

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Gly Leu Leu Leu Pro Val Glu Pro Ser Ala Arg Leu Ile Thr Gln Thr
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gag ctt tat cac atc gct cgc aac gtg gtg aac aac tac gac ggt gag 144
Glu Leu Tyr His Ile Ala Arg Asn Val Val Asn Asn Tyr Asp Gly Glu
35 40 45

ctc acc gcc acc caa acg ccg gcc act gtc acg gaa tac ctc ctc aag 192
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Leu Val Ser Glu Met Asp Asn His Met Val Thr Ala Glu Asp Ile Arg
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Glu Glu Ser Asp Pro Phe Ile Lys Leu Phe Asp Glu Leu Pro Lys Gly
85 90 95

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Lys Gly Gln Arg Asp Asn Leu Asn Ala Glu Met Thr Lys Trp Arg Asp
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Thr Gln Val Ala Arg Leu Gln Tyr Leu Pro Leu Val Lys Ala Leu Lys	
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gag gaa ctg cac aat cag gct gtg gtg acg ttt ggt gag cag atg tct	432
Glu Glu Leu His Asn Gln Ala Val Val Thr Phe Gly Glu Gln Met Ser	
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aag gca gct cat ctc gca tcg acg cat cct cag gtg ggc tat tcg cag	480
Lys Ala Ala His Leu Ala Ser Thr His Pro Gln Val Gly Tyr Ser Gln	
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agg cga cgg ttc cgc gtt gtc atg ctt gat gag tat cag gac acc agc	528
Arg Arg Arg Phe Arg Val Val Met Leu Asp Glu Tyr Gln Asp Thr Ser	
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His Ser Gln Arg Val Leu Leu Ser Ser Leu Phe Gly Gly Thr Asp Pro	
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Gly Leu Thr Val Asn Ala Val Gly Asp Pro Met Gln Ala Ile Tyr Gly	
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Trp Arg Gly Ala Thr Ala Ala Asn Leu Glu Asn Phe Val Asp Asp Phe	
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Pro Val Ile His Leu Asp Gly Lys Thr Arg Ala Pro Lys Asn Glu Leu	
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Thr Thr Ser Trp Arg Asn Pro Pro Glu Val Leu Thr Leu Ala Asn Ala	
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Gln Pro Leu Gln Pro Arg Glu Gly Ala Pro Thr Gly Glu Val Ser Leu	
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Gly Trp Phe Gly Thr Ala Ala Gln Glu Arg Glu Phe Val Ala Asp Glu	
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Met Val Lys His Trp Asn Ala Arg Glu Glu Lys Gly Thr Phe Thr Ala	
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gcg gtg ttg gtg cgt aag aag cgt cat tcg gca ccg atg gcg gag gag	1008
Ala Val Leu Val Arg Lys Lys Arg His Ser Ala Pro Met Ala Glu Glu	
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Leu Thr Lys Arg Gly Ile Pro Val Glu Ile Val Gly Leu Ser Gly Leu	
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Glu	Glu	Asn	Ser	Arg	Leu	Phe	Tyr	Val	Gly	Ile	Thr	Arg	Ser	Glu	Arg		
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aaa	gtt	ccc	tac	ggc	cac	ttg	gag	atc	ctt	cgg	gat	aaa	gcg	ccg	gag	2064	
Lys	Val	Pro	Tyr	Gly	His	Leu	Glu	Ile	Leu	Arg	Asp	Lys	Ala	Pro	Glu		
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Cys	Val	Val	Ser	Trp	Trp	Glu	Gly	Glu	Glu	Gly	Asp	Val	Glu	Lys	Gln		
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Ala	Arg	Arg	Met	Arg	Arg	Pro	Val	Pro	Phe	Lys	Pro	Asn	Thr	Tyr	Ala		
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Lys	Arg	Gly	Thr	Leu	Phe	His	Gln	Trp	Leu	Glu	Asp	Arg	Phe	Gly	Ser		
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acc	gcg	ctt	ctc	gac	gaa	acc	gag	ctc	ccc	ggc	atc	gac	gag	gac	tac	2496	
Thr	Ala	Leu	Leu	Asp	Glu	Thr	Glu	Leu	Pro	Gly	Ile	Asp	Glu	Asp	Tyr		
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tcg	gat	gac	gca	ttc	atc	gaa	ctc	cgc	gac	gcg	ttc	cta	gga	tct	act	2544	
Ser	Asp	Asp	Ala	Phe	Ile	Glu	Leu	Arg	Asp	Ala	Phe	Leu	Gly	Ser	Thr		

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Trp Glu Asn Arg Thr Pro Glu Phe Val Glu His Pro Phe Glu Val Thr			
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atc ggc gaa cac gtc atc cgc ggc cgc atg gac gcc gtc ttc cac acc			2640
Ile Gly Glu His Val Ile Arg Gly Arg Met Asp Ala Val Phe His Thr			
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gat ggc acc tgg atg gtg gtc gac tgg aaa acc gga cgc acc cca acc			2688
Asp Gly Thr Trp Met Val Val Asp Trp Lys Thr Gly Arg Thr Pro Thr			
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Gly Pro Glu Met Asp Ala Ala Ile Ile Gln Leu Ala Val Tyr Arg Leu			
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Ala Trp Ala Arg Leu Lys Gly Leu Glu Pro Glu Glu Val Arg Ala Ala			
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Phe His Tyr Val Ala His Asp His Thr Phe Glu Pro Asn Asp Leu Pro			
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Glu Glu Ser Asp Pro Phe Ile Lys Leu Phe Asp Glu Leu Pro Lys Gly			
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Lys Gly Gln Arg Asp Asn Leu Asn Ala Glu Met Thr Lys Trp Arg Asp			
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Thr Gln Val Ala Arg Leu Gln Tyr Leu Pro Leu Val Lys Ala Leu Lys			

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Arg	Arg	Arg	Phe	Arg	Val	Val	Met	Leu	Asp	Glu	Tyr	Gln	Asp	Thr	Ser
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His	Ser	Gln	Arg	Val	Leu	Leu	Ser	Ser	Leu	Phe	Gly	Gly	Thr	Asp	Pro
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Val	Ser	Arg	Glu	Val	Leu	Gly	Ser	Pro	Asp	Ala	Pro	Thr	Arg	Thr	Val
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Gln	Pro	Leu	Gln	Pro	Arg	Glu	Gly	Ala	Pro	Thr	Gly	Glu	Val	Ser	Leu
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 Lys Val Pro Tyr Gly His Leu Glu Ile Leu Arg Asp Lys Ala Pro Glu
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 Gly Leu Glu Ser Leu Trp Glu Lys Glu Val Ser Ala Leu Ile Asp Glu
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Gly Pro Val Ala Glu Arg Met Trp Val Ala Thr Phe His Ser Val Cys	
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Thr	Ala	Lys	Gly	Leu	Glu	Phe	Pro	Ile	Val	Phe	Leu	Thr	Gly	Trp	Glu	
		600					605					610				
gac	gga	cag	ttc	cca	cac	ctg	cgt	tcc	ctt	ggc	gat	gcc	aaa	gaa	ctt	1987
Asp	Gly	Gln	Phe	Pro	His	Leu	Arg	Ser	Leu	Gly	Asp	Ala	Lys	Glu	Leu	
	615					620				625						
gcc	gag	gaa	cgc	cgc	ctc	gcc	tac	gtg	ggc	atc	acc	cgc	gcc	cgc	aag	2035
Ala	Glu	Glu	Arg	Arg	Leu	Ala	Tyr	Val	Gly	Ile	Thr	Arg	Ala	Arg	Lys	
630					635					640					645	
cgc	ctc	tac	atg	acc	aga	gcc	atg	ctg	cgt	agc	tcc	tgg	ggc	aac	ccg	2083
Arg	Leu	Tyr	Met	Thr	Arg	Ala	Met	Leu	Arg	Ser	Ser	Trp	Gly	Asn	Pro	
				650					655					660		
gtg	acc	aac	cca	ccg	tca	cgt	ttc	ctc	caa	gaa	gtg	ccc	gca	gaa	ctc	2131
Val	Thr	Asn	Pro	Pro	Ser	Arg	Phe	Leu	Gln	Glu	Val	Pro	Ala	Glu	Leu	
			665					670				675				
atc	gat	tgg	agg	cgc	gaa	gaa	ccc	cag	atg	tct	tcc	gcc	tgg	gct	cct	2179
Ile	Asp	Trp	Arg	Arg	Glu	Glu	Pro	Gln	Met	Ser	Ser	Ala	Trp	Ala	Pro	
		680					685					690				
cga	ccc	acc	cga	agc	atc	ccc	acc	aaa	act	cgc	acc	aac	aat	aag	cag	2227
Arg	Pro	Thr	Arg	Ser	Ile	Pro	Thr	Lys	Thr	Arg	Thr	Asn	Asn	Lys	Gln	
	695					700				705						
ttg	gat	ctg	tcg	gtg	ggg	gat	cgc	gtc	aat	cac	gac	aag	tac	ggc	ttg	2275
Leu	Asp	Leu	Ser	Val	Gly	Asp	Arg	Val	Asn	His	Asp	Lys	Tyr	Gly	Leu	
710					715					720					725	
gga	acc	gtg	ctc	tct	tca	gat	ggc	agc	ggc	ccc	cga	gcc	acc	gtc	acc	2323
Gly	Thr	Val	Leu	Ser	Ser	Asp	Gly									

760

<210> 56

<211> 763

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 56

Met	Asn	Thr	Ser	Pro	Phe	Thr	Pro	Gly	Ser	Pro	Asp	Leu	Ile	Asp	Gly
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Leu	Asn	Glu	Gln	Gln	Arg	Ala	Ala	Val	Glu	His	Ile	Gly	Ser	Pro	Leu
			20					25					30		

Leu	Ile	Val	Ala	Gly	Ala	Gly	Ser	Gly	Lys	Thr	Ala	Val	Leu	Thr	Arg
		35					40					45			

Arg	Ile	Ala	Tyr	Leu	Met	Arg	Tyr	Arg	Gly	Val	His	Pro	Gln	Gln	Ile
	50					55					60				

Leu	Ala	Ile	Thr	Phe	Thr	Asn	Lys	Ala	Ala	Ala	Glu	Met	Arg	Glu	Arg
65					70					75					80

Val	Ser	Gln	Leu	Val	Gly	Pro	Val	Ala	Glu	Arg	Met	Trp	Val	Ala	Thr
			85						90					95	

Phe	His	Ser	Val	Cys	Val	Arg	Ile	Leu	Arg	Gln	Gln	Ala	Gln	Leu	Val
			100					105					110		

Glu	Gly	Leu	Asn	Thr	Asn	Phe	Thr	Ile	Tyr	Asp	Ser	Asp	Asp	Ser	Arg
		115					120					125			

Arg	Leu	Leu	Thr	Met	Ile	Ala	Lys	Asp	Leu	Glu	Leu	Asp	Ile	Lys	Lys
	130					135					140				

Phe	Ser	Ala	Arg	Thr	Leu	Leu	Gly	Ala	Ile	Ser	Asn	Leu	Lys	Asn	Glu
145					150					155					160

Leu	Val	Thr	Pro	Gln	Glu	Ala	Leu	Ala	Asp	Ala	Glu	Arg	Thr	His	Asn
				165					170					175	

Pro	Tyr	Glu	Thr	Val	Val	Ala	Arg	Ala	Phe	Ser	Glu	Tyr	Gln	Ser	Arg
		180						185					190		

Leu	Arg	Arg	Ala	Asn	Ala	Val	Asp	Phe	Asp	Asp	Leu	Ile	Gly	Glu	Thr
		195					200					205			

Val	Arg	Ile	Phe	Arg	Glu	His	Pro	Pro	Val	Ala	Glu	Tyr	Tyr	Arg	Arg
	210					215					220				

Arg	Phe	Arg	His	Val	Leu	Ile	Asp	Glu	Tyr	Gln	Asp	Thr	Asn	His	Ala
225					230					235					240

Gln	Tyr	Glu	Leu	Ile	Ser	Thr	Leu	Val	Gly	Lys	Pro	Asp	Gln	Asp	Pro
			245						250					255	

Ser	Glu	Leu	Cys	Val	Val	Gly	Asp	Ser	Asp	Gln	Ser	Ile	Tyr	Ala	Phe
		260						265					270		

Arg	Gly	Ala	Thr	Ile	Arg	Asn	Ile	Glu	Glu	Phe	Glu	Arg	Asp	Phe	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

275					280					285					
Asn	Ala	Arg	Thr	Ile	Leu	Leu	Glu	Gln	Asn	Tyr	Arg	Ser	Thr	Gln	Thr
290						295					300				
Ile	Leu	Ser	Ala	Ala	Asn	Ala	Val	Ile	Ser	Gln	Asn	Glu	Asn	Arg	Arg
305					310					315					320
Pro	Lys	Asn	Leu	Trp	Thr	Ala	Leu	Gly	Glu	Gly	Glu	Gln	Ile	Ile	Gly
				325					330					335	
Tyr	Val	Ala	Asp	Asn	Glu	His	Asp	Glu	Ala	Arg	Phe	Ile	Ala	Ser	Glu
			340					345					350		
Ile	Asp	Asn	Leu	Val	Asp	His	Gly	Met	Ser	Tyr	Ser	Asp	Ile	Ala	Ile
	355						360					365			
Met	Tyr	Arg	Thr	Asn	Asn	Ser	Ser	Arg	Ala	Leu	Glu	Asp	Val	Phe	Met
	370					375					380				
Arg	Thr	Gly	Val	Pro	Tyr	Lys	Val	Val	Gly	Gly	Thr	Lys	Phe	Tyr	Glu
385					390					395					400
Arg	Lys	Glu	Ile	Arg	Asp	Ile	Ile	Ala	Tyr	Leu	Arg	Val	Leu	Glu	Asn
				405					410					415	
Pro	Asp	Asp	Thr	Val	Asn	Leu	Arg	Arg	Ile	Ile	Asn	Thr	Pro	Lys	Arg
			420					425					430		
Gly	Ile	Gly	Asp	Arg	Ala	Gln	Ala	Phe	Ile	Ala	Leu	His	Ser	Glu	Asn
		435				440						445			
Asn	Gln	Ile	Ser	Phe	Gly	Gln	Ala	Leu	Leu	Asp	Ala	Ala	Leu	Gly	Lys
	450					455					460				
Val	Asp	Leu	Leu	Gly	Ala	Arg	Gly	Lys	Asn	Ala	Ala	Ile	Lys	Phe	Asn
465					470					475					480
Glu	Leu	Phe	Asp	Ala	Leu	Arg	Ser	Glu	Leu	Pro	Thr	Met	Val	Asn	Glu
			485					490					495		
Val	Thr	Gly	Leu	Pro	Asp	Ile	Gly	Gln	Val	Ile	Ser	Arg	Ile	Leu	Asp
			500					505					510		
Ile	Thr	Gly	Tyr	Lys	Ala	Glu	Leu	Glu	Ala	Ser	Asn	Asp	Pro	Gln	Asp
	515					520						525			
Gly	Ala	Arg	Leu	Asp	Asn	Leu	Asn	Glu	Leu	Val	Ser	Val	Ala	Arg	Glu
	530					535					540				
Phe	Ser	Ser	Asp	Ala	Ala	Asn	Arg	Met	Val	Asn	Glu	Val	Pro	Glu	Gly
545					550					555					560
Glu	Ala	Gln	Pro	Gly	Ser	Leu	Gln	Ala	Phe	Leu	Glu	Arg	Val	Ser	Leu
			565						570					575	
Val	Ala	Asp	Ala	Asp	Gln	Ile	Pro	Asp	Ser	Asp	Asn	Gly	Val	Val	Thr
		580					585					590			
Leu	Met	Thr	Leu	His	Thr	Ala	Lys	Gly	Leu	Glu	Phe	Pro	Ile	Val	Phe
	595					600						605			

Leu Thr Gly Trp Glu Asp Gly Gln Phe Pro His Leu Arg Ser Leu Gly
 610 615 620
 Asp Ala Lys Glu Leu Ala Glu Glu Arg Arg Leu Ala Tyr Val Gly Ile
 625 630 635 640
 Thr Arg Ala Arg Lys Arg Leu Tyr Met Thr Arg Ala Met Leu Arg Ser
 645 650 655
 Ser Trp Gly Asn Pro Val Thr Asn Pro Pro Ser Arg Phe Leu Gln Glu
 660 665 670
 Val Pro Ala Glu Leu Ile Asp Trp Arg Arg Glu Glu Pro Gln Met Ser
 675 680 685
 Ser Ala Trp Ala Pro Arg Pro Thr Arg Ser Ile Pro Thr Lys Thr Arg
 690 695 700
 Thr Asn Asn Lys Gln Leu Asp Leu Ser Val Gly Asp Arg Val Asn His
 705 710 715 720
 Asp Lys Tyr Gly Leu Gly Thr Val Leu Ser Ser Asp Gly Ser Gly Pro
 725 730 735
 Arg Ala Thr Val Thr Ile Asp Phe Gly Ser Ser Gly Lys Val Arg Leu
 740 745 750
 Met Leu Leu Gly Gly Val Pro Met Glu Lys Leu
 755 760

<210> 57

<211> 1070

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1047)

<223> RXN02819

<400> 57

aag ctg caa atc ggt gat gtc att gcc atg cct ggt aga aaa cga cca 48
 Lys Leu Gln Ile Gly Asp Val Ile Ala Met Pro Gly Arg Lys Arg Pro
 1 5 10 15

gtt ctc gca gta gtg atg acg cct gct aat cag agc aga gat ccc cgc 96
 Val Leu Ala Val Val Met Thr Pro Ala Asn Gln Ser Arg Asp Pro Arg
 20 25 30

cca tgg gtg acc acc gaa tct ggt tgg tca ggt cgt gtg gat gcg gaa 144
 Pro Trp Val Thr Thr Glu Ser Gly Trp Ser Gly Arg Val Asp Ala Glu
 35 40 45

tcc ttt act aat ccg ccg atc acc att ggg cat atg cgt ctg cct cgc 192
 Ser Phe Thr Asn Pro Pro Ile Thr Ile Gly His Met Arg Leu Pro Arg
 50 55 60

caa gct att gaa gag cct cgc cgc aat gcc cgg cgc gtc cag gaa ctg 240
 Gln Ala Ile Glu Glu Pro Arg Arg Asn Ala Arg Arg Val Gln Glu Leu

65					70					75					80					
ttt	agg	cgt	gag	cac	ttc	aag	cga	ccc	aac	aag	atg	cgg	gag	ttt	gct	288				
Phe	Arg	Arg	Glu	His	Phe	Lys	Arg	Pro	Asn	Lys	Met	Arg	Glu	Phe	Ala					
85					90					95										
cgg	gtt	cgt	ccc	aat	gag	gca	gtg	acc	aaa	ctg	cgt	aat	gct	att	cgg	336				
Arg	Val	Arg	Pro	Asn	Glu	Ala	Val	Thr	Lys	Leu	Arg	Asn	Ala	Ile	Arg					
100					105					110										
gat	cat	gag	gcg	cat	cat	tgg	cct	gat	cgg	gag	cac	ttg	gct	cgc	acc	384				
Asp	His	Glu	Ala	His	His	Trp	Pro	Asp	Arg	Glu	His	Leu	Ala	Arg	Thr					
115					120					125										
gcg	gag	cgt	atg	atc	cgt	aaa	gaa	cgt	gat	ctg	gct	aag	ttg	acc	ggc	432				
Ala	Glu	Arg	Met	Ile	Arg	Lys	Glu	Arg	Asp	Leu	Ala	Lys	Leu	Thr	Gly					
130					135					140										
aat	gtg	gat	aaa	gcc	agg	gaa	acc	ctc	ggt	agg	acg	ttt	gag	cgc	att	480				
Asn	Val	Asp	Lys	Ala	Arg	Glu	Thr	Leu	Gly	Arg	Thr	Phe	Glu	Arg	Ile					
145					150					155					160					
ttg	tcg	ctg	ctc	agt	gaa	atg	gac	tat	gtg	gat	tac	tct	aat	cca	gat	528				
Leu	Ser	Leu	Leu	Ser	Glu	Met	Asp	Tyr	Val	Asp	Tyr	Ser	Asn	Pro	Asp					
165					170					175										
aat	cca	gtg	atc	act	gat	gaa	ggt	gag	cgt	ttg	gcg	aaa	atc	cac	agt	576				
Asn	Pro	Val	Ile	Thr	Asp	Glu	Gly	Glu	Arg	Leu	Ala	Lys	Ile	His	Ser					
180					185					190										
gag	gca	gac	ctg	ttg	gtt	gct	cag	tgc	ctc	aag	cgt	ggc	att	tgg	gac	624				
Glu	Ala	Asp	Leu	Leu	Val	Ala	Gln	Cys	Leu	Lys	Arg	Gly	Ile	Trp	Asp					
195					200					205										
aac	ctt	gat	ccc	gca	gag	ctc	gcc	ggt	gtg	gtg	agt	atg	tgc	acg	ttt	672				
Asn	Leu	Asp	Pro	Ala	Glu	Leu	Ala	Gly	Val	Val	Ser	Met	Cys	Thr	Phe					
210					215					220										
gaa	aat	cgt	cgc	gaa	acc	ggt	ggt	gag	gct	caa	gct	gtc	aca	gag	gcc	720				
Glu	Asn	Arg	Arg	Glu	Thr	Gly	Gly	Glu	Ala	Gln	Ala	Val	Thr	Glu	Ala					
225					230					235					240					
atg	gct	gat	tcc	atg	aat	agc	gtg	gaa	cgt	att	tgg	ggt	gag	ctg	gtt	768				
Met	Ala	Asp	Ser	Met	Asn	Ser	Val	Glu	Arg	Ile	Trp	Gly	Glu	Leu	Val					
245					250					255										
gaa	gat	gag	cgc	cgt	cac	cgt	ctg	cca	att	act	cgc	cag	ccg	gaa	gca	816				
Glu	Asp	Glu	Arg	Arg	His	Arg	Leu	Pro	Ile	Thr	Arg	Gln	Pro	Glu	Ala					
260					265					270										
ggt	ttt	gcc	acc	gcg	atc	cac	cag	tgg	gct	tca	ggt	gct	ccg	ctg	gga	864				
Gly	Phe	Ala	Thr	Ala	Ile	His	Gln	Trp	Ala	Ser	Gly	Ala	Pro	Leu	Gly					
275					280					285										
tat	tgc	atg	gct	gcg	gca	gcg	gaa	aac	ggc	gcg	gag	ttg	acc	cct	ggt	912				
Tyr	Cys	Met	Ala	Ala	Ala	Ala	Glu	Asn	Gly	Ala	Glu	Leu	Thr	Pro	Gly					
290					295					300										
gac	ttc	gtg	cgc	tgg	tgc	cgt	caa	gtc	atc	gat	ctt	cta	gag	cag	gtt	960				
Asp	Phe	Val	Arg	Trp	Cys	Arg	Gln	Val	Ile	Asp	Leu	Leu	Glu	Gln	Val					
305					310					315					320					

gct aag act gcc tac ttt gat gag acc aca cgg aat gct cgt cag gct 1008
 Ala Lys Thr Ala Tyr Phe Asp Glu Thr Thr Arg Asn Ala Arg Gln Ala
 325 330 335

att gat gcg att agg cgt gga gtt gtg gcg atc ggt tcc tagcgagcta 1057
 Ile Asp Ala Ile Arg Arg Gly Val Val Ala Ile Gly Ser
 340 345

gctatgttcg agc 1070

<210> 58

<211> 349

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 58

Lys Leu Gln Ile Gly Asp Val Ile Ala Met Pro Gly Arg Lys Arg Pro
 1 5 10 15

Val Leu Ala Val Val Met Thr Pro Ala Asn Gln Ser Arg Asp Pro Arg
 20 25 30

Pro Trp Val Thr Thr Glu Ser Gly Trp Ser Gly Arg Val Asp Ala Glu
 35 40 45

Ser Phe Thr Asn Pro Pro Ile Thr Ile Gly His Met Arg Leu Pro Arg
 50 55 60

Gln Ala Ile Glu Glu Pro Arg Arg Asn Ala Arg Arg Val Gln Glu Leu
 65 70 75 80

Phe Arg Arg Glu His Phe Lys Arg Pro Asn Lys Met Arg Glu Phe Ala
 85 90 95

Arg Val Arg Pro Asn Glu Ala Val Thr Lys Leu Arg Asn Ala Ile Arg
 100 105 110

Asp His Glu Ala His His Trp Pro Asp Arg Glu His Leu Ala Arg Thr
 115 120 125

Ala Glu Arg Met Ile Arg Lys Glu Arg Asp Leu Ala Lys Leu Thr Gly
 130 135 140

Asn Val Asp Lys Ala Arg Glu Thr Leu Gly Arg Thr Phe Glu Arg Ile
 145 150 155 160

Leu Ser Leu Leu Ser Glu Met Asp Tyr Val Asp Tyr Ser Asn Pro Asp
 165 170 175

Asn Pro Val Ile Thr Asp Glu Gly Glu Arg Leu Ala Lys Ile His Ser
 180 185 190

Glu Ala Asp Leu Leu Val Ala Gln Cys Leu Lys Arg Gly Ile Trp Asp
 195 200 205

Asn Leu Asp Pro Ala Glu Leu Ala Gly Val Val Ser Met Cys Thr Phe
 210 215 220

Glu Asn Arg Arg Glu Thr Gly Gly Glu Ala Gln Ala Val Thr Glu Ala

225		230		235		240
Met Ala Asp Ser	Met Asn Ser Val	Glu Arg Ile Trp	Gly Glu Leu Val			
	245	250	255			
Glu Asp Glu Arg	Arg His Arg Leu	Pro Ile Thr Arg	Gln Pro Glu Ala			
	260	265	270			
Gly Phe Ala Thr	Ala Ile His Gln	Trp Ala Ser Gly	Ala Pro Leu Gly			
	275	280	285			
Tyr Cys Met Ala	Ala Ala Ala Glu	Asn Gly Ala Glu	Leu Thr Pro Gly			
	290	295	300			
Asp Phe Val Arg	Trp Cys Arg Gln	Val Ile Asp Leu	Leu Glu Gln Val			
305	310	315	320			
Ala Lys Thr Ala	Tyr Phe Asp Glu	Thr Thr Arg Asn	Ala Arg Gln Ala			
	325	330	335			
Ile Asp Ala Ile	Arg Arg Gly Val	Val Ala Ile Gly	Ser			
	340	345				

<210> 59

<211> 612

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(612)

<223> FRXA02819

<400> 59

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Lys Leu Gln Ile	Gly Asp Val Ile	Ala Met Pro Gly	Arg Lys Arg Pro	
1	5	10	15	

ggt ctc gca gta	gtg atg acg cct	gct aat cag agc	aga gat ccc cgc	96
Val Leu Ala Val	Val Met Thr Pro	Ala Asn Gln Ser	Arg Asp Pro Arg	
20	25	30		

cca tgg gtg acc	acc gaa tct ggt	tgg tca ggt cgt	gtg gat gcg gaa	144
Pro Trp Val Thr	Thr Glu Ser Gly	Trp Ser Gly Arg	Val Asp Ala Glu	
35	40	45		

tcc ttt act aat	ccg ccg atc acc	att ggg cat atg	cgt ctg cct cgc	192
Ser Phe Thr Asn	Pro Pro Ile Thr	Ile Gly His Met	Arg Leu Pro Arg	
50	55	60		

caa gct att gaa	gag cct cgc cgc	aat gcc cgg cgc	gtc cag gaa ctg	240
Gln Ala Ile Glu	Glu Pro Arg Arg	Asn Ala Arg Arg	Val Gln Glu Leu	
65	70	75	80	

ttt agg cgt gag	cac ttc aag cga	ccc aac aag atg	cgg gag ttt gct	288
Phe Arg Arg Glu	His Phe Lys Arg	Pro Asn Lys Met	Arg Glu Phe Ala	
85	90	95		

cgg gtt cgt ccc	aat gag gca gtg	acc aaa ctg cgt	aat gct att cgg	336
Arg Val Arg Pro	Asn Glu Ala Val	Thr Lys Leu Arg	Asn Ala Ile Arg	

100	105	110	
gat cat gag gcg cat cat tgg cct gat cgg gag cac ttg gct cgc acc			384
Asp His Glu Ala His His Trp Pro Asp Arg Glu His Leu Ala Arg Thr			
115	120	125	
gcg gag cgt atg atc cgt aaa gaa cgt gat ctg gct aag ttg acc ggc			432
Ala Glu Arg Met Ile Arg Lys Glu Arg Asp Leu Ala Lys Leu Thr Gly			
130	135	140	
aat gtg gat aaa gcc agg gaa acc ctc ggt agg acg ttt gag cgc att			480
Asn Val Asp Lys Ala Arg Glu Thr Leu Gly Arg Thr Phe Glu Arg Ile			
145	150	155	160
ttg tcg ctg ctc agt gaa atg gac tat gtg gat tac tct aat cca gat			528
Leu Ser Leu Leu Ser Glu Met Asp Tyr Val Asp Tyr Ser Asn Pro Asp			
165	170	175	
aat cca gtg atc act gat gaa ggt gag cgt ttg gcg aaa atc cac agt			576
Asn Pro Val Ile Thr Asp Glu Gly Glu Arg Leu Ala Lys Ile His Ser			
180	185	190	
gag gca gac ctg ttg gtt gct cag tgc ctc aag cgt			612
Glu Ala Asp Leu Leu Val Ala Gln Cys Leu Lys Arg			
195	200		
<210> 60			
<211> 204			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 60			
Lys Leu Gln Ile Gly Asp Val Ile Ala Met Pro Gly Arg Lys Arg Pro			
1	5	10	15
Val Leu Ala Val Val Met Thr Pro Ala Asn Gln Ser Arg Asp Pro Arg			
20	25	30	
Pro Trp Val Thr Thr Glu Ser Gly Trp Ser Gly Arg Val Asp Ala Glu			
35	40	45	
Ser Phe Thr Asn Pro Pro Ile Thr Ile Gly His Met Arg Leu Pro Arg			
50	55	60	
Gln Ala Ile Glu Glu Pro Arg Arg Asn Ala Arg Arg Val Gln Glu Leu			
65	70	75	80
Phe Arg Arg Glu His Phe Lys Arg Pro Asn Lys Met Arg Glu Phe Ala			
85	90	95	
Arg Val Arg Pro Asn Glu Ala Val Thr Lys Leu Arg Asn Ala Ile Arg			
100	105	110	
Asp His Glu Ala His His Trp Pro Asp Arg Glu His Leu Ala Arg Thr			
115	120	125	
Ala Glu Arg Met Ile Arg Lys Glu Arg Asp Leu Ala Lys Leu Thr Gly			
130	135	140	
Asn Val Asp Lys Ala Arg Glu Thr Leu Gly Arg Thr Phe Glu Arg Ile			

145 150 155 160

Leu Ser Leu Leu Ser Glu Met Asp Tyr Val Asp Tyr Ser Asn Pro Asp
 165 170 175

Asn Pro Val Ile Thr Asp Glu Gly Glu Arg Leu Ala Lys Ile His Ser
 180 185 190

Glu Ala Asp Leu Leu Val Ala Gln Cys Leu Lys Arg
 195 200

<210> 61
 <211> 1705
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1705)
 <223> RXA01157

<400> 61
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ggtgacgtgc tctagggcct agccaggtac ccttagaggc atg agt ttt tct gcc 115
 Met Ser Phe Ser Ala
 1 5

gaa aag ggc acc cac ctt tca gag ttc ata gca gac ctg ggc ttt gat 163
 Glu Lys Gly Thr His Leu Ser Glu Phe Ile Ala Asp Leu Gly Phe Asp
 10 15 20

ctg gac gag ttc caa atc aaa ggc tgc cac gct gtg gaa gaa gac cac 211
 Leu Asp Glu Phe Gln Ile Lys Gly Cys His Ala Val Glu Glu Asp His
 25 30 35

ggt gtt tta gta tgt gcg ccc acc ggc gcg ggc aaa aca att gtt ggt 259
 Gly Val Leu Val Cys Ala Pro Thr Gly Ala Gly Lys Thr Ile Val Gly
 40 45 50

gaa ttc gca gtg tcc ctc gca tta tcg cgg ggg aca aag tgt ttc tac 307
 Glu Phe Ala Val Ser Leu Ala Leu Ser Arg Gly Thr Lys Cys Phe Tyr
 55 60 65

acc acc ccc atc aaa gcg ctg agc aac cag aag tac cac gat ttg gtg 355
 Thr Thr Pro Ile Lys Ala Leu Ser Asn Gln Lys Tyr His Asp Leu Val
 70 75 80 85

gct aaa cac ggc tcc gat gcc gtt ggt ctg ctc acc ggt gat gtt tcc 403
 Ala Lys His Gly Ser Asp Ala Val Gly Leu Leu Thr Gly Asp Val Ser
 90 95 100

att aac cat gat gct gac atc gtg gtc atg acc acc gaa gtg ctg cgc 451
 Ile Asn His Asp Ala Asp Ile Val Val Met Thr Thr Glu Val Leu Arg
 105 110 115

aac atg att tac gcg ggc tct ttt gcg ctt gag cgc tta agc cac gtg 499
 Asn Met Ile Tyr Ala Gly Ser Phe Ala Leu Glu Arg Leu Ser His Val
 120 125 130

gtc atg gat gag atc cac ttc ctt gct gat gcc tcc cgt ggc gcg gtg	547
Val Met Asp Glu Ile His Phe Leu Ala Asp Ala Ser Arg Gly Ala Val	
135 140 145	
tgg gaa gaa gtg atc ctc aac ttg gat gat tcc gtc aac atc atc ggt	595
Trp Glu Glu Val Ile Leu Asn Leu Asp Asp Ser Val Asn Ile Ile Gly	
150 155 160 165	
cta tct gcc acg gtg tcc aac tca gag gag ttt ggt gag tgg ctg acc	643
Leu Ser Ala Thr Val Ser Asn Ser Glu Glu Phe Gly Glu Trp Leu Thr	
170 175 180	
act gtt cgc ggc gat acc cgt gtg att gtt act gat cac cgc ccc gtt	691
Thr Val Arg Gly Asp Thr Arg Val Ile Val Thr Asp His Arg Pro Val	
185 190 195	
ccg ctt gat cag tac atg atg gtg cag cgc aaa gtg atg cca ctg ttt	739
Pro Leu Asp Gln Tyr Met Met Val Gln Arg Lys Val Met Pro Leu Phe	
200 205 210	
gag cct ggc acc gat gga cgc gtg aac aag gag tta gag gca acg att	787
Glu Pro Gly Thr Asp Gly Arg Val Asn Lys Glu Leu Glu Ala Thr Ile	
215 220 225	
gat cgc ctc aac agc aag caa agc gaa caa ggc cgt gcg gca tac cgc	835
Asp Arg Leu Asn Ser Lys Gln Ser Glu Gln Gly Arg Ala Ala Tyr Arg	
230 235 240 245	
tct ggt gaa ggc ttc cgt gca cgc agc aaa ggc gat aag cag gat tct	883
Ser Gly Glu Gly Phe Arg Ala Arg Ser Lys Gly Asp Lys Gln Asp Ser	
250 255 260	
cgc act ggt aag cca cgg gaa caa gac cgc cac agg cca ctg ggt cgg	931
Arg Thr Gly Lys Pro Arg Glu Gln Asp Arg His Arg Pro Leu Gly Arg	
265 270 275	
cct gaa gtg ctc agc atc ctc aag ggc atc aac atg ctg cca gcg att	979
Pro Glu Val Leu Ser Ile Leu Lys Gly Ile Asn Met Leu Pro Ala Ile	
280 285 290	
acg ttt atc ttc tcc cgc gcg ggc tgt gat ggt gcg ctg tac caa tgc	1027
Thr Phe Ile Phe Ser Arg Ala Gly Cys Asp Gly Ala Leu Tyr Gln Cys	
295 300 305	
ttg cgt tct aag ttg gtc ttg acg gat caa gca gaa tca gaa gag att	1075
Leu Arg Ser Lys Leu Val Leu Thr Asp Gln Ala Glu Ser Glu Glu Ile	
310 315 320 325	
gca cgc att gtc gac gcc ggc gtg gtg ggg atc ccc gag gaa gac ctt	1123
Ala Arg Ile Val Asp Ala Gly Val Val Gly Ile Pro Glu Glu Asp Leu	
330 335 340	
caa gta ctg aac ttt aag cag tgg cgt gct gca ctg atg cgc ggt ttc	1171
Gln Val Leu Asn Phe Lys Gln Trp Arg Ala Ala Leu Met Arg Gly Phe	
345 350 355	
gca gcc cac cac gcg ggt atg ctt cca gcg ttt agg cac atc gtg gaa	1219
Ala Ala His His Ala Gly Met Leu Pro Ala Phe Arg His Ile Val Glu	
360 365 370	
gag ctc ttt gtt aaa ggt ctt gtc cgc gcg gtg ttt gcc acg gaa acc	1267

Glu Leu Phe Val Lys Gly Leu Val Arg Ala Val Phe Ala Thr Glu Thr
 375 380 385
 ctg gca ttg gga atc aac atg cca gcg cgc acc gtg gtg ttg gaa aag 1315
 Leu Ala Leu Gly Ile Asn Met Pro Ala Arg Thr Val Val Leu Glu Lys
 390 395 400 405
 atg gtc aaa ttt gac ggc gaa ggc cac gtt gat ctc acc cct ggc caa 1363
 Met Val Lys Phe Asp Gly Glu Gly His Val Asp Leu Thr Pro Gly Gln
 410 415 420
 tac acg cag ctg acc ggt cgt gct ggt cga cgt ggc atc gat gtg ttg 1411
 Tyr Thr Gln Leu Thr Gly Arg Ala Gly Arg Arg Gly Ile Asp Val Leu
 425 430 435
 ggt aat gct gtg gtg cag tgg tca cca gca ctt gat cca cga tgg gtg 1459
 Gly Asn Ala Val Val Gln Trp Ser Pro Ala Leu Asp Pro Arg Trp Val
 440 445 450
 gca ggt ctt gcc tct acg cgt acc tac ccg ctg atc tct acg ttc cag 1507
 Ala Gly Leu Ala Ser Thr Arg Thr Tyr Pro Leu Ile Ser Thr Phe Gln
 455 460 465
 ccg ggc tac aac atg tcg gtt aac ctg ctg aaa acc att ggt tat gag 1555
 Pro Gly Tyr Asn Met Ser Val Asn Leu Leu Lys Thr Ile Gly Tyr Glu
 470 475 480 485
 cct tcg ctg cgc ctt ttg gaa aaa tct ttt gca cag ttc caa gcc gat 1603
 Pro Ser Leu Arg Leu Leu Glu Lys Ser Phe Ala Gln Phe Gln Ala Asp
 490 495 500
 ggt tcc gtc gtg ggc gat gtg cgt gaa att gaa cgt gca gaa gcc aag 1651
 Gly Ser Val Val Gly Asp Val Arg Glu Ile Glu Arg Ala Glu Ala Lys
 505 510 515
 gtg gca gaa ttg cgt gcc cag ctg aac aaa gag att gct gcc acc aac 1699
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 cct gcg 1705
 Pro Ala
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<210> 62

<211> 535

<212> PRT

<213> Corynebacterium glutamicum

<400> 62

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Val Glu Glu Asp His Gly Val Leu Val Cys Ala Pro Thr Gly Ala Gly
 35 40 45

Lys Thr Ile Val Gly Glu Phe Ala Val Ser Leu Ala Leu Ser Arg Gly
 50 55 60

Thr Lys Cys Phe Tyr Thr Thr Pro Ile Lys Ala Leu Ser Asn Gln Lys
 65 70 75 80
 Tyr His Asp Leu Val Ala Lys His Gly Ser Asp Ala Val Gly Leu Leu
 85 90 95
 Thr Gly Asp Val Ser Ile Asn His Asp Ala Asp Ile Val Val Met Thr
 100 105 110
 Thr Glu Val Leu Arg Asn Met Ile Tyr Ala Gly Ser Phe Ala Leu Glu
 115 120 125
 Arg Leu Ser His Val Val Met Asp Glu Ile His Phe Leu Ala Asp Ala
 130 135 140
 Ser Arg Gly Ala Val Trp Glu Glu Val Ile Leu Asn Leu Asp Asp Ser
 145 150 155 160
 Val Asn Ile Ile Gly Leu Ser Ala Thr Val Ser Asn Ser Glu Glu Phe
 165 170 175
 Gly Glu Trp Leu Thr Thr Val Arg Gly Asp Thr Arg Val Ile Val Thr
 180 185 190
 Asp His Arg Pro Val Pro Leu Asp Gln Tyr Met Met Val Gln Arg Lys
 195 200 205
 Val Met Pro Leu Phe Glu Pro Gly Thr Asp Gly Arg Val Asn Lys Glu
 210 215 220
 Leu Glu Ala Thr Ile Asp Arg Leu Asn Ser Lys Gln Ser Glu Gln Gly
 225 230 235 240
 Arg Ala Ala Tyr Arg Ser Gly Glu Gly Phe Arg Ala Arg Ser Lys Gly
 245 250 255
 Asp Lys Gln Asp Ser Arg Thr Gly Lys Pro Arg Glu Gln Asp Arg His
 260 265 270
 Arg Pro Leu Gly Arg Pro Glu Val Leu Ser Ile Leu Lys Gly Ile Asn
 275 280 285
 Met Leu Pro Ala Ile Thr Phe Ile Phe Ser Arg Ala Gly Cys Asp Gly
 290 295 300
 Ala Leu Tyr Gln Cys Leu Arg Ser Lys Leu Val Leu Thr Asp Gln Ala
 305 310 315 320
 Glu Ser Glu Glu Ile Ala Arg Ile Val Asp Ala Gly Val Val Gly Ile
 325 330 335
 Pro Glu Glu Asp Leu Gln Val Leu Asn Phe Lys Gln Trp Arg Ala Ala
 340 345 350
 Leu Met Arg Gly Phe Ala Ala His His Ala Gly Met Leu Pro Ala Phe
 355 360 365
 Arg His Ile Val Glu Glu Leu Phe Val Lys Gly Leu Val Arg Ala Val
 370 375 380

Phe Ala Thr Glu Thr Leu Ala Leu Gly Ile Asn Met Pro Ala Arg Thr
385 390 395 400

Val Val Leu Glu Lys Met Val Lys Phe Asp Gly Glu Gly His Val Asp
405 410 415

Leu Thr Pro Gly Gln Tyr Thr Gln Leu Thr Gly Arg Ala Gly Arg Arg
420 425 430

Gly Ile Asp Val Leu Gly Asn Ala Val Val Gln Trp Ser Pro Ala Leu
435 440 445

Asp Pro Arg Trp Val Ala Gly Leu Ala Ser Thr Arg Thr Tyr Pro Leu
450 455 460

Ile Ser Thr Phe Gln Pro Gly Tyr Asn Met Ser Val Asn Leu Leu Lys
465 470 475 480

Thr Ile Gly Tyr Glu Pro Ser Leu Arg Leu Leu Glu Lys Ser Phe Ala
485 490 495

Gln Phe Gln Ala Asp Gly Ser Val Val Gly Asp Val Arg Glu Ile Glu
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Arg Ala Glu Ala Lys Val Ala Glu Leu Arg Ala Gln Leu Asn Lys Glu
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Ile Ala Ala Thr Asn Pro Ala
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<211> 1974

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1951)

<223> RXN01876

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Met Ala Arg Pro Phe
1 5

tat ctg gcc acc acc gtt tca ccg gag ggc gtg cat atc cgc cgg cac 163
Tyr Leu Ala Thr Thr Val Ser Pro Glu Gly Val His Ile Arg Arg His
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att cgc acc cgt ggg cgc gtt gtc acg ggt gtt gat gat gag gta ttg 211
Ile Arg Thr Arg Gly Arg Val Val Thr Gly Val Asp Asp Glu Val Leu
25 30 35

acc ggt gag atg gcc gat gtt atc gag cag ggt ggt gtc ggc tct gaa 259
Thr Gly Glu Met Ala Asp Val Ile Glu Gln Gly Gly Val Gly Ser Glu
40 45 50

tct gtg ctg cac cag gcg ttg gaa cag gcc cgc agc ggc cac atg cgc 307

Ser	Val	Leu	His	Gln	Ala	Leu	Glu	Gln	Ala	Arg	Ser	Gly	His	Met	Arg	
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Asn	Ile	Val	Glu	Thr	Ile	Gln	Arg	Glu	Gln	Asp	Glu	Ile	Ile	Arg	Asp	
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acc	acc	cgc	ggt	gtc	atg	gtt	gtt	caa	ggt	ggc	cct	gga	aca	ggt	aaa	403
Thr	Thr	Arg	Gly	Val	Met	Val	Val	Gln	Gly	Gly	Pro	Gly	Thr	Gly	Lys	
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act	gcg	gtc	gcg	ttg	cac	cgt	gtg	gct	tat	ctg	ctt	tat	acc	tgg	cgc	451
Thr	Ala	Val	Ala	Leu	His	Arg	Val	Ala	Tyr	Leu	Leu	Tyr	Thr	Trp	Arg	
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Asp	Gln	Leu	Ala	Lys	Ser	Gly	Val	Leu	Ile	Ile	Gly	Pro	Asn	Lys	Thr	
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Phe	Leu	Glu	Tyr	Ile	Ser	His	Val	Leu	Pro	Glu	Leu	Gly	Glu	Thr	Gly	
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gtg	gtg	ttg	tcc	acc	gtc	ggt	gag	ctg	ttc	ccc	ggt	atc	gtc	cca	acg	595
Val	Val	Leu	Ser	Thr	Val	Gly	Glu	Leu	Phe	Pro	Gly	Ile	Val	Pro	Thr	
	150				155					160					165	
ggt	tcc	gag	gac	act	ttg	acc	agg	gaa	att	aag	ggc	agc	gag	gaa	atg	643
Gly	Ser	Glu	Asp	Thr	Leu	Thr	Arg	Glu	Ile	Lys	Gly	Ser	Glu	Glu	Met	
				170				175						180		
gcc	agc	att	ttg	gcc	gag	gca	gtc	aag	gcg	tat	caa	gtg	ctg	cca	gag	691
Ala	Ser	Ile	Leu	Ala	Glu	Ala	Val	Lys	Ala	Tyr	Gln	Val	Leu	Pro	Glu	
			185					190					195			
aag	acc	atc	gtg	gtc	tct	gtt	gat	ggc	atc	gag	att	tcc	att	gat	gag	739
Lys	Thr	Ile	Val	Val	Ser	Val	Asp	Gly	Ile	Glu	Ile	Ser	Ile	Asp	Glu	
		200					205					210				
aaa	acg	gtg	gca	aaa	tcc	cgc	acc	cga	gct	cgt	cgt	gcc	agg	cag	tcg	787
Lys	Thr	Val	Ala	Lys	Ser	Arg	Thr	Arg	Ala	Arg	Arg	Ala	Arg	Gln	Ser	
	215					220					225					
cac	aat	tcc	gca	cgc	cca	att	ttc	cgc	gag	cat	tta	gtc	gaa	caa	ctc	835
His	Asn	Ser	Ala	Arg	Pro	Ile	Phe	Arg	Glu	His	Leu	Val	Glu	Gln	Leu	
	230				235				240						245	
gcg	cac	caa	atg	gct	caa	acg	atc	ggc	gcg	gat	ccg	ctg	ggc	ggc	aaa	883
Ala	His	Gln	Met	Ala	Gln	Thr	Ile	Gly	Ala	Asp	Pro	Leu	Gly	Gly	Lys	
				250				255						260		
aac	ctg	ctg	tca	gcc	gcc	gac	atc	gat	cag	ctg	cac	gat	gat	ttg	ctt	931
Asn	Leu	Leu	Ser	Ala	Ala	Asp	Ile	Asp	Gln	Leu	His	Asp	Asp	Leu	Leu	
			265					270					275			
gac	gac	gcg	gcc	ctc	cag	tcc	gtc	atc	gac	gat	ttc	tgg	ccg	gag	ctc	979
Asp	Asp	Ala	Ala	Leu	Gln	Ser	Val	Ile	Asp	Asp	Phe	Trp	Pro	Glu	Leu	
		280					285					290				
cgg	cct	cag	gac	gtc	ctg	cat	gat	ctg	ttg	att	tcc	gaa	gag	cgc	att	1027
Arg	Pro	Gln	Asp	Val	Leu	His	Asp	Leu	Leu	Ile	Ser	Glu	Glu	Arg	Ile	

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gag tta gcc ctg ctc atc ggt ctt ccc gat cca gag gag gca cgg gag Glu Leu Ala Leu Leu Ile Gly Leu Pro Asp Pro Glu Glu Ala Arg Glu 345 350 355			1171
aag gct gag gcc aaa tgg cgc gag cag atc gat gac gct cag gaa gtc Lys Ala Glu Ala Lys Trp Arg Glu Gln Ile Asp Asp Ala Gln Glu Val 360 365 370			1219
ctg gac gtt ctt agt tca tca cag tca tcg gat att gat gat gtc acg Leu Asp Val Leu Ser Ser Ser Gln Ser Ser Asp Ile Asp Asp Val Thr 375 380 385			1267
gaa gct gaa gtt ctc tcc gct ttc gac gtc atc gat gcg gaa act ttg Glu Ala Glu Val Leu Ser Ala Phe Asp Val Ile Asp Ala Glu Thr Leu 390 395 400 405			1315
gca caa cgc caa act gtc acg gat aat cgc acc act gcg gaa cgt gca Ala Gln Arg Gln Thr Val Thr Asp Asn Arg Thr Thr Ala Glu Arg Ala 410 415 420			1363
cag gcg gat cat aag tgg gca tat ggt cac gtg att gta gat gaa gct Gln Ala Asp His Lys Trp Ala Tyr Gly His Val Ile Val Asp Glu Ala 425 430 435			1411
cag gag ctc agt ccg atg gaa tgg cgc atg gtg ttt cgc cgt agc cct Gln Glu Leu Ser Pro Met Glu Trp Arg Met Val Phe Arg Arg Ser Pro 440 445 450			1459
tcg cga tgg atg acc ctt gtg ggc gat att gca caa act ggt tgg cct Ser Arg Trp Met Thr Leu Val Gly Asp Ile Ala Gln Thr Gly Trp Pro 455 460 465			1507
gcc ggc gtt gac gat tgg gca gaa tca ctg tgg ccc ttc gtc gaa aag Ala Gly Val Asp Asp Trp Ala Glu Ser Leu Trp Pro Phe Val Glu Lys 470 475 480 485			1555
cgt ttc agg cac cac gag ctc acc gtt aac tac cgc acc ccg gcc gag Arg Phe Arg His His Glu Leu Thr Val Asn Tyr Arg Thr Pro Ala Glu 490 495 500			1603
atc atg tcg gtg gcc aat gag ctt ttg acg cag atc aat cct gat att Ile Met Ser Val Ala Asn Glu Leu Leu Thr Gln Ile Asn Pro Asp Ile 505 510 515			1651
gcg ccg gca atg gcg atc cgc gaa tct ggt cga gag gta gtg aac ttg Ala Pro Ala Met Ala Ile Arg Glu Ser Gly Arg Glu Val Val Asn Leu 520 525 530			1699
ccg ctt gat gcc gat ttg tcg gca gtg atg gat agt ttg cgt gag gag Pro Leu Asp Ala Asp Leu Ser Ala Val Met Asp Ser Leu Arg Glu Glu 535 540 545			1747

gat tca cag cgc acc atc gcg gtg att tct tcg cgc cgc cac cac gaa 1795
 Asp Ser Gln Arg Thr Ile Ala Val Ile Ser Ser Arg Arg His His Glu
 550 555 560 565
 agc gat ttc tac ctg gtc gat gac atc aag ggc tta gag ttt gac cac 1843
 Ser Asp Phe Tyr Leu Val Asp Asp Ile Lys Gly Leu Glu Phe Asp His
 570 575 580
 gtc atc gtg gtg gat cct gcg gga atc gtt gaa gaa tcc ccc cag gga 1891
 Val Ile Val Val Asp Pro Ala Gly Ile Val Glu Glu Ser Pro Gln Gly
 585 590 595
 ttg caa gac ctc tac gtt gcg gtc act cgt gca acg cag agc ctc acc 1939
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 600 605 610
 att tta ggt gag tagcagggtta tgagctcagg gcc 1974
 Ile Leu Gly Glu
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<210> 64
 <211> 617
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 64
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 Asp Asp Glu Val Leu Thr Gly Glu Met Ala Asp Val Ile Glu Gln Gly
 35 40 45
 Gly Val Gly Ser Glu Ser Val Leu His Gln Ala Leu Glu Gln Ala Arg
 50 55 60
 Ser Gly His Met Arg Asn Ile Val Glu Thr Ile Gln Arg Glu Gln Asp
 65 70 75 80
 Glu Ile Ile Arg Asp Thr Thr Arg Gly Val Met Val Val Gln Gly Gly
 85 90 95
 Pro Gly Thr Gly Lys Thr Ala Val Ala Leu His Arg Val Ala Tyr Leu
 100 105 110
 Leu Tyr Thr Trp Arg Asp Gln Leu Ala Lys Ser Gly Val Leu Ile Ile
 115 120 125
 Gly Pro Asn Lys Thr Phe Leu Glu Tyr Ile Ser His Val Leu Pro Glu
 130 135 140
 Leu Gly Glu Thr Gly Val Val Leu Ser Thr Val Gly Glu Leu Phe Pro
 145 150 155 160
 Gly Ile Val Pro Thr Gly Ser Glu Asp Thr Leu Thr Arg Glu Ile Lys
 165 170 175

Gly Ser Glu Glu Met Ala Ser Ile Leu Ala Glu Ala Val Lys Ala Tyr
 180 185 190
 Gln Val Leu Pro Glu Lys Thr Ile Val Val Ser Val Asp Gly Ile Glu
 195 200 205
 Ile Ser Ile Asp Glu Lys Thr Val Ala Lys Ser Arg Thr Arg Ala Arg
 210 215 220
 Arg Ala Arg Gln Ser His Asn Ser Ala Arg Pro Ile Phe Arg Glu His
 225 230 235 240
 Leu Val Glu Gln Leu Ala His Gln Met Ala Gln Thr Ile Gly Ala Asp
 245 250 255
 Pro Leu Gly Gly Lys Asn Leu Leu Ser Ala Ala Asp Ile Asp Gln Leu
 260 265 270
 His Asp Asp Leu Leu Asp Asp Ala Ala Leu Gln Ser Val Ile Asp Asp
 275 280 285
 Phe Trp Pro Glu Leu Arg Pro Gln Asp Val Leu His Asp Leu Leu Ile
 290 295 300
 Ser Glu Glu Arg Ile Asn Val Ala Ala Ala Gly Tyr Asp Glu Glu Thr
 305 310 315 320
 Lys Ser Ala Leu Leu Arg Gly Glu Leu Asp Pro Trp Ala Pro Ser Asp
 325 330 335
 Ala Ala Leu Leu Asp Glu Leu Ala Leu Leu Ile Gly Leu Pro Asp Pro
 340 345 350
 Glu Glu Ala Arg Glu Lys Ala Glu Ala Lys Trp Arg Glu Gln Ile Asp
 355 360 365
 Asp Ala Gln Glu Val Leu Asp Val Leu Ser Ser Ser Gln Ser Ser Asp
 370 375 380
 Ile Asp Asp Val Thr Glu Ala Glu Val Leu Ser Ala Phe Asp Val Ile
 385 390 395 400
 Asp Ala Glu Thr Leu Ala Gln Arg Gln Thr Val Thr Asp Asn Arg Thr
 405 410 415
 Thr Ala Glu Arg Ala Gln Ala Asp His Lys Trp Ala Tyr Gly His Val
 420 425 430
 Ile Val Asp Glu Ala Gln Glu Leu Ser Pro Met Glu Trp Arg Met Val
 435 440 445
 Phe Arg Arg Ser Pro Ser Arg Trp Met Thr Leu Val Gly Asp Ile Ala
 450 455 460
 Gln Thr Gly Trp Pro Ala Gly Val Asp Asp Trp Ala Glu Ser Leu Trp
 465 470 475 480
 Pro Phe Val Glu Lys Arg Phe Arg His His Glu Leu Thr Val Asn Tyr
 485 490 495
 Arg Thr Pro Ala Glu Ile Met Ser Val Ala Asn Glu Leu Leu Thr Gln

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530					535					540						
Ser	Leu	Arg	Glu	Glu	Asp	Ser	Gln	Arg	Thr	Ile	Ala	Val	Ile	Ser	Ser	
545					550					555					560	
Arg	Arg	His	His	Glu	Ser	Asp	Phe	Tyr	Leu	Val	Asp	Asp	Ile	Lys	Gly	
565					570					575						
Leu	Glu	Phe	Asp	His	Val	Ile	Val	Val	Asp	Pro	Ala	Gly	Ile	Val	Glu	
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Glu	Ser	Pro	Gln	Gly	Leu	Gln	Asp	Leu	Tyr	Val	Ala	Val	Thr	Arg	Ala	
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 <222> (1)..(1473)
 <223> FRXA01876

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cct gaa ctc ggc gag act ggc gtg gtg ttg tcc acc gtc ggt gag ctg															96	
Pro	Glu	Leu	Gly	Glu	Thr	Gly	Val	Val	Leu	Ser	Thr	Val	Gly	Glu	Leu	
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Phe	Pro	Gly	Ile	Val	Pro	Thr	Gly	Ser	Glu	Asp	Thr	Leu	Thr	Arg	Glu	
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gct cgt cgt gcc agg cag tcg cac aat tcc gca cgc cca att ttc cgc															336	
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100							105					110					
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Glu	His	Leu	Val	Glu	Gln	Leu	Ala	His	Gln	Met	Ala	Gln	Thr	Ile	Gly		
		115					120					125					
gcg	gat	ccg	ctg	ggc	ggc	aaa	aac	ctg	ctg	tca	gcc	gcc	gac	atc	gat	432	
Ala	Asp	Pro	Leu	Gly	Gly	Lys	Asn	Leu	Leu	Ser	Ala	Ala	Asp	Ile	Asp		
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cag	ctg	cac	gat	gat	ttg	ctt	gac	gac	gcg	gcc	ctc	cag	tcc	gtc	atc	480	
Gln	Leu	His	Asp	Asp	Leu	Leu	Asp	Asp	Ala	Ala	Leu	Gln	Ser	Val	Ile		
		145			150					155					160		
gac	gat	ttc	tgg	ccg	gag	ctc	cgg	cct	cag	gac	gtc	ctg	cat	gat	ctg	528	
Asp	Asp	Phe	Trp	Pro	Glu	Leu	Arg	Pro	Gln	Asp	Val	Leu	His	Asp	Leu		
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ttg	att	tcc	gaa	gag	cgc	att	aat	gtt	gct	gcc	gcg	ggg	tat	gac	gag	576	
Leu	Ile	Ser	Glu	Glu	Arg	Ile	Asn	Val	Ala	Ala	Ala	Gly	Tyr	Asp	Glu		
			180					185					190				
gaa	act	aag	tct	gct	ttg	ctg	cgt	ggc	gaa	ctc	gat	ccg	tgg	gca	cca	624	
Glu	Thr	Lys	Ser	Ala	Leu	Leu	Arg	Gly	Glu	Leu	Asp	Pro	Trp	Ala	Pro		
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tcg	gac	gct	gca	ttg	ctt	gat	gag	tta	gcc	ctg	ctc	atc	ggc	ctt	ccc	672	
Ser	Asp	Ala	Ala	Leu	Leu	Asp	Glu	Leu	Ala	Leu	Leu	Ile	Gly	Leu	Pro		
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Asp	Pro	Glu	Glu	Ala	Arg	Glu	Lys	Ala	Glu	Ala	Lys	Trp	Arg	Glu	Gln		
		225			230					235					240		
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Ile	Asp	Asp	Ala	Gln	Glu	Val	Leu	Asp	Val	Leu	Ser	Ser	Ser	Gln	Ser		
				245					250					255			
tcg	gat	att	gat	gat	gtc	acg	gaa	gct	gaa	gtt	ctc	tcc	gct	ttc	gac	816	
Ser	Asp	Ile	Asp	Asp	Val	Thr	Glu	Ala	Glu	Val	Leu	Ser	Ala	Phe	Asp		
			260					265					270				
gtc	atc	gat	gcg	gaa	act	ttg	gca	caa	cgc	caa	act	gtc	acg	gat	aat	864	
Val	Ile	Asp	Ala	Glu	Thr	Leu	Ala	Gln	Arg	Gln	Thr	Val	Thr	Asp	Asn		
		275					280					285					
cgc	acc	act	gcg	gaa	cgt	gca	cag	gcg	gat	cat	aag	tgg	gca	tat	ggc	912	
Arg	Thr	Thr	Ala	Glu	Arg	Ala	Gln	Ala	Asp	His	Lys	Trp	Ala	Tyr	Gly		
		290				295					300						
cac	gtg	att	gta	gat	gaa	gct	cag	gag	ctc	agt	ccg	atg	gaa	tgg	cgc	960	
His	Val	Ile	Val	Asp	Glu	Ala	Gln	Glu	Leu	Ser	Pro	Met	Glu	Trp	Arg		
		305			310					315					320		
atg	gtg	ttt	cgc	cgt	agc	cct	tcg	cga	tgg	atg	acc	ctt	gtg	ggc	gat	1008	
Met	Val	Phe	Arg	Arg	Ser	Pro	Ser	Arg	Trp	Met	Thr	Leu	Val	Gly	Asp		
				325					330					335			
att	gca	caa	act	ggt	tgg	cct	gcc	ggc	gtt	gac	gat	tgg	gca	gaa	tca	1056	
Ile	Ala	Gln	Thr	Gly	Trp	Pro	Ala	Gly	Val	Asp	Asp	Trp	Ala	Glu	Ser		
			340					345					350				

ctg tgg ccc ttc gtc gaa aag cgt ttc agg cac cac gag ctc acc gtt 1104
 Leu Trp Pro Phe Val Glu Lys Arg Phe Arg His His Glu Leu Thr Val
 355 360 365

 aac tac cgc acc ccg gcc gag atc atg tcg gtg gcc aat gag ctt ttg 1152
 Asn Tyr Arg Thr Pro Ala Glu Ile Met Ser Val Ala Asn Glu Leu Leu
 370 375 380

 acg cag atc aat cct gat att gcg ccg gca atg gcg atc cgc gaa tct 1200
 Thr Gln Ile Asn Pro Asp Ile Ala Pro Ala Met Ala Ile Arg Glu Ser
 385 390 395 400

 ggt cga gag gta gtg aac ttg ccg ctt gat gcc gat ttg tcg gca gtg 1248
 Gly Arg Glu Val Val Asn Leu Pro Leu Asp Ala Asp Leu Ser Ala Val
 405 410 415

 atg gat agt ttg cgt gag gag gat tca cag cgc acc atc gcg gtg att 1296
 Met Asp Ser Leu Arg Glu Glu Asp Ser Gln Arg Thr Ile Ala Val Ile
 420 425 430

 tct tcg cgc cgc cac cac gaa agc gat ttc tac ctg gtc gat gac atc 1344
 Ser Ser Arg Arg His His Glu Ser Asp Phe Tyr Leu Val Asp Asp Ile
 435 440 445

 aag ggc tta gag ttt gac cac gtc atc gtg gtg gat cct gcg gga atc 1392
 Lys Gly Leu Glu Phe Asp His Val Ile Val Val Asp Pro Ala Gly Ile
 450 455 460

 gtt gaa gaa tcc ccc cag gga ttg caa gac ctc tac gtt gcg gtc act 1440
 Val Glu Glu Ser Pro Gln Gly Leu Gln Asp Leu Tyr Val Ala Val Thr
 465 470 475 480

 cgt gca acg cag agc ctc acc att tta ggt gag tagcagggtta tgagctcagg 1493
 Arg Ala Thr Gln Ser Leu Thr Ile Leu Gly Glu
 485 490

 gcc 1496

<210> 66

<211> 491

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

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Pro Glu Leu Gly Glu Thr Gly Val Val Leu Ser Thr Val Gly Glu Leu
 20 25 30

Phe Pro Gly Ile Val Pro Thr Gly Ser Glu Asp Thr Leu Thr Arg Glu
 35 40 45

Ile Lys Gly Ser Glu Glu Met Ala Ser Ile Leu Ala Glu Ala Val Lys
 50 55 60

Ala Tyr Gln Val Leu Pro Glu Lys Thr Ile Val Val Ser Val Asp Gly
 65 70 75 80

Ile Glu Ile Ser Ile Asp Glu Lys Thr Val Ala Lys Ser Arg Thr Arg
 85 90 95
 Ala Arg Arg Ala Arg Gln Ser His Asn Ser Ala Arg Pro Ile Phe Arg
 100 105 110
 Glu His Leu Val Glu Gln Leu Ala His Gln Met Ala Gln Thr Ile Gly
 115 120 125
 Ala Asp Pro Leu Gly Gly Lys Asn Leu Leu Ser Ala Ala Asp Ile Asp
 130 135 140
 Gln Leu His Asp Asp Leu Leu Asp Asp Ala Ala Leu Gln Ser Val Ile
 145 150 155 160
 Asp Asp Phe Trp Pro Glu Leu Arg Pro Gln Asp Val Leu His Asp Leu
 165 170 175
 Leu Ile Ser Glu Glu Arg Ile Asn Val Ala Ala Ala Gly Tyr Asp Glu
 180 185 190
 Glu Thr Lys Ser Ala Leu Leu Arg Gly Glu Leu Asp Pro Trp Ala Pro
 195 200 205
 Ser Asp Ala Ala Leu Leu Asp Glu Leu Ala Leu Leu Ile Gly Leu Pro
 210 215 220
 Asp Pro Glu Glu Ala Arg Glu Lys Ala Glu Ala Lys Trp Arg Glu Gln
 225 230 235 240
 Ile Asp Asp Ala Gln Glu Val Leu Asp Val Leu Ser Ser Ser Gln Ser
 245 250 255
 Ser Asp Ile Asp Asp Val Thr Glu Ala Glu Val Leu Ser Ala Phe Asp
 260 265 270
 Val Ile Asp Ala Glu Thr Leu Ala Gln Arg Gln Thr Val Thr Asp Asn
 275 280 285
 Arg Thr Thr Ala Glu Arg Ala Gln Ala Asp His Lys Trp Ala Tyr Gly
 290 295 300
 His Val Ile Val Asp Glu Ala Gln Glu Leu Ser Pro Met Glu Trp Arg
 305 310 315 320
 Met Val Phe Arg Arg Ser Pro Ser Arg Trp Met Thr Leu Val Gly Asp
 325 330 335
 Ile Ala Gln Thr Gly Trp Pro Ala Gly Val Asp Asp Trp Ala Glu Ser
 340 345 350
 Leu Trp Pro Phe Val Glu Lys Arg Phe Arg His His Glu Leu Thr Val
 355 360 365
 Asn Tyr Arg Thr Pro Ala Glu Ile Met Ser Val Ala Asn Glu Leu Leu
 370 375 380
 Thr Gln Ile Asn Pro Asp Ile Ala Pro Ala Met Ala Ile Arg Glu Ser
 385 390 395 400
 Gly Arg Glu Val Val Asn Leu Pro Leu Asp Ala Asp Leu Ser Ala Val

405	Met Asp Ser Leu Arg Glu Glu Asp Ser Gln Arg Thr Ile Ala Val Ile	410	415
420		425	430
Ser Ser Arg Arg His His Glu Ser Asp Phe Tyr Leu Val Asp Asp Ile			
435		440	445
Lys Gly Leu Glu Phe Asp His Val Ile Val Val Asp Pro Ala Gly Ile			
450		455	460
Val Glu Glu Ser Pro Gln Gly Leu Gln Asp Leu Tyr Val Ala Val Thr			
465		470	475
Arg Ala Thr Gln Ser Leu Thr Ile Leu Gly Glu			
485		490	

<210> 67

<211> 1653

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1630)

<223> RXA00544

<400> 67

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ggggctagag tgaacttaga atcagattgg ggaaaagaaa atg gct aca gat aca	115
Met Ala Thr Asp Thr	
1 5	

cac gcc gca agt ttt gat gat gac tac gta cct cca cag gag cca agc	163
His Ala Ala Ser Phe Asp Asp Asp Tyr Val Pro Pro Gln Glu Pro Ser	
10 15 20	

gat tcc ttc gcg gat gac gca cac gta gat gtc cct gct ccg gcg ttt	211
Asp Ser Phe Ala Asp Asp Ala His Val Asp Val Pro Ala Pro Ala Phe	
25 30 35	

gaa gat ttc tcc ccg gcc cag gcc ttt ggt cag gga act agg gga gga	259
Glu Asp Phe Ser Pro Ala Gln Ala Phe Gly Gln Gly Thr Arg Gly Gly	
40 45 50	

gac tct cag ggc ttc aag aag agg ggt cgc aag gac gag tcc cgt gaa	307
Asp Ser Gln Gly Phe Lys Lys Arg Gly Arg Lys Asp Glu Ser Arg Glu	
55 60 65	

tac cga gac ttc cgc caa cct ccc tat gac aat gac gct gag atg ggc	355
Tyr Arg Asp Phe Arg Gln Pro Pro Tyr Asp Asn Asp Ala Glu Met Gly	
70 75 80 85	

gtg ctg ggc gcg atg ctg ctc agt ccg acc acg gtc atc gac att ctg	403
Val Leu Gly Ala Met Leu Leu Ser Pro Thr Thr Val Ile Asp Ile Leu	
90 95 100	

gat atc ctc acc cca gaa gac ttc tac agg ccg tcc cac cag ctg att	451
Asp Ile Leu Thr Pro Glu Asp Phe Tyr Arg Pro Ser His Gln Leu Ile	

105	110	115	
ttc cag gcg atc att gac ctg ttc agt gac aac cgt gat att gac ccc Phe Gln Ala Ile Ile Asp Leu Phe Ser Asp Asn Arg Asp Ile Asp Pro 120 125 130			499
gtg att gtc tcc ggt cgc ctc gat cga acc aac gat ctg gac cgc gtc Val Ile Val Ser Gly Arg Leu Asp Arg Thr Asn Asp Leu Asp Arg Val 135 140 145			547
ggc ggt ggc gcg tac ctc cac gac ctc atc cag tcc gtt ccc acc gca Gly Gly Gly Ala Tyr Leu His Asp Leu Ile Gln Ser Val Pro Thr Ala 150 155 160 165			595
gcc aac gcg cgc tac tat gcg gaa atc gtt tcg gaa aag gca gtg ctt Ala Asn Ala Arg Tyr Tyr Ala Glu Ile Val Ser Glu Lys Ala Val Leu 170 175 180			643
cgc agg ctt gtc gac gcc ggc acc cgc gtc gtc cag ctc ggc tac gag Arg Arg Leu Val Asp Ala Gly Thr Arg Val Val Gln Leu Gly Tyr Glu 185 190 195			691
ggc gat gaa ggc gcc gaa att gac gcg gtg att gac cgc gcg cag caa Gly Asp Glu Gly Ala Glu Ile Asp Ala Val Ile Asp Arg Ala Gln Gln 200 205 210			739
gaa gtc ttc gcc gtt tcc caa aag aat cag agc gaa gac tat gca gtc Glu Val Phe Ala Val Ser Gln Lys Asn Gln Ser Glu Asp Tyr Ala Val 215 220 225			787
cta gcc gat att ctg gat gaa acc atg gct gag ctg gaa atg ctc aac Leu Ala Asp Ile Leu Asp Glu Thr Met Ala Glu Leu Glu Met Leu Asn 230 235 240 245			835
gac ggc ggc atc gcc acc ggt att cca acc ggc ttc aaa gat ctc gat Asp Gly Gly Ile Ala Thr Gly Ile Pro Thr Gly Phe Lys Asp Leu Asp 250 255 260			883
gac ctc acc aac ggt ctg cgc ggt ggc cag atg atc atc gtt gca gct Asp Leu Thr Asn Gly Leu Arg Gly Gly Gln Met Ile Ile Val Ala Ala 265 270 275			931
cgt cct ggt gtg ggt aaa tcc acc atc gcc ttg gac ttc atg cgt tcg Arg Pro Gly Val Gly Lys Ser Thr Ile Ala Leu Asp Phe Met Arg Ser 280 285 290			979
gca tcc atc aag aac aac atg gcg tct gtc att ttc tcc ttg gaa atg Ala Ser Ile Lys Asn Asn Met Ala Ser Val Ile Phe Ser Leu Glu Met 295 300 305			1027
tcc aag tca gag atc gtg atg cgt ttg ctc tct gca gaa aca gaa atc Ser Lys Ser Glu Ile Val Met Arg Leu Leu Ser Ala Glu Thr Glu Ile 310 315 320 325			1075
cgc ctg gct gat atg cgt ggt gga aag atg gat gaa acc gca tgg gaa Arg Leu Ala Asp Met Arg Gly Gly Lys Met Asp Glu Thr Ala Trp Glu 330 335 340			1123
aag atg gtg cag aag tta gac aag gta gcc cag gca cct ttg ttc atc Lys Met Val Gln Lys Leu Asp Lys Val Ala Gln Ala Pro Leu Phe Ile 345 350 355			1171

gat gac tcc gcg aac ctc acc atg atg gaa atc cgc tcc aag gcc aga 1219
Asp Asp Ser Ala Asn Leu Thr Met Met Glu Ile Arg Ser Lys Ala Arg
360 365 370
aag ctg aag cag aag cat gat ctg aaa atg atc gtg gtg gac tac ctc 1267
Lys Leu Lys Gln Lys His Asp Leu Lys Met Ile Val Val Asp Tyr Leu
375 380 385
cag ctg atg agc tcc ggt aaa cgc gtg gaa tcc cgt cag cag gaa gtc 1315
Gln Leu Met Ser Ser Gly Lys Arg Val Glu Ser Arg Gln Gln Glu Val
390 395 400 405
tcc gag ttc tcc cgt cag ctc aag ctg ctg gcc aaa gaa ctc gat gtg 1363
Ser Glu Phe Ser Arg Gln Leu Lys Leu Leu Ala Lys Glu Leu Asp Val
410 415 420
ccg ttg atc gcg att tcc cag ctg aac cgt gga cct gaa tcc cgt acc 1411
Pro Leu Ile Ala Ile Ser Gln Leu Asn Arg Gly Pro Glu Ser Arg Thr
425 430 435
gat aag cga cca cag ctt gct gac ctt cgt gaa tcc ggc tcg ctg gag 1459
Asp Lys Arg Pro Gln Leu Ala Asp Leu Arg Glu Ser Gly Ser Leu Glu
440 445 450
cag gac gcc gat atc gtt atg ctg cta tac cgc cca gac tcc cag gat 1507
Gln Asp Ala Asp Ile Val Met Leu Leu Tyr Arg Pro Asp Ser Gln Asp
455 460 465
aag gac gac gag cgc gcg ggc gag gcc gac atc att ttg gct aag cac 1555
Lys Asp Asp Glu Arg Ala Gly Glu Ala Asp Ile Ile Leu Ala Lys His
470 475 480 485
cgt ggt ggc ccg atc gat acc gtc cag gtg gcg cac cag ctg cac tat 1603
Arg Gly Gly Pro Ile Asp Thr Val Gln Val Ala His Gln Leu His Tyr
490 495 500
tca cgt ttt gtg gac atg gcg cgc ggt taagaaaaagt tcatttttct 1650
Ser Arg Phe Val Asp Met Ala Arg Gly
505 510
aaa 1653

<210> 68

<211> 510

<212> PRT

<213> Corynebacterium glutamicum

<400> 68

Met Ala Thr Asp Thr His Ala Ala Ser Phe Asp Asp Asp Tyr Val Pro
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Pro Gln Glu Pro Ser Asp Ser Phe Ala Asp Asp Ala His Val Asp Val
20 25 30

Pro Ala Pro Ala Phe Glu Asp Phe Ser Pro Ala Gln Ala Phe Gly Gln
35 40 45

Gly Thr Arg Gly Gly Asp Ser Gln Gly Phe Lys Lys Arg Gly Arg Lys
50 55 60

Asp Glu Ser Arg Glu Tyr Arg Asp Phe Arg Gln Pro Pro Tyr Asp Asn
 65 70 75 80
 Asp Ala Glu Met Gly Val Leu Gly Ala Met Leu Leu Ser Pro Thr Thr
 85 90 95
 Val Ile Asp Ile Leu Asp Ile Leu Thr Pro Glu Asp Phe Tyr Arg Pro
 100 105 110
 Ser His Gln Leu Ile Phe Gln Ala Ile Ile Asp Leu Phe Ser Asp Asn
 115 120 125
 Arg Asp Ile Asp Pro Val Ile Val Ser Gly Arg Leu Asp Arg Thr Asn
 130 135 140
 Asp Leu Asp Arg Val Gly Gly Gly Ala Tyr Leu His Asp Leu Ile Gln
 145 150 155 160
 Ser Val Pro Thr Ala Ala Asn Ala Arg Tyr Tyr Ala Glu Ile Val Ser
 165 170 175
 Glu Lys Ala Val Leu Arg Arg Leu Val Asp Ala Gly Thr Arg Val Val
 180 185 190
 Gln Leu Gly Tyr Glu Gly Asp Glu Gly Ala Glu Ile Asp Ala Val Ile
 195 200 205
 Asp Arg Ala Gln Gln Glu Val Phe Ala Val Ser Gln Lys Asn Gln Ser
 210 215 220
 Glu Asp Tyr Ala Val Leu Ala Asp Ile Leu Asp Glu Thr Met Ala Glu
 225 230 235 240
 Leu Glu Met Leu Asn Asp Gly Gly Ile Ala Thr Gly Ile Pro Thr Gly
 245 250 255
 Phe Lys Asp Leu Asp Asp Leu Thr Asn Gly Leu Arg Gly Gly Gln Met
 260 265 270
 Ile Ile Val Ala Ala Arg Pro Gly Val Gly Lys Ser Thr Ile Ala Leu
 275 280 285
 Asp Phe Met Arg Ser Ala Ser Ile Lys Asn Asn Met Ala Ser Val Ile
 290 295 300
 Phe Ser Leu Glu Met Ser Lys Ser Glu Ile Val Met Arg Leu Leu Ser
 305 310 315 320
 Ala Glu Thr Glu Ile Arg Leu Ala Asp Met Arg Gly Gly Lys Met Asp
 325 330 335
 Glu Thr Ala Trp Glu Lys Met Val Gln Lys Leu Asp Lys Val Ala Gln
 340 345 350
 Ala Pro Leu Phe Ile Asp Asp Ser Ala Asn Leu Thr Met Met Glu Ile
 355 360 365
 Arg Ser Lys Ala Arg Lys Leu Lys Gln Lys His Asp Leu Lys Met Ile
 370 375 380

Val	Val	Asp	Tyr	Leu	Gln	Leu	Met	Ser	Ser	Gly	Lys	Arg	Val	Glu	Ser	385	390	395	400
Arg	Gln	Gln	Glu	Val	Ser	Glu	Phe	Ser	Arg	Gln	Leu	Lys	Leu	Leu	Ala	405	410	415	
Lys	Glu	Leu	Asp	Val	Pro	Leu	Ile	Ala	Ile	Ser	Gln	Leu	Asn	Arg	Gly	420	425	430	
Pro	Glu	Ser	Arg	Thr	Asp	Lys	Arg	Pro	Gln	Leu	Ala	Asp	Leu	Arg	Glu	435	440	445	
Ser	Gly	Ser	Leu	Glu	Gln	Asp	Ala	Asp	Ile	Val	Met	Leu	Leu	Tyr	Arg	450	455	460	
Pro	Asp	Ser	Gln	Asp	Lys	Asp	Asp	Glu	Arg	Ala	Gly	Glu	Ala	Asp	Ile	465	470	475	480
Ile	Leu	Ala	Lys	His	Arg	Gly	Gly	Pro	Ile	Asp	Thr	Val	Gln	Val	Ala	485	490	495	
His	Gln	Leu	His	Tyr	Ser	Arg	Phe	Val	Asp	Met	Ala	Arg	Gly			500	505	510	

<210> 69

<211> 421

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(421)

<223> RXA01866

<400> 69

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tggattaaag ccagcctgat tcttcgatct cagctaccac ttg aaa ccc ggc cac 115
                                   Leu Lys Pro Gly His
                                   1 5

cgc gat gac ggc gtc aca gtc ctc atc ccc att cca gtg ctg ggt gga 163
Arg Asp Asp Gly Val Thr Val Leu Ile Pro Ile Pro Val Leu Gly Gly
                                   10 15 20

ctt gat acc gaa ggc ttc gat tgg cta gtt cca ggc tta agg ctt gat 211
Leu Asp Thr Glu Gly Phe Asp Trp Leu Val Pro Gly Leu Arg Leu Asp
                                   25 30 35

ttg gtg acc gag tta atc cgc acc atg cct aag gct tta cga cgc acc 259
Leu Val Thr Glu Leu Ile Arg Thr Met Pro Lys Ala Leu Arg Arg Thr
                                   40 45 50

gtt gtc cct gcc ccg gat ttc gcc gag cgg gtc ttg ccg tta ctg cgt 307
Val Val Pro Ala Pro Asp Phe Ala Glu Arg Val Leu Pro Leu Leu Arg
                                   55 60 65

ccc tac atg aca cca ctg acc acc caa ctt gcc gat gca ctc cat acc 355
Pro Tyr Met Thr Pro Leu Thr Thr Gln Leu Ala Asp Ala Leu His Thr
                                   70 75 80 85

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ctg ggc ggc caa gga atc aac gcc tct gat ttc gat cct gcc aaa ctc 403
 Leu Gly Gly Gln Gly Ile Asn Ala Ser Asp Phe Asp Pro Ala Lys Leu
 90 95 100

ccc gat cac ctg cgc att 421
 Pro Asp His Leu Arg Ile
 105

<210> 70

<211> 107

<212> PRT

<213> Corynebacterium glutamicum

<400> 70

Leu Lys Pro Gly His Arg Asp Asp Gly Val Thr Val Leu Ile Pro Ile
 1 5 10 15

Pro Val Leu Gly Gly Leu Asp Thr Glu Gly Phe Asp Trp Leu Val Pro
 20 25 30

Gly Leu Arg Leu Asp Leu Val Thr Glu Leu Ile Arg Thr Met Pro Lys
 35 40 45

Ala Leu Arg Arg Thr Val Val Pro Ala Pro Asp Phe Ala Glu Arg Val
 50 55 60

Leu Pro Leu Leu Arg Pro Tyr Met Thr Pro Leu Thr Thr Gln Leu Ala
 65 70 75 80

Asp Ala Leu His Thr Leu Gly Gly Gln Gly Ile Asn Ala Ser Asp Phe
 85 90 95

Asp Pro Ala Lys Leu Pro Asp His Leu Arg Ile
 100 105

<210> 71

<211> 515

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(492)

<223> RXA01867

<400> 71

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 1 5 10 15

tct gaa ccg tat tgg tcc tca aag cgt ggc gct gcc atg gtg cac cgc 96
 Ser Glu Pro Tyr Trp Ser Ser Lys Arg Gly Ala Ala Met Val His Arg
 20 25 30

aaa tca acg ctc ttc ggt gtg aca att gtt gcc gtc aag gta gtt ccc 144
 Lys Ser Thr Leu Phe Gly Val Thr Ile Val Ala Val Lys Val Val Pro
 35 40 45

tac cac acg gtt gat ccc gtg gct gcg cgc gat atg ttc atc cgc cat 192
 Tyr His Thr Val Asp Pro Val Ala Ala Arg Asp Met Phe Ile Arg His
 50 55 60

gcc ctc atc gaa ggc gat tgg tcc act cac cac cgc ttc tac cac gac 240
 Ala Leu Ile Glu Gly Asp Trp Ser Thr His His Arg Phe Tyr His Asp
 65 70 75 80

aac gtg gcc aaa ttg gag gca atc gga gaa ctt gaa gcc aag gcg cgt 288
 Asn Val Ala Lys Leu Glu Ala Ile Gly Glu Leu Glu Ala Lys Ala Arg
 85 90 95

cgc cgc gac atc gtc gta gat gaa gac acc ctg ttt gat ttc tac gat 336
 Arg Arg Asp Ile Val Val Asp Glu Asp Thr Leu Phe Asp Phe Tyr Asp
 100 105 110

gcc aag ctt cca agc aac gcc acc acc acc cgc aat ttc gat tcc tgg 384
 Ala Lys Leu Pro Ser Asn Ala Thr Thr Arg Asn Phe Asp Ser Trp
 115 120 125

tgg aag aaa aca tca cgc gtc aca cca gat ctt ctc gat ttc gac cca 432
 Trp Lys Lys Thr Ser Arg Val Thr Pro Asp Leu Leu Asp Phe Asp Pro
 130 135 140

gat agt ctg atc aag gaa gac gct ggg gcg tta cga aga agc ctt tcc 480
 Asp Ser Leu Ile Lys Glu Asp Ala Gly Ala Leu Arg Arg Ser Leu Ser
 145 150 155 160

cga caa gtg gat taaagccagc ctgattcttc gat 515
 Arg Gln Val Asp

<210> 72

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 72

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 20 25 30

Lys Ser Thr Leu Phe Gly Val Thr Ile Val Ala Val Lys Val Val Pro
 35 40 45

Tyr His Thr Val Asp Pro Val Ala Ala Arg Asp Met Phe Ile Arg His
 50 55 60

Ala Leu Ile Glu Gly Asp Trp Ser Thr His His Arg Phe Tyr His Asp
 65 70 75 80

Asn Val Ala Lys Leu Glu Ala Ile Gly Glu Leu Glu Ala Lys Ala Arg
 85 90 95

Arg Arg Asp Ile Val Val Asp Glu Asp Thr Leu Phe Asp Phe Tyr Asp
 100 105 110

Ala Lys Leu Pro Ser Asn Ala Thr Thr Thr Arg Asn Phe Asp Ser Trp

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<210> 73
<211> 2358
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101) .. (2335)  
<223> RXN03166
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											atg Met 1	act Thr	act Thr	tct Ser	gaa Glu 5	115
act	gcc	cca	tca	aag	gct	tcc	ctg	tat	gaa	ctt	tta	gag	ggc	gta	tcc	163
Thr	Ala	Pro	Ser	Lys 10	Ala	Ser	Leu	Tyr	Glu 15	Leu	Leu	Glu	Gly	Val 20	Ser	
ctc tcc gac gag cgc acg ttt agg cgc cga ctg tcc aaa gcc cgc gcg																211
Leu	Ser	Asp	Glu 25	Arg	Thr	Phe	Arg 30	Arg	Arg	Leu	Ser	Lys	Ala 35	Arg	Ala	
ccc aag gcg ctt ggt gcg att aag gct gat atc gat aag gca cgc ttg																259
Pro	Lys	Ala 40	Leu	Gly	Ala	Ile	Lys 45	Ala	Asp	Ile	Asp	Lys 50	Ala	Arg	Leu	
ctt atc gac gaa aag agc cag tta att ccg tct atc acc tac cca gaa																307
Leu	Ile 55	Asp	Glu	Lys	Ser	Gln 60	Leu	Ile	Pro	Ser	Ile 65	Thr	Tyr	Pro	Glu	
aac ctt ccg gtg agt tcc cgg cgc gat gat atc gcc gag gct atc cgt																355
Asn 70	Leu	Pro	Val	Ser	Ser 75	Arg	Arg	Asp	Asp	Ile 80	Ala	Glu	Ala	Ile	Arg 85	
gat aat cag gtg gtt att atc gcc ggt gag act ggt tcg ggt aag acg																403
Asp	Asn	Gln	Val 90	Val	Ile	Ile	Ala	Gly	Glu 95	Thr	Gly	Ser	Gly	Lys 100	Thr	
act cag att cct aag att tgt ttg gac cta ggc cgt ggc cgg cgt ggg																451
Thr	Gln	Ile	Pro 105	Lys	Ile	Cys	Leu	Asp 110	Leu	Gly	Arg	Gly	Arg 115	Arg	Gly	
ctc att ggc cac aca cag cca cgt cga tta gca gct agg acc gtc gcc																499
Leu	Ile	Gly 120	His	Thr	Gln	Pro	Arg 125	Arg	Leu	Ala	Ala	Arg 130	Thr	Val	Ala	

gag cgc atc gcc gat gaa ttg ggg caa gac atc ggc gaa tcg gtg ggt	547
Glu Arg Ile Ala Asp Glu Leu Gly Gln Asp Ile Gly Glu Ser Val Gly	
135 140 145	
tat gcg att cgt ttt gat gat cga gtt tcc tcg cat aca tcc gtg aag	595
Tyr Ala Ile Arg Phe Asp Asp Arg Val Ser Ser His Thr Ser Val Lys	
150 155 160 165	
ttg atg acg gat ggt att ttg ctt gct gaa atg cag cgg gat cgt ttc	643
Leu Met Thr Asp Gly Ile Leu Leu Ala Glu Met Gln Arg Asp Arg Phe	
170 175 180	
ctc aat gcg tat gac acc atc atc atc gat gag gcg cat gaa cgt tcc	691
Leu Asn Ala Tyr Asp Thr Ile Ile Ile Asp Glu Ala His Glu Arg Ser	
185 190 195	
ctc aac att gac ttc att ctg ggt tat ttg cgc cag ttg ttg cct aag	739
Leu Asn Ile Asp Phe Ile Leu Gly Tyr Leu Arg Gln Leu Leu Pro Lys	
200 205 210	
cgc cct gat ctt aaa gtc att att acc tcc gca acg att gac cct gag	787
Arg Pro Asp Leu Lys Val Ile Ile Thr Ser Ala Thr Ile Asp Pro Glu	
215 220 225	
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Ile Glu Val Ser Gly Arg Thr Phe Pro Val Glu Ile Arg Tyr Arg Pro	
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Leu Glu Val Leu Asp Gly Asp Lys Ile Ile Asp Thr Asp Pro Leu Asp	
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Gly Leu Cys Ser Ala Leu Glu Glu Leu Met Ala Glu Gly Asp Gly Asp	
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Gly Arg Arg Ile Val Leu Ser Thr Asn Ile Ala Glu Thr Ser Leu Thr	
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Val Pro Gly Ile His Tyr Val Val Asp Thr Gly Thr Ala Arg Ile Ser	
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Pro	Glu	Phe	Thr	Asp	Pro	Glu	Ile	Leu	Arg	Thr	Asn	Leu	Ala	Ser	Val	
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Ile	Leu	Arg	Met	Ala	Ser	Leu	Arg	Leu	Gly	Asp	Ile	Asn	Asp	Phe	Pro	
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Phe	Val	Gln	Ala	Pro	Glu	Gln	Arg	Ser	Ile	Arg	Asp	Gly	Ile	Leu	Leu	
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ctc	cac	gag	ttg	ggc	gca	ctc	acc	gac	gac	acc	caa	gcc	gat	ggg	tca	1555
Leu	His	Glu	Leu	Gly	Ala	Leu	Thr	Asp	Asp	Thr	Gln	Ala	Asp	Gly	Ser	
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His	Ser	Val	Met	Val	Ile	Val	Ser	Ala	Leu	Thr	Ile	Gln	Asp	Val	Arg	
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Glu	Arg	Pro	Leu	Glu	Phe	Gln	Ala	Gln	Ala	Asp	Gln	Ala	His	Ala	Arg	
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Phe	Lys	Asp	Thr	Thr	Ser	Asp	Phe	Leu	Gly	Phe	Leu	Lys	Leu	Trp	Glu	
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Tyr	Ile	Ala	Asp	Gln	Arg	Asn	Gln	Ser	Ser	Gly	Asn	Ser	Phe	Arg	Lys	
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cag	atg	aaa	aaa	gaa	ttc	ctc	cac	tac	atg	cgt	atc	cgc	gag	tgg	tgg	1891
Gln	Met	Lys	Lys	Glu	Phe	Leu	His	Tyr	Met	Arg	Ile	Arg	Glu	Trp	Trp	
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Asp	Leu	Val	Arg	Gln	Leu	Glu	Gln	Ile	Gly	Gln	Gln	Leu	Gly	Trp	Ala	
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Lys	Lys	Glu	Gln	Val	Ala	Gly	Thr	Ala	Ser	Pro	Asp	Ile	Ile	His	Gln	

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Ser Lys Glu Phe Thr Gly Ala Arg Gly Thr Lys Phe Leu Val Phe Pro			
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Gly Ser Ala Leu Thr Lys Lys Pro Pro Gln Phe Ile Met Ala Gly Gln			
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Pro Glu Trp Val Glu Lys Ala Ala Gly Pro Leu Leu Lys His Gln Tyr			
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Ser Glu Pro Tyr Trp Ser Ser Lys Arg Gly Gly Cys His Gly Ala Pro			
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 Ala His Glu Arg Ser Leu Asn Ile Asp Phe Ile Leu Gly Tyr Leu Arg
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 Gln Ala Asp Gly Ser Pro Gln Leu Thr Gln Ile Gly Lys Asp Leu Ala
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Tyr Asp Thr Ile Ile Ile Asp Glu Ala His Glu Arg Ser Leu Asn Ile	
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Glu His Phe Ala Asp Ala Ser Gly Lys Pro Ala Pro Ile Ile Glu Val	
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Ser Gly Arg Thr Phe Pro Val Glu Ile Arg Tyr Arg Pro Leu Glu Val	
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Leu Asp Gly Asp Lys Ile Ile Asp Thr Asp Pro Leu Asp Gly Leu Cys	
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Ile His Tyr Val Val Asp Thr Gly Thr Ala Arg Ile Ser Arg Tyr Ser	
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Val Arg Thr Lys Val Gln Arg Leu Pro Ile Glu Asn Ile Ser Gln Ala	
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Asp Ser Asp Leu Leu Leu Gly Met Leu Ala Glu Leu Ser Gln Leu Arg
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Asp Asp Phe Ser Leu Ile Ala Met Ser Ala Thr Leu Asp Ser Asp Lys
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Phe Ala Asn Leu Leu Asp Ala Gln Val Leu Ser Val Glu Ala Pro Ile
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Gly Val Arg Glu Ile Asp Arg Val Met Ser Thr Leu Lys Ser Leu Gly	
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His Asn Asn Val Phe Pro Leu His Gly Gln Leu Ser Pro Thr Glu Gln	
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Asp Arg Ala Leu Ala Pro Ser Gln Gln Gln Arg Ile Ile Val Ser Thr	
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Pro Val Ala Glu Ser Ser Leu Thr Val Pro Gly Val Arg Ile Gly Val	
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Leu Gly Thr Lys Val Gly Phe Ser Val Arg Gly Glu His Ile Ser Gly
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Gly Phe Ser Val Arg Gly Glu His Ile Ser Gly Ser His Val Gln Phe
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Lys	Val	Lys	Ala	Ala	Gly	Ala	Ile	Glu	Leu	Ser	Ser	Thr	Pro	Thr	Lys	
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cca	aca	ccc	gcc	gaa	gcc	tcg	gaa	aca	atc	gcc	aca	gcc	ctt	gcc	aaa	1939
Pro	Thr	Pro	Ala	Glu	Ala	Ser	Glu	Thr	Ile	Ala	Thr	Ala	Leu	Ala	Lys	
		600					605					610				
ggc	gga	atc	gac	cta	ttc	cac	ttc	tcc	gac	aaa	gcg	gca	tcc	ttg	cgt	1987
Gly	Gly	Ile	Asp	Leu	Phe	His	Phe	Ser	Asp	Lys	Ala	Ala	Ser	Leu	Arg	
	615					620					625					
gac	cga	ctg	aaa	ttc	atc	cac	gaa	cac	cgt	ggc	gaa	ccc	tgg	cca	gat	2035
Asp	Arg	Leu	Lys	Phe	Ile	His	Glu	His	Arg	Gly	Glu	Pro	Trp	Pro	Asp	
630					635				640						645	
att	gaa	act	gcg	gac	ccg	cac	ctg	tgg	tta	tct	cca	gaa	att	gag	gcg	2083
Ile	Glu	Thr	Ala	Asp	Pro	His	Leu	Trp	Leu	Ser	Pro	Glu	Ile	Glu	Ala	
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ctc	agc	cac	gga	aca	cga	cta	aac	aat	atc	gat	atg	tat	ccc	gca	ctc	2131
Leu	Ser	His	Gly	Thr	Arg	Leu	Asn	Asn	Ile	Asp	Met	Tyr	Pro	Ala	Leu	
			665					670					675			

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 Gln Arg Leu Leu Pro Trp Pro Glu Ala Thr Asn Phe Glu Glu Phe Ala
 680 685 690

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 Ser Ser Gly Arg Pro Val Ile Arg Val Lys Leu Gln Glu Cys Phe Gly
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 Phe Trp Ser Gly Pro Tyr Ser Gln Val Arg Ala Glu Met Arg Gly Arg
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 Tyr Pro Lys His Pro Trp Pro Glu Asp Pro Trp Thr Ala Pro Ala Thr
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Gly Pro Lys Asn Leu Val Ile Gln Ala Pro Pro Gly Thr Gly Lys Thr
 35 40 45

Thr Leu Leu Pro Pro Leu Val Ala Asn Ile Leu Cys Asn Glu Gly Ala
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Gly Asn Ala Thr Pro Thr Lys Val Leu Val Thr Ala Pro Arg Arg Val
 65 70 75 80

Ala Val Arg Ala Ala Arg Arg Leu Ala Gln Leu Asp Asp Ser Gln
 85 90 95

Leu Gly Thr Lys Val Gly Phe Ser Val Arg Gly Glu His Ile Ser Gly
 100 105 110

Ser His Val Gln Phe Met Thr Pro Gly Val Leu Ile Arg Gln Leu Leu

115					120					125					
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His	Glu	Arg	Gln	Leu	Asp	Ser	Asp	Leu	Leu	Leu	Gly	Met	Leu	Ala	Glu
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Leu	Ser	Gln	Leu	Arg	Asp	Asp	Phe	Ser	Leu	Ile	Ala	Met	Ser	Ala	Thr
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Leu	Asp	Ser	Asp	Lys	Phe	Ala	Asn	Leu	Leu	Asp	Ala	Gln	Val	Leu	Ser
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Val	Glu	Ala	Pro	Ile	Phe	Pro	Leu	Asp	Ile	Ser	Tyr	Ala	Pro	Ala	Arg
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Ala	Pro	Arg	Leu	Asn	Ala	Lys	Gly	Val	Asp	Trp	Asp	Phe	Leu	Asp	His
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Met	Ala	Gln	Lys	Thr	His	Asp	Ala	Val	Thr	His	Ser	Glu	His	Ser	Ala
225					230					235					240
Leu	Ile	Phe	Val	Pro	Gly	Val	Arg	Glu	Ile	Asp	Arg	Val	Met	Ser	Thr
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Leu	Lys	Ser	Leu	Gly	His	Asn	Asn	Val	Phe	Pro	Leu	His	Gly	Gln	Leu
			260					265					270		
Ser	Pro	Thr	Glu	Gln	Asp	Arg	Ala	Leu	Ala	Pro	Ser	Gln	Gln	Gln	Arg
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Ile	Ile	Val	Ser	Thr	Pro	Val	Ala	Glu	Ser	Ser	Leu	Thr	Val	Pro	Gly
			290			295					300				
Val	Arg	Ile	Gly	Val	Asp	Ser	Gly	Leu	Ser	Arg	Ser	Pro	Lys	Arg	Asp
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Ser	Ala	Arg	Gly	Met	Thr	Gly	Leu	Ile	Thr	Ser	Ser	Cys	Ala	Gln	Ala
				325					330					335	
Ser	Ala	Gly	Gln	Arg	Ala	Gly	Arg	Ala	Gly	Arg	Glu	Gly	Pro	Gly	Gln
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Ile	Ile	Arg	Cys	Tyr	Ser	Glu	Glu	Asp	Phe	Ser	His	Phe	Pro	Arg	Phe
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Val	Thr	Pro	Glu	Ile	Ser	Ser	Ala	Asp	Leu	Thr	Gln	Ala	Ala	Leu	Trp
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Leu	Ala	Gln	Trp	Gly	Thr	Ser	Pro	Ala	Asp	Leu	Pro	Leu	Leu	Asp	Gln
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Pro	Pro	His	Ala	Ala	Trp	Thr	Ala	Ala	Gln	Gln	Ile	Leu	Arg	Leu	Ile
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Gly	Ala	Leu	Glu	Gly	Asp	Ala	Ile	Thr	Ser	Leu	Gly	His	Arg	Leu	Ser
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Thr	Leu	Pro	Leu	Cys	Pro	Gln	Leu	Ser	Ala	Ser	Leu	Leu	Arg	Phe	Gly
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Glu Gln Ser Ala Lys Ile Leu Ala Val Val Ser Glu Asn Pro Gln Gly
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 Asp Val Glu Lys Gln Gln Pro Asp Lys Arg Glu Val Glu Arg Leu Arg
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 Arg Leu Ala Pro Ala Ser Val Gly Lys Ala Ser Ala Gly Gln Ile Val
 485 490 495
 Gly Ala Ala Phe Pro Gln Leu Ile Gly Arg Lys Ile Asp Asn Gly Glu
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 Tyr Leu Leu Ala Ser Gly Thr Arg Ala Arg Leu Met Asp Ser Asp Leu
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 Lys Asp Ala Glu Trp Ile Ser Val Ala Ala Ile Asn Arg Ser Gln Asn
 530 535 540
 Ser Ala Ile Ile Arg Ala Ala Ala Arg Ile Ser Glu Asp Asp Ala Ile
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 Asp Ile Ile Gly Val Val Glu Glu Thr Arg Ala Ile Phe Val Asn Gly
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 Lys Val Gln Ala Arg Lys Val Lys Ala Ala Gly Ala Ile Glu Leu Ser
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 Ser Thr Pro Thr Lys Pro Thr Pro Ala Glu Ala Ser Glu Thr Ile Ala
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 Thr Ala Leu Ala Lys Gly Gly Ile Asp Leu Phe His Phe Ser Asp Lys
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 Ala Ala Ser Leu Arg Asp Arg Leu Lys Phe Ile His Glu His Arg Gly
 625 630 635 640
 Glu Pro Trp Pro Asp Ile Glu Thr Ala Asp Pro His Leu Trp Leu Ser
 645 650 655
 Pro Glu Ile Glu Ala Leu Ser His Gly Thr Arg Leu Asn Asn Ile Asp
 660 665 670
 Met Tyr Pro Ala Leu Gln Arg Leu Leu Pro Trp Pro Glu Ala Thr Asn
 675 680 685
 Phe Glu Glu Phe Ala Pro Ser His Leu Ser Val Pro Ser Gly Asn Gln
 690 695 700
 His Arg Leu Asp Tyr Ser Ser Gly Arg Pro Val Ile Arg Val Lys Leu
 705 710 715 720
 Gln Glu Cys Phe Gly Leu Glu Glu Ser Pro Gln Leu Cys Gly Ile Pro
 725 730 735
 Val Gln Phe His Leu Leu Ser Pro Ala Gly Arg Pro Leu Ala Val Thr
 740 745 750
 Asp Asp Leu Arg Ser Phe Trp Ser Gly Pro Tyr Ser Gln Val Arg Ala
 755 760 765

gag gat atc tcg tgg tta ggt aag cac att gtg cgc ctt aat gag tgg 595

Glu Asp Ile Ser Trp Leu Gly Lys His Ile Val Arg Leu Asn Glu Trp	
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gcc aat gag act gag act ggc gat cgt gat gat ttg gat ccg ggt gtt	643
Ala Asn Glu Thr Glu Thr Gly Asp Arg Asp Asp Leu Asp Pro Gly Val	
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cct gat ctt gcg tgg aag cag gta agt gtt act gcc cgt gag tgc att	691
Pro Asp Leu Ala Trp Lys Gln Val Ser Val Thr Ala Arg Glu Cys Ile	
185 190 195	
ggc gcg tca agg tgc ccg cat ggc gag gat tgt ttc gct gag att gcc	739
Gly Ala Ser Arg Cys Pro His Gly Glu Asp Cys Phe Ala Glu Ile Ala	
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cgc ggg aag gca aag gag gct gat gtg gtg gtc acc aac cat gcg tta	787
Arg Gly Lys Ala Lys Glu Ala Asp Val Val Val Thr Asn His Ala Leu	
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ctt gct att gat gcg ttg tcg gat gtt tct gtg ctt cct gaa cat gat	835
Leu Ala Ile Asp Ala Leu Ser Asp Val Ser Val Leu Pro Glu His Asp	
230 235 240 245	
gtg gtg gtc atc gat gag gcc cat gag cta gat ggt cgc atc act gct	883
Val Val Val Ile Asp Glu Ala His Glu Leu Asp Gly Arg Ile Thr Ala	
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gtg gcg tcg gct gag atc acg gtg aat tcg ctc aat tta gct gct cgc	931
Val Ala Ser Ala Glu Ile Thr Val Asn Ser Leu Asn Leu Ala Ala Arg	
265 270 275	
cgt gcg tcc aag ttg gat tcc gat aag cgg gaa gaa cgc gtc cag gaa	979
Arg Ala Ser Lys Leu Asp Ser Asp Lys Arg Glu Glu Arg Val Gln Glu	
280 285 290	
atc gct ggc gat ttg gaa acc ttg ttg caa acc atg cag ccg ggc cgg	1027
Ile Ala Gly Asp Leu Glu Thr Leu Leu Gln Thr Met Gln Pro Gly Arg	
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Trp Asn Asp Met Asp Glu Gly Ser Lys Gly Thr Leu Val Ala Leu Lys	
310 315 320 325	
gac gcg ttg tgg gca ttg cgt gct cag atc gcg gga gca cct gag ggt	1123
Asp Ala Leu Trp Ala Leu Arg Ala Gln Ile Ala Gly Ala Pro Glu Gly	
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gag gct gcg aat gat ccg gag cgt ttc gcc gag cga cag aat tta agc	1171
Glu Ala Ala Asn Asp Pro Glu Arg Phe Ala Glu Arg Gln Asn Leu Ser	
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aat cac ttg atg gaa atc cat gat gcc aac gtg cgc att ttg gag gtc	1219
Asn His Leu Met Glu Ile His Asp Ala Asn Val Arg Ile Leu Glu Val	
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ttc gcg gag gag gat ccc tcc aag cag tac gac gtg gtg tgg cat aac	1267
Phe Ala Glu Glu Asp Pro Ser Lys Gln Tyr Asp Val Val Trp His Asn	
375 380 385	
cac gat gat cgt cgc ggg gat tcc ctc aat gtg gcg ccg ctg tcg gtt	1315
His Asp Asp Arg Arg Gly Asp Ser Leu Asn Val Ala Pro Leu Ser Val	

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Ala Gly Leu Leu His Glu Lys Leu Phe Ala Glu Asn Thr Val Val Leu	410	415	420	
gcc agt gcg acg ctg acc att ggt ggc aat ttc aac gca atg gct gcc				1411
Ala Ser Ala Thr Leu Thr Ile Gly Gly Asn Phe Asn Ala Met Ala Ala	425	430	435	
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Ser Trp Gly Leu Pro Lys Gly Ser Trp Asp Ser Met Asp Ala Gly Thr	440	445	450	
ccg ttt gat cca gcg aag tcg ggt att ttg tac acc gct cga cac ctt				1507
Pro Phe Asp Pro Ala Lys Ser Gly Ile Leu Tyr Thr Ala Arg His Leu	455	460	465	
ccg gac cct ggc cgc gat ggg ttg ccg gag gaa acg ctt gat gaa atc				1555
Pro Asp Pro Gly Arg Asp Gly Leu Pro Glu Glu Thr Leu Asp Glu Ile	470	475	480	485
tac gag ttg atc act gcg gcg ggt ggc cga act ttg ggg ctc ttt tcg				1603
Tyr Glu Leu Ile Thr Ala Ala Gly Gly Arg Thr Leu Gly Leu Phe Ser	490	495	500	
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Ser Lys Arg Ala Ala Glu Gln Ala Thr Lys Ala Met Arg Leu Arg Leu	505	510	515	
cct ttt gat gtg ctc tgc cag gga gat gac aat act gcc gcg ctg gtg				1699
Pro Phe Asp Val Leu Cys Gln Gly Asp Asp Asn Thr Ala Ala Leu Val	520	525	530	
aag aag ttt tcc gac agc gaa aac acg tgc ctt ttt ggc act ctc acg				1747
Lys Lys Phe Ser Asp Ser Glu Asn Thr Cys Leu Phe Gly Thr Leu Thr	535	540	545	
ctg tgg cag ggc gtc gac gtc ccc ggc cgt tcg ctg tcg ttg gtg ttg				1795
Leu Trp Gln Gly Val Asp Val Pro Gly Arg Ser Leu Ser Leu Val Leu	550	555	560	565
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Ile Asp Arg Ile Pro Phe Pro Arg Pro Asp Asp Pro Leu Leu Gln Ala	570	575	580	
cgc aag gag gcc gcc gat gcc gaa ggc cgc aac ggt ttc atg gag gtc				1891
Arg Lys Glu Ala Ala Asp Ala Glu Gly Arg Asn Gly Phe Met Glu Val	585	590	595	
gca gcc acc cac gcg gcg ttg ttg atg gcg cag ggc gcg ggc cgg ttg				1939
Ala Ala Thr His Ala Ala Leu Leu Met Ala Gln Gly Ala Gly Arg Leu	600	605	610	
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Leu Arg His Val Gly Asp Arg Gly Val Val Ala Val Leu Asp His Arg	615	620	625	
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Leu Ser Thr Lys Arg Tyr Gly Gly Phe Leu Arg Phe Ser Met Pro Arg	630	635	640	645

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		35					40					45				
Phe	Asp	Thr	Glu	Arg	His	Leu	Ala	Val	Gln	Ala	Gly	Thr	Gly	Thr	Gly	
50						55					60					
Lys	Ser	Leu	Ala	Tyr	Leu	Val	Pro	Ser	Ile	Arg	His	Ala	Gln	Lys	Ser	
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Asp	Ser	Thr	Val	Ile	Val	Ser	Thr	Ala	Thr	Ile	Ala	Leu	Gln	Arg	Gln	
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Leu	Val	Asn	Arg	Asp	Leu	Pro	Arg	Leu	Val	Asp	Ala	Leu	Glu	Pro	Leu	
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 260 265 270
 Asn Leu Ala Ala Arg Arg Ala Ser Lys Leu Asp Ser Asp Lys Arg Glu
 275 280 285
 Glu Arg Val Gln Glu Ile Ala Gly Asp Leu Glu Thr Leu Leu Gln Thr
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 Met Gln Pro Gly Arg Trp Asn Asp Met Asp Glu Gly Ser Lys Gly Thr
 305 310 315 320
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 325 330 335
 Gly Ala Pro Glu Gly Glu Ala Ala Asn Asp Pro Glu Arg Phe Ala Glu
 340 345 350
 Arg Gln Asn Leu Ser Asn His Leu Met Glu Ile His Asp Ala Asn Val
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 370 375 380
 Val Val Trp His Asn His Asp Asp Arg Arg Gly Asp Ser Leu Asn Val
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 Met Asp Ala Gly Thr Pro Phe Asp Pro Ala Lys Ser Gly Ile Leu Tyr
 450 455 460
 Thr Ala Arg His Leu Pro Asp Pro Gly Arg Asp Gly Leu Pro Glu Glu
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 485 490 495
 Leu Gly Leu Phe Ser Ser Lys Arg Ala Ala Glu Gln Ala Thr Lys Ala
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 515 520 525
 Thr Ala Ala Leu Val Lys Lys Phe Ser Asp Ser Glu Asn Thr Cys Leu
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Met Ser Glu Ser Gly
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gcg cta agt tct act gac tct cta tcc ccg ggt gtc acc att gaa gtc 163
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Arg Asp Glu Ile Trp Leu Val Thr His Val Thr Arg Ser Thr Asp Gly
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Phe Arg Val Lys Ala Arg Gly Leu Ser Asp Tyr Val Arg Asp His Glu
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Ala Thr Phe Phe Thr Ala Leu Asp Lys Asp Leu Lys Val Ile Asp Pro
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acc cag gtc acc gtc agt ctt gat gat tcc tcc aat tac cgt cgc acc 355
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atg Met 150	ggc Gly	atg Met	atc Ile	ttg Leu	gcg Ala 155	gaa Glu	ctt Leu	atc Ile	cgc Arg	cgt Arg 160	ggc Gly	cgt Arg	ggg Gly	gag Glu	cgc Arg 165	595
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<211> 414

<212> PRT

<213> Corynebacterium glutamicum

<400> 84

Met Ser Glu Ser Gly Ala Leu Ser Ser Thr Asp Ser Leu Ser Pro Gly
 1 5 10 15

Val Thr Ile Glu Val Arg Asp Glu Ile Trp Leu Val Thr His Val Thr
 20 25 30

Arg Ser Thr Asp Gly Phe Arg Val Lys Ala Arg Gly Leu Ser Asp Tyr
 35 40 45

Val Arg Asp His Glu Ala Thr Phe Phe Thr Ala Leu Asp Lys Asp Leu
 50 55 60

Lys Val Ile Asp Pro Thr Gln Val Thr Val Ser Leu Asp Asp Ser Ser
 65 70 75 80

Asn Tyr Arg Arg Thr Arg Leu Trp Leu Glu Ala Thr Met Arg Lys Thr
 85 90 95

Pro Val Pro Leu Tyr Gln Glu Ser Leu Ser Val Ala Asp Gln Met Leu
 100 105 110

Ala Asp Pro Leu Glu Tyr Gln Leu Ala Ala Val Arg Lys Thr Leu Ser
 115 120 125

Ser Ala Asn Leu Arg Pro Arg Val Leu Ile Ala Asp Ala Val Gly Leu
 130 135 140

Gly Lys Thr Leu Glu Met Gly Met Ile Leu Ala Glu Leu Ile Arg Arg
 145 150 155 160

Gly Arg Gly Glu Arg Ile Leu Val Val Thr Pro Arg His Ile Met Glu
 165 170 175

Gln Phe Gln Gln Glu Met Trp Thr Arg Phe Ala Ile Pro Leu Val Arg
 180 185 190
 Leu Asp Ser Val Gly Ile Gln Gln Val Arg Gln Lys Leu Pro Ala Ser
 195 200 205
 Arg Asn Pro Phe Thr Tyr Phe Pro Arg Val Ile Val Ser Met Asp Thr
 210 215 220
 Leu Lys Ser Pro Lys Tyr Arg Ala Gln Leu Glu Lys Val His Trp Asp
 225 230 235 240
 Ala Val Val Ile Asp Glu Ile His Asn Ala Thr Asn Ala Gly Thr Gln
 245 250 255
 Asn Asn Glu Leu Ala Gly Thr Leu Gly Pro Thr Ala Glu Ala Leu Ile
 260 265 270
 Leu Ala Ser Ala Thr Pro His Asn Gly Asp Pro Glu Ser Phe Lys Glu
 275 280 285
 Ile Leu Arg Leu Leu Asp Pro Thr Ala Val Met Pro Asp Gly Thr Ile
 290 295 300
 Asp Ala Glu Ala Ala Gln Arg Leu Ile Ile Arg Arg His Arg Asn Ser
 305 310 315 320
 Pro Glu Val Ser Gly Phe Val Gly Glu Lys Trp Ala Pro Arg Asn Glu
 325 330 335
 Pro Gln Asn Phe Leu Val Ala Ala Ser Lys Glu Glu Asn Gly Val Ala
 340 345 350
 Ala Glu Leu Asn His Val Trp Ile Ser Pro Gly Ala Ser Asn Pro Ile
 355 360 365
 Lys Asp Arg Leu Phe Pro Leu Asp Ile Gly Glu Gly Phe Ser Leu Leu
 370 375 380
 Pro Cys Ser Leu Gly Arg Asn Ser Val Gln Ser Pro Gln Lys Gly Leu
 385 390 395 400
 Cys Thr Arg Arg Lys Thr Arg Pro Arg Asn Pro Phe Thr Thr
 405 410

<210> 85

<211> 982

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(982)

<223> FRXA01374

<400> 85

tccccgcagc ccaccaccgt gggctgcggg gtgtggcggt tttgccacaa agtggaccgt 60

attcgcaaat actttgttaa gacgcgttaa tctttaacct atg tct gaa tca ggt 115

	Met	Ser	Glu	Ser	Gly	
	1				5	
gcg cta agt tct act gac tct cta tcc ccg ggt gtc acc att gaa gtc						163
Ala Leu Ser Ser Thr Asp Ser Leu Ser Pro Gly Val Thr Ile Glu Val						
				10	20	
cga gat gaa att tgg ctg gtt act cac gtt act cgc tcc aca gat ggt						211
Arg Asp Glu Ile Trp Leu Val Thr His Val Thr Arg Ser Thr Asp Gly						
			25	30	35	
ttt agg gtt aaa gct cgt ggt ctc tct gat tat gtg cgg gac cac gaa						259
Phe Arg Val Lys Ala Arg Gly Leu Ser Asp Tyr Val Arg Asp His Glu						
		40		45	50	
gct acg ttc ttc acc gca ctt gat aaa gat ttg aag gtc att gac cct						307
Ala Thr Phe Phe Thr Ala Leu Asp Lys Asp Leu Lys Val Ile Asp Pro						
	55		60		65	
acc cag gtc acc gtc agt ctt gat gat tcc tcc aat tac cgt cgc acc						355
Thr Gln Val Thr Val Ser Leu Asp Asp Ser Ser Asn Tyr Arg Arg Thr						
	70		75		80	85
cgc ctg tgg ttg gag gcc acc atg cgt aaa act ccg gta ccg ctc tat						403
Arg Leu Trp Leu Glu Ala Thr Met Arg Lys Thr Pro Val Pro Leu Tyr						
		90		95	100	
caa gag tca ctt tcc gtg gca gat caa atg ctc gcc gat cca ctg gag						451
Gln Glu Ser Leu Ser Val Ala Asp Gln Met Leu Ala Asp Pro Leu Glu						
		105		110	115	
tac caa tta gca gcc gtg cgc aaa acc ctc tct agt gct aac ttg cgc						499
Tyr Gln Leu Ala Ala Val Arg Lys Thr Leu Ser Ser Ala Asn Leu Arg						
		120		125	130	
ccc cgc gtg ctt att gct gat gcc gtg gga ctt ggc aaa acc cta gaa						547
Pro Arg Val Leu Ile Ala Asp Ala Val Gly Leu Gly Lys Thr Leu Glu						
	135		140		145	
atg ggc atg atc ttg gcg gaa ctt atc cgc cgt ggc cgt ggt gag cgc						595
Met Gly Met Ile Leu Ala Glu Leu Ile Arg Arg Gly Arg Gly Glu Arg						
	150		155		160	165
att ttg gta gtc acc ccg cgc cac att atg gag cag ttc cag cag gaa						643
Ile Leu Val Val Thr Pro Arg His Ile Met Glu Gln Phe Gln Gln Glu						
		170		175	180	
atg tgg acc cgt ttt gcc atc ccg ctc gtt cgt cta gat tcc gtg ggc						691
Met Trp Thr Arg Phe Ala Ile Pro Leu Val Arg Leu Asp Ser Val Gly						
		185		190	195	
atc cag caa gtg cgc caa aaa ttg cca gca tca cgc aac cct ttt act						739
Ile Gln Gln Val Arg Gln Lys Leu Pro Ala Ser Arg Asn Pro Phe Thr						
	200		205		210	
tat ttc ccg cgc gtg att gtc tct atg gat act ttg aaa tct ccg aag						787
Tyr Phe Pro Arg Val Ile Val Ser Met Asp Thr Leu Lys Ser Pro Lys						
	215		220		225	
tac cgc gcg caa cta gaa aag gtg cac tgg gat gcg gtg gtt ata gat						835
Tyr Arg Ala Gln Leu Glu Lys Val His Trp Asp Ala Val Val Ile Asp						

230	235	240	245	
gaa atc cac aat gca acc aat gct ggc acc caa aat aat gag cta gcc				883
Glu Ile His Asn Ala Thr Asn Ala Gly Thr Gln Asn Asn Glu Leu Ala	250	255	260	
cgc aca ctt gcg cct act gcc gag gct ctt att ttg gcc tct gcc acc				931
Arg Thr Leu Ala Pro Thr Ala Glu Ala Leu Ile Leu Ala Ser Ala Thr	265	270	275	
ccg cac aat ggt gat cca gaa tcc ttt aag gag atc ttg cgt ttg ctt				979
Pro His Asn Gly Asp Pro Glu Ser Phe Lys Glu Ile Leu Arg Leu Leu	280	285	290	
gat				982
Asp				

<210> 86

<211> 294

<212> PRT

<213> Corynebacterium glutamicum

<400> 86

Met Ser Glu Ser Gly Ala Leu Ser Ser Thr Asp Ser Leu Ser Pro Gly	
1 5 10 15	

Val Thr Ile Glu Val Arg Asp Glu Ile Trp Leu Val Thr His Val Thr	
20 25 30	

Arg Ser Thr Asp Gly Phe Arg Val Lys Ala Arg Gly Leu Ser Asp Tyr	
35 40 45	

Val Arg Asp His Glu Ala Thr Phe Phe Thr Ala Leu Asp Lys Asp Leu	
50 55 60	

Lys Val Ile Asp Pro Thr Gln Val Thr Val Ser Leu Asp Asp Ser Ser	
65 70 75 80	

Asn Tyr Arg Arg Thr Arg Leu Trp Leu Glu Ala Thr Met Arg Lys Thr	
85 90 95	

Pro Val Pro Leu Tyr Gln Glu Ser Leu Ser Val Ala Asp Gln Met Leu	
100 105 110	

Ala Asp Pro Leu Glu Tyr Gln Leu Ala Ala Val Arg Lys Thr Leu Ser	
115 120 125	

Ser Ala Asn Leu Arg Pro Arg Val Leu Ile Ala Asp Ala Val Gly Leu	
130 135 140	

Gly Lys Thr Leu Glu Met Gly Met Ile Leu Ala Glu Leu Ile Arg Arg	
145 150 155 160	

Gly Arg Gly Glu Arg Ile Leu Val Val Thr Pro Arg His Ile Met Glu	
165 170 175	

Gln Phe Gln Gln Glu Met Trp Thr Arg Phe Ala Ile Pro Leu Val Arg	
180 185 190	

Leu Asp Ser Val Gly Ile Gln Gln Val Arg Gln Lys Leu Pro Ala Ser
 195 200 205
 Arg Asn Pro Phe Thr Tyr Phe Pro Arg Val Ile Val Ser Met Asp Thr
 210 215 220
 Leu Lys Ser Pro Lys Tyr Arg Ala Gln Leu Glu Lys Val His Trp Asp
 225 230 235 240
 Ala Val Val Ile Asp Glu Ile His Asn Ala Thr Asn Ala Gly Thr Gln
 245 250 255
 Asn Asn Glu Leu Ala Arg Thr Leu Ala Pro Thr Ala Glu Ala Leu Ile
 260 265 270
 Leu Ala Ser Ala Thr Pro His Asn Gly Asp Pro Glu Ser Phe Lys Glu
 275 280 285
 Ile Leu Arg Leu Leu Asp
 290

<210> 87
 <211> 2517
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2494)
 <223> RXN00817

<400> 87
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 tcagtccecat ttatacagcc cagcgaaagg gggtaaattc ttg act acc ccc gat 115
 Leu Thr Thr Pro Asp
 1 5
 ttt gag agt gaa aag act caa gct atg agg ccc agc ttt ggt gaa gag 163
 Phe Glu Ser Glu Lys Thr Gln Ala Met Arg Pro Ser Phe Gly Glu Glu
 10 15 20
 ctg gcc gca atc gtt tcc aaa cgt tac tcc gaa tcg acg ctc act cat 211
 Leu Ala Ala Ile Val Ser Lys Arg Tyr Ser Glu Ser Thr Leu Thr His
 25 30 35
 atg gtg acg ttg ccc gca tcg aaa gct aaa tac gtc gat tgg ccg agt 259
 Met Val Thr Leu Pro Ala Ser Lys Ala Lys Tyr Val Asp Trp Pro Ser
 40 45 50
 tgg gta cct gct agc ctg cgc gat gcg ttg gtg aat cgt ggt atc aat 307
 Trp Val Pro Ala Ser Leu Arg Asp Ala Leu Val Asn Arg Gly Ile Asn
 55 60 65
 aag ctc ttt tcc cac cag gag cag acc gca cat ctg gcg tgg aat ggc 355
 Lys Leu Phe Ser His Gln Glu Gln Thr Ala His Leu Ala Trp Asn Gly
 70 75 80 85
 cag cat gtg gtg gtt gcc acc ggt aca tct tcg gga aaa tct ttg ggt 403
 Gln His Val Val Val Ala Thr Gly Thr Ser Ser Gly Lys Ser Leu Gly

	90	95	100	
tat cag ctg ccc att ttg tca gcg ctc ggc acg gat cct acc gcc tgt	451			
Tyr Gln Leu Pro Ile Leu Ser Ala Leu Gly Thr Asp Pro Thr Ala Cys				
105	110	115		
gcg ttg tat cta act ccc acc aag gct ttg gga tct gat cag cta acc	499			
Ala Leu Tyr Leu Thr Pro Thr Lys Ala Leu Gly Ser Asp Gln Leu Thr				
120	125	130		
tcc acg tcc acg ttg ctg cgc gac att ccg gat ttc cac ccg att aat	547			
Ser Thr Ser Thr Leu Leu Arg Asp Ile Pro Asp Phe His Pro Ile Asn				
135	140	145		
ccg gcg ccc tac gat ggc gat acc ccc tcc gag gcg ccg tcc gcc atc	595			
Pro Ala Pro Tyr Asp Gly Asp Thr Pro Ser Glu Ala Arg Ser Gly Ile				
150	155	160	165	
cgc gat ttg agt cgt ttt gtg ttc acc aat ccg gat atg gtg cat gcg	643			
Arg Asp Leu Ser Arg Phe Val Phe Thr Asn Pro Asp Met Val His Ala				
170	175	180		
tcg atg ctg gcg aat cat ccc cgc tgg gcc agg ttg ttg cgc cat ttg	691			
Ser Met Leu Ala Asn His Pro Arg Trp Ala Arg Leu Leu Arg His Leu				
185	190	195		
aag ttc atc gtg att gat gaa tgc cat gcc tac cgt ggt gtg ttt gcc	739			
Lys Phe Ile Val Ile Asp Glu Cys His Ala Tyr Arg Gly Val Phe Gly				
200	205	210		
gcg aac gtg tcg atg gtg ctt cgt cgt cta ctg cgc atc gcc gcg ttt	787			
Ala Asn Val Ser Met Val Leu Arg Arg Leu Leu Arg Ile Ala Ala Phe				
215	220	225		
tat gga tcc cac ccg acg gtc att ttg gcg tcc gcg acc agc tcc gat	835			
Tyr Gly Ser His Pro Thr Val Ile Leu Ala Ser Ala Thr Ser Ser Asp				
230	235	240	245	
ccg gaa att cat gct tcc aga ttg ttg ggc gcg ccg gtt aaa gca gtg	883			
Pro Glu Ile His Ala Ser Arg Leu Leu Gly Ala Pro Val Lys Ala Val				
250	255	260		
acg gaa gat ggc gcc ccg acg ggt gaa cgc acc gtt ttg ctg tgg gag	931			
Thr Glu Asp Gly Ala Pro Thr Gly Glu Arg Thr Val Leu Leu Trp Glu				
265	270	275		
ccc ggt ttc atc gaa ggc gcc gag ggc gag aac ggc gcg ccg gtg cgt	979			
Pro Gly Phe Ile Glu Gly Ala Glu Gly Glu Asn Gly Ala Pro Val Arg				
280	285	290		
cgc gca gcc agc acc gaa gca gca aac att atg gcc acg ctc att tcc	1027			
Arg Ala Ala Ser Thr Glu Ala Ala Asn Ile Met Ala Thr Leu Ile Ser				
295	300	305		
gag ggt gca cgc acg ttg acg ttc gtc cgt tca cgt cga caa gca gaa	1075			
Glu Gly Ala Arg Thr Leu Thr Phe Val Arg Ser Arg Arg Gln Ala Glu				
310	315	320	325	
atc gtt gcc ctg cgc gcg cag gaa gag ctc agc acg ctg ggc cgc ccc	1123			
Ile Val Ala Leu Arg Ala Gln Glu Glu Ser Thr Leu Gly Arg Pro				
330	335	340		

gat ttc gcc cgg cgc gtc gcg tcc tac cgg gcg ggg tac ttg gcg gag	1171
Asp Phe Ala Arg Arg Val Ala Ser Tyr Arg Ala Gly Tyr Leu Ala Glu	
345 350 355	
gac cgc cgt agg ttg gag aga ttg ctt gac gac ggc acc ctc ctc ggt	1219
Asp Arg Arg Arg Leu Glu Arg Leu Leu Asp Asp Gly Thr Leu Leu Gly	
360 365 370	
gtt gct tcc acc aat gcg ctt gaa ctg ggc att gat gtc ggt gga ctg	1267
Val Ala Ser Thr Asn Ala Leu Glu Leu Gly Ile Asp Val Gly Gly Leu	
375 380 385	
gat gct gtg gtc acg gct ggt ttt cca gga act gtg gcg tcg ttt tgg	1315
Asp Ala Val Val Thr Ala Gly Phe Pro Gly Thr Val Ala Ser Phe Trp	
390 395 400 405	
cag cag gcg ggg cga gct ggt cgg cgt ggg cag ggt tcg ttg gtg gtg	1363
Gln Gln Ala Gly Arg Ala Gly Arg Arg Gly Gln Gly Ser Leu Val Val	
410 415 420	
ctt gtt gct cgt gat gag ccg atg gat acg tat ttg gtg cat cat ccg	1411
Leu Val Ala Arg Asp Glu Pro Met Asp Thr Tyr Leu Val His His Pro	
425 430 435	
gca gcc ctg ttg gag aag ccg gtt gag gct gcg gtg ttt gat ccg acg	1459
Ala Ala Leu Leu Glu Lys Pro Val Glu Ala Ala Val Phe Asp Pro Thr	
440 445 450	
aat ccg cat gtt att cgg ggt cat gtt tat tgc gct gcg gtg gaa aag	1507
Asn Pro His Val Ile Arg Gly His Val Tyr Cys Ala Ala Val Glu Lys	
455 460 465	
cct ctg aca gag gcg gag gtc gcg gcg ttt ggt gcc caa aag gtg gtg	1555
Pro Leu Thr Glu Ala Glu Val Ala Ala Phe Gly Ala Gln Lys Val Val	
470 475 480 485	
gag aag ctc gag att gaa ggg ctg ttg cgc aag cgt ccg cgt ggc tgg	1603
Glu Lys Leu Glu Ile Glu Gly Leu Leu Arg Lys Arg Pro Arg Gly Trp	
490 495 500	
ttt gcg gtg gaa aag ccc atg tca gag gat ccg gat gag ctg agt cct	1651
Phe Ala Val Glu Lys Pro Met Ser Glu Asp Pro Asp Glu Leu Ser Pro	
505 510 515	
gat tcg gca cac cag cag gtg agt ttg cgt ggt ggg tct ggt tcg gag	1699
Asp Ser Ala His Gln Gln Val Ser Leu Arg Gly Gly Ser Gly Ser Glu	
520 525 530	
ttc atg att gtt gat atc act gac ggc cgg ttg tta ggc acc atc gat	1747
Phe Met Ile Val Asp Ile Thr Asp Gly Arg Leu Leu Gly Thr Ile Asp	
535 540 545	
tcc gcg aag gcg atg tcg cag act cat ccc ggc gcg gtg tat ctc cac	1795
Ser Ala Lys Ala Met Ser Gln Thr His Pro Gly Ala Val Tyr Leu His	
550 555 560 565	
cag ggt gaa tcc ttt gtc att gat gag ttg gat ttg gag gag aat ctg	1843
Gln Gly Glu Ser Phe Val Ile Asp Glu Leu Asp Leu Glu Glu Asn Leu	
570 575 580	

gca ctg gcc agg cct gag ctg cct gat tac acc acc tat gcc aga agt	1891
Ala Leu Ala Arg Pro Glu Leu Pro Asp Tyr Thr Thr Tyr Ala Arg Ser	
585 590 595	
gac acg gac atc agg att acc tct gcc ccg ttg gag gac gag gtt ttt	1939
Asp Thr Asp Ile Arg Ile Thr Ser Ala Pro Leu Glu Asp Glu Val Phe	
600 605 610	
gat gct ggt ggt ggt ttg tgg gtc gcc aac gta gag gtg cag gtc acc	1987
Asp Ala Gly Gly Gly Leu Trp Val Ala Asn Val Glu Val Gln Val Thr	
615 620 625	
gac cgt gtg act ggc tat gtc acc cgc ctt agt gat ggc acc acg ttg	2035
Asp Arg Val Thr Gly Tyr Val Thr Arg Leu Ser Asp Gly Thr Thr Leu	
630 635 640 645	
gat gcg act ccg ttg tat ctt cct cct caa att ctt cag act cgt gcg	2083
Asp Ala Thr Pro Leu Tyr Leu Pro Pro Gln Ile Leu Gln Thr Arg Ala	
650 655 660	
gtg gcg tac acg att gat ccg ttg gcg ttg gaa gcg atg ggc att ccc	2131
Val Ala Tyr Thr Ile Asp Pro Leu Ala Leu Glu Ala Met Gly Ile Pro	
665 670 675	
gcc gct gat att ccc ggt gct ctt cac gca gcg gag cat gcg gcg att	2179
Ala Ala Asp Ile Pro Gly Ala Leu His Ala Ala Glu His Ala Ala Ile	
680 685 690	
ggt atg ttg ccg ctg ctt gcg acg tgt gat cgt tgg gat atc ggc ggc	2227
Gly Met Leu Pro Leu Leu Ala Thr Cys Asp Arg Trp Asp Ile Gly Gly	
695 700 705	
gta tcc acg gca ctt cat gcg gat acg ggc tac ccc act gtg ttt gtc	2275
Val Ser Thr Ala Leu His Ala Asp Thr Gly Tyr Pro Thr Val Phe Val	
710 715 720 725	
tat gac ggt atg gac ggc gga gct ggt ttt gcg gat act ggt ttt cga	2323
Tyr Asp Gly Met Asp Gly Gly Ala Gly Phe Ala Asp Thr Gly Phe Arg	
730 735 740	
cgt ttc gcc cag tgg att gag gcc aca ttt gag gtc gtc cgc agc tgt	2371
Arg Phe Ala Gln Trp Ile Glu Ala Thr Phe Glu Val Val Arg Ser Cys	
745 750 755	
agc tgt gaa tct ggg tgc ccg agc tgt gtg cag tcc ccg aaa tgc ggc	2419
Ser Cys Glu Ser Gly Cys Pro Ser Cys Val Gln Ser Pro Lys Cys Gly	
760 765 770	
aat gga aac aat ccg ttg gat aag gca ggt gcc atc aag tta ctg ggt	2467
Asn Gly Asn Asn Pro Leu Asp Lys Ala Gly Ala Ile Lys Leu Leu Gly	
775 780 785	
gcg atg gtg acc ttg ttg gga acc tca taaaggtcct gcttttgcgt	2514
Ala Met Val Thr Leu Leu Gly Thr Ser	
790 795	
ggg	2517

<210> 88

<211> 798

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 88

Leu Thr Thr Pro Asp Phe Glu Ser Glu Lys Thr Gln Ala Met Arg Pro
 1 5 10 15

Ser Phe Gly Glu Glu Leu Ala Ala Ile Val Ser Lys Arg Tyr Ser Glu
 20 25 30

Ser Thr Leu Thr His Met Val Thr Leu Pro Ala Ser Lys Ala Lys Tyr
 35 40 45

Val Asp Trp Pro Ser Trp Val Pro Ala Ser Leu Arg Asp Ala Leu Val
 50 55 60

Asn Arg Gly Ile Asn Lys Leu Phe Ser His Gln Glu Gln Thr Ala His
 65 70 75 80

Leu Ala Trp Asn Gly Gln His Val Val Val Ala Thr Gly Thr Ser Ser
 85 90 95

Gly Lys Ser Leu Gly Tyr Gln Leu Pro Ile Leu Ser Ala Leu Gly Thr
 100 105 110

Asp Pro Thr Ala Cys Ala Leu Tyr Leu Thr Pro Thr Lys Ala Leu Gly
 115 120 125

Ser Asp Gln Leu Thr Ser Thr Ser Thr Leu Leu Arg Asp Ile Pro Asp
 130 135 140

Phe His Pro Ile Asn Pro Ala Pro Tyr Asp Gly Asp Thr Pro Ser Glu
 145 150 155 160

Ala Arg Ser Gly Ile Arg Asp Leu Ser Arg Phe Val Phe Thr Asn Pro
 165 170 175

Asp Met Val His Ala Ser Met Leu Ala Asn His Pro Arg Trp Ala Arg
 180 185 190

Leu Leu Arg His Leu Lys Phe Ile Val Ile Asp Glu Cys His Ala Tyr
 195 200 205

Arg Gly Val Phe Gly Ala Asn Val Ser Met Val Leu Arg Arg Leu Leu
 210 215 220

Arg Ile Ala Ala Phe Tyr Gly Ser His Pro Thr Val Ile Leu Ala Ser
 225 230 235 240

Ala Thr Ser Ser Asp Pro Glu Ile His Ala Ser Arg Leu Leu Gly Ala
 245 250 255

Pro Val Lys Ala Val Thr Glu Asp Gly Ala Pro Thr Gly Glu Arg Thr
 260 265 270

Val Leu Leu Trp Glu Pro Gly Phe Ile Glu Gly Ala Glu Gly Glu Asn
 275 280 285

Gly Ala Pro Val Arg Arg Ala Ala Ser Thr Glu Ala Ala Asn Ile Met
 290 295 300

Ala Thr Leu Ile Ser Glu Gly Ala Arg Thr Leu Thr Phe Val Arg Ser
 305 310 315 320
 Arg Arg Gln Ala Glu Ile Val Ala Leu Arg Ala Gln Glu Glu Leu Ser
 325 330 335
 Thr Leu Gly Arg Pro Asp Phe Ala Arg Arg Val Ala Ser Tyr Arg Ala
 340 345 350
 Gly Tyr Leu Ala Glu Asp Arg Arg Arg Leu Glu Arg Leu Leu Asp Asp
 355 360 365
 Gly Thr Leu Leu Gly Val Ala Ser Thr Asn Ala Leu Glu Leu Gly Ile
 370 375 380
 Asp Val Gly Gly Leu Asp Ala Val Val Thr Ala Gly Phe Pro Gly Thr
 385 390 395 400
 Val Ala Ser Phe Trp Gln Gln Ala Gly Arg Ala Gly Arg Arg Gly Gln
 405 410 415
 Gly Ser Leu Val Val Leu Val Ala Arg Asp Glu Pro Met Asp Thr Tyr
 420 425 430
 Leu Val His His Pro Ala Ala Leu Leu Glu Lys Pro Val Glu Ala Ala
 435 440 445
 Val Phe Asp Pro Thr Asn Pro His Val Ile Arg Gly His Val Tyr Cys
 450 455 460
 Ala Ala Val Glu Lys Pro Leu Thr Glu Ala Glu Val Ala Ala Phe Gly
 465 470 475 480
 Ala Gln Lys Val Val Glu Lys Leu Glu Ile Glu Gly Leu Leu Arg Lys
 485 490 495
 Arg Pro Arg Gly Trp Phe Ala Val Glu Lys Pro Met Ser Glu Asp Pro
 500 505 510
 Asp Glu Leu Ser Pro Asp Ser Ala His Gln Gln Val Ser Leu Arg Gly
 515 520 525
 Gly Ser Gly Ser Glu Phe Met Ile Val Asp Ile Thr Asp Gly Arg Leu
 530 535 540
 Leu Gly Thr Ile Asp Ser Ala Lys Ala Met Ser Gln Thr His Pro Gly
 545 550 555 560
 Ala Val Tyr Leu His Gln Gly Glu Ser Phe Val Ile Asp Glu Leu Asp
 565 570 575
 Leu Glu Glu Asn Leu Ala Leu Ala Arg Pro Glu Leu Pro Asp Tyr Thr
 580 585 590
 Thr Tyr Ala Arg Ser Asp Thr Asp Ile Arg Ile Thr Ser Ala Pro Leu
 595 600 605
 Glu Asp Glu Val Phe Asp Ala Gly Gly Gly Leu Trp Val Ala Asn Val
 610 615 620
 Glu Val Gln Val Thr Asp Arg Val Thr Gly Tyr Val Thr Arg Leu Ser

625		630		635		640
Asp Gly Thr Thr	Leu	Asp Ala Thr	Pro Leu Tyr	Leu Pro Pro	Gln Ile	
	645		650		655	
Leu Gln Thr Arg	Ala Val	Ala Tyr Thr	Ile Asp Pro	Leu Ala Leu	Glu	
	660		665		670	
Ala Met Gly Ile	Pro Ala Ala	Asp Ile Pro	Gly Ala Leu	His Ala Ala		
	675		680		685	
Glu His Ala Ala	Ile Gly Met	Leu Pro Leu	Leu Ala Thr	Cys Asp Arg		
	690		695		700	
Trp Asp Ile Gly	Gly Val Ser	Thr Ala Leu	His Ala Asp	Thr Gly Tyr		
	705		710		715	
Pro Thr Val Phe	Val Tyr Asp	Gly Met Asp	Gly Gly Ala	Gly Phe Ala		
	725		730		735	
Asp Thr Gly Phe	Arg Arg Phe	Ala Gln Trp	Ile Glu Ala	Thr Phe Glu		
	740		745		750	
Val Val Arg Ser	Cys Ser Cys	Glu Ser Gly	Cys Pro Ser	Cys Val Gln		
	755		760		765	
Ser Pro Lys Cys	Gly Asn Gly	Asn Asn Pro	Leu Asp Lys	Ala Gly Ala		
	770		775		780	
Ile Lys Leu Leu	Gly Ala Met	Val Thr Leu	Leu Gly Thr	Ser		
	785		790		795	

<210> 89

<211> 610

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(610)

<223> FRXA00809

<400> 89

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tcagtccecat ttatacagcc cagcgaaagg gggtaaattc	ttg act acc ccc gat	115
	Leu Thr Thr Pro Asp	
	1 5	

ttt gag agt gaa aag act caa gct atg agg ccc agc ttt ggt gaa gag	163
Phe Glu Ser Glu Lys Thr Gln Ala Met Arg Pro Ser Phe Gly Glu Glu	
	10 15 20

ctg gcc gca atc gtt tcc aaa cgt tac tcc gaa tcg acg ctc act cat	211
Leu Ala Ala Ile Val Ser Lys Arg Tyr Ser Glu Ser Thr Leu Thr His	
	25 30 35

atg gtg acg ttg ccc gca tcg aaa gct aaa tac gtc gat tgg ccg agt	259
Met Val Thr Leu Pro Ala Ser Lys Ala Lys Tyr Val Asp Trp Pro Ser	
	40 45 50

tgg gta cct gct agc ctg cgc gat gcg ttg gtg aat cgt ggt atc aat 307
 Trp Val Pro Ala Ser Leu Arg Asp Ala Leu Val Asn Arg Gly Ile Asn
 55 60 65
 aag ctc ttt tcc cac cag gag cag acc gca cat ctg gcg tgg aat ggc 355
 Lys Leu Phe Ser His Gln Glu Gln Thr Ala His Leu Ala Trp Asn Gly
 70 75 80 85
 cag cat gtg gtg gtt gcc acc ggt aca tct tcg gga aaa tct ttg ggt 403
 Gln His Val Val Val Ala Thr Gly Thr Ser Ser Gly Lys Ser Leu Gly
 90 95 100
 tat cag ctg ccc att ttg tca gcg ctc ggc acg gat cct acc gcc tgt 451
 Tyr Gln Leu Pro Ile Leu Ser Ala Leu Gly Thr Asp Pro Thr Ala Cys
 105 110 115
 gcg ttg tat cta act ccc acc aag gct ttg gga tct gat cag cta acc 499
 Ala Leu Tyr Leu Thr Pro Thr Lys Ala Leu Gly Ser Asp Gln Leu Thr
 120 125 130
 tcc acg tcc acg ttg ctg cgc gac att ccg gat ttc cac ccg att aat 547
 Ser Thr Ser Thr Leu Leu Arg Asp Ile Pro Asp Phe His Pro Ile Asn
 135 140 145
 ccg gcg ccc tac gat ggc gat acc ccc tcc gag gcg cgg tcc ggc atc 595
 Pro Ala Pro Tyr Asp Gly Asp Thr Pro Ser Glu Ala Arg Ser Gly Ile
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 Arg Asp Leu Ser Arg
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<213> Corynebacterium glutamicum

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 35 40 45
 Val Asp Trp Pro Ser Trp Val Pro Ala Ser Leu Arg Asp Ala Leu Val
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 Asn Arg Gly Ile Asn Lys Leu Phe Ser His Gln Glu Gln Thr Ala His
 65 70 75 80
 Leu Ala Trp Asn Gly Gln His Val Val Val Ala Thr Gly Thr Ser Ser
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 Gly Lys Ser Leu Gly Tyr Gln Leu Pro Ile Leu Ser Ala Leu Gly Thr
 100 105 110

Asp Pro Thr Ala Cys Ala Leu Tyr Leu Thr Pro Thr Lys Ala Leu Gly
 115 120 125

Ser Asp Gln Leu Thr Ser Thr Ser Thr Leu Leu Arg Asp Ile Pro Asp
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Phe His Pro Ile Asn Pro Ala Pro Tyr Asp Gly Asp Thr Pro Ser Glu
 145 150 155 160

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Asp Pro Glu Ile His Ala Ser Arg Leu Leu Gly Ala Pro Val Lys Ala	
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Val Thr Glu Asp Gly Ala Pro Thr Gly Glu Arg Thr Val Leu Leu Trp	
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Glu Pro Gly Phe Ile Glu Gly Ala Glu Gly Glu Asn Gly Ala Pro Val	
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Arg Arg Ala Ala Ser Thr Glu Ala Ala Asn Ile Met Ala Thr Leu Ile	
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Ser Glu Gly Ala Arg Thr Leu Thr Phe Val Arg Ser Arg Arg Gln Ala	
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Glu Ile Val Ala Leu Arg Ala Gln Glu Leu Ser Thr Leu Gly Arg	
100 105 110	
ccc gat ttc gcc cgg cgc gtc gcg tcc tac cgg gcg ggg tac ttg gcg	384
Pro Asp Phe Ala Arg Arg Val Ala Ser Tyr Arg Ala Gly Tyr Leu Ala	
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Glu Asp Arg Arg Arg Leu Glu Arg Leu Leu Asp Asp Gly Thr Leu Leu	
130 135 140	
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Gly 145	Val	Ala	Ser	Thr	Asn 150	Ala	Leu	Glu	Leu	Gly 155	Ile	Asp	Val	Gly	Gly 160	
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Leu	Asp	Ala	Val	Val 165	Thr	Ala	Gly	Phe	Pro 170	Gly	Thr	Val	Ala	Ser 175	Phe	
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Trp	Gln	Gln	Ala 180	Gly	Arg	Ala	Gly	Arg 185	Arg	Gly	Gln	Gly	Ser 190	Leu	Val	
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Val	Leu	Val 195	Ala	Arg	Asp	Glu	Pro 200	Met	Asp	Thr	Tyr	Leu 205	Val	His	His	
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Pro	Ala 210	Ala	Leu	Leu	Glu	Lys 215	Pro	Val	Glu	Ala 220	Ala	Val	Phe	Asp	Pro	
acg	aat	ccg	cat	gtt	att	cgg	ggg	cat	gtt	tat	tgc	gct	gcg	gtg	gaa	720
Thr	Asn	Pro	His	Val 230	Ile	Arg	Gly	His	Val	Tyr 235	Cys	Ala	Ala	Val	Glu 240	
aag	cct	ctg	aca	gag	gcg	gag	gtc	gcg	gcg	ttt	ggg	gcc	caa	aag	gtg	768
Lys	Pro	Leu	Thr 245	Glu	Ala	Glu	Val	Ala	Ala 250	Phe	Gly	Ala	Gln	Lys 255	Val	
gtg	gag	aag	ctc	gag	att	gaa	ggg	ctg	ttg	cgc	aag	cgt	ccg	cgt	ggc	816
Val	Glu	Lys	Leu 260	Glu	Ile	Glu	Gly	Leu 265	Leu	Arg	Lys	Arg	Pro 270	Arg	Gly	
tgg	ttt	gcg	gtg	gaa	aag	ccc	atg	tca	gag	gat	ccg	gat	gag	ctg	agt	864
Trp	Phe	Ala 275	Val	Glu	Lys	Pro 280	Met	Ser	Glu	Asp	Pro 285	Asp	Glu	Leu	Ser	
cct	gat	tcg	gca	cac	cag	cag	gtg	agt	ttg	cgt	ggg	ggg	tct	ggg	tcg	912
Pro	Asp	Ser	Ala	His	Gln 295	Gln	Val	Ser	Leu	Arg	Gly 300	Gly	Ser	Gly	Ser	
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Glu	Phe	Met	Ile	Val 310	Asp	Ile	Thr	Asp	Gly 315	Arg	Leu	Leu	Gly	Thr	Ile 320	
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Asp	Ser	Ala	Lys 325	Ala	Met	Ser	Gln	Thr	His 330	Pro	Gly	Ala	Val	Tyr 335	Leu	
cac	cag	ggg	gaa	tcc	ttt	gtc	att	gat	gag	ttg	gat	ttg	gag	gag	aat	1056
His	Gln	Gly	Glu 340	Ser	Phe	Val	Ile	Asp 345	Glu	Leu	Asp	Leu	Glu	Glu	Asn	
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Leu	Ala	Leu	Ala 355	Arg	Pro	Glu	Leu	Pro 360	Asp	Tyr	Thr	Thr	Tyr	Ala	Arg	
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Ser	Asp	Thr	Asp 370	Ile	Arg	Ile 375	Thr	Ser	Ala	Pro	Leu 380	Glu	Asp	Glu	Val	
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Phe	Asp	Ala	Gly	Gly	Gly	Leu	Trp	Val	Ala	Asn	Val	Glu	Val	Gln	Val	

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Thr Asp Arg Val Thr Gly Tyr Val Thr Arg Leu Ser Asp Gly Thr Thr				
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ttg gat gcg act ccg ttg tat ctt cct cct caa att ctt cag act cgt				1296
Leu Asp Ala Thr Pro Leu Tyr Leu Pro Pro Gln Ile Leu Gln Thr Arg				
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Ala Val Ala Tyr Thr Ile Asp Pro Leu Ala Leu Glu Ala Met Gly Ile				
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ccc gcc gct gat att ccc ggt gct ctt cac gca gcg gag cat gcg gcg				1392
Pro Ala Ala Asp Ile Pro Gly Ala Leu His Ala Ala Glu His Ala Ala				
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att ggt atg ttg ccg ctg ctt gcg acg tgt gat cgt tgg gat atc ggc				1440
Ile Gly Met Leu Pro Leu Leu Ala Thr Cys Asp Arg Trp Asp Ile Gly				
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Gly Val Ser Thr Ala Leu His Ala Asp Thr Gly Tyr Pro Thr Val Phe				
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Val Tyr Asp Gly Met Asp Gly Gly Ala Gly Phe Ala Asp Thr Gly Phe				
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cga cgt ttc gcc cag tgg att gag gcc aca ttt gag gtc gtc cgc agc				1584
Arg Arg Phe Ala Gln Trp Ile Glu Ala Thr Phe Glu Val Val Arg Ser				
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Cys Ser Cys Glu Ser Gly Cys Pro Ser Cys Val Gln Ser Pro Lys Cys				
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Gly Asn Gly Asn Asn Pro Leu Asp Lys Ala Gly Ala Ile Lys Leu Leu				
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Asp Pro Glu Ile His Ala Ser Arg Leu Leu Gly Ala Pro Val Lys Ala				
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1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

355	360	365
Ser Asp Thr Asp Ile Arg Ile Thr Ser Ala Pro Leu Glu Asp Glu Val 370	375	380
Phe Asp Ala Gly Gly Gly Leu Trp Val Ala Asn Val Glu Val Gln Val 385	390	400
Thr Asp Arg Val Thr Gly Tyr Val Thr Arg Leu Ser Asp Gly Thr Thr 405	410	415
Leu Asp Ala Thr Pro Leu Tyr Leu Pro Pro Gln Ile Leu Gln Thr Arg 420	425	430
Ala Val Ala Tyr Thr Ile Asp Pro Leu Ala Leu Glu Ala Met Gly Ile 435	440	445
Pro Ala Ala Asp Ile Pro Gly Ala Leu His Ala Ala Glu His Ala Ala 450	455	460
Ile Gly Met Leu Pro Leu Leu Ala Thr Cys Asp Arg Trp Asp Ile Gly 465	470	475
Gly Val Ser Thr Ala Leu His Ala Asp Thr Gly Tyr Pro Thr Val Phe 485	490	495
Val Tyr Asp Gly Met Asp Gly Gly Ala Gly Phe Ala Asp Thr Gly Phe 500	505	510
Arg Arg Phe Ala Gln Trp Ile Glu Ala Thr Phe Glu Val Val Arg Ser 515	520	525
Cys Ser Cys Glu Ser Gly Cys Pro Ser Cys Val Gln Ser Pro Lys Cys 530	535	540
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 Met Ala Lys Ser Ile
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 Leu Ser Arg Phe Arg Pro Gln Val Ala Glu Trp Phe Arg Asp Val Phe

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Gly Lys Asn Ala Leu Val Val Ala Pro Thr Gly Ser Gly Lys Thr Leu															
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Ala Ala Phe Leu Trp Ala Leu Asp Ser Leu Thr Glu Gln Thr Gly Gln															
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cag gtt tta gac acg gga aca ccg gtg cct gtt cgt ggt ggg aaa gtg	355														
Gln Val Leu Asp Thr Gly Thr Pro Val Pro Val Arg Gly Gly Lys Val															
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Lys Val Leu Tyr Ile Ser Pro Leu Lys Ala Leu Gly Val Asp Val Glu															
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aat aat ctg cgt gca ccg ttg acc ggt att gcg agg act gcc tct cgg	451														
Asn Asn Leu Arg Ala Pro Leu Thr Gly Ile Ala Arg Thr Ala Ser Arg															
105	110					115									
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Met Gly Leu Asp Val Pro Asn Ile Thr Val Ala Val Arg Ser Gly Asp															
120	125					130									
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Thr Pro Ser Ala Glu Arg Ala Arg Gln Val Arg Lys Pro Pro Asp Ile															
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Leu Ile Thr Thr Pro Glu Ser Ala Tyr Leu Met Leu Thr Ser Lys Ala															
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ggg gcg acc ctt tcg gat gtt gat gtg gtg atc atc gat gaa atc cac	643														
Gly Ala Thr Leu Ser Asp Val Asp Val Val Ile Ile Asp Glu Ile His															
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gcc atg gcc gga acc aaa ccg gga gtg cat ctg gcg ttg acg ctg gag	691														
Ala Met Ala Gly Thr Lys Arg Gly Val His Leu Ala Leu Thr Leu Glu															
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Arg Leu Glu Lys Leu Val Gly Arg Pro Val Gln Arg Val Gly Leu Ser															
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gca acg gtg cgt cct ttg gaa acg gtg gcg ggt ttc ttg ggc ggt ggc	787														
Ala Thr Val Arg Pro Leu Glu Thr Val Ala Gly Phe Leu Gly Gly Gly															
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Arg Pro Val Glu Ile Val Ala Pro Pro Ala Glu Lys Lys Trp Asp Leu															
230	235					240					245				
act gtc act gtg ccg gtg gaa gac atg tcg gat ttg ccg gtt cag gag	883														
Thr Val Thr Val Pro Val Glu Asp Met Ser Asp Leu Pro Val Gln Glu															
250	255					260									

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Pro Gly Ser Thr Ile Gly Glu Leu Val Met Asp Asp Pro Leu Gly Ile	
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Thr Gly Glu Ser Ala Leu Pro Thr Gln Gly Ser Ile Trp Pro His Ile	
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Glu Gln Gln Val Tyr Asn Gln Val Met Ser Ala Lys Ser Thr Ile Val	
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Phe Val Asn Ser Arg Arg Ser Ala Glu Arg Leu Thr Ser Arg Leu Asn	
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Glu Ile Trp Ala Met Glu His Asp Pro Glu Ser Leu Ser Pro Gln Leu	
330 335 340	
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Ser Phe Tyr Pro Lys His Arg Ser Asp Leu Val Gln Thr Ala Val Thr	
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Val Gln Arg Met Lys Glu Gly Leu Ile Glu Glu Ile His Val Pro Lys	
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470 475 480 485	
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Lys Asp Val Gln Val Asp Glu Trp Tyr Glu Thr Ile Arg Lys Ala Tyr	
490 495 500	

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Pro Tyr Arg Asp Leu Ala Arg Glu Val Phe Asp Ser Val Ile Asp Leu	
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Val Ser Gly Val Tyr Pro Ser Thr Asp Phe Ala Glu Leu Lys Pro Arg	
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Val Val Tyr Asp Arg Val Ser Gly Val Leu Glu Gly Arg Pro Gly Ser	
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Gln Arg Val Ala Val Thr Ser Gly Gly Thr Ile Pro Asp Arg Gly Met	
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Phe Gly Val Phe Leu Val Gly Asp Gly Pro Arg Arg Val Gly Glu Leu	
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Val Thr Pro Ala Pro Gly His Thr Gly Arg Leu Pro Phe Trp Thr Gly	
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Asp Ala Ala Gly Arg Pro Ala Glu Leu Gly Lys Ala Leu Gly Ala Phe	
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Arg Arg Ser Thr Leu Thr Asp Pro Ser Ser Ser Gly Leu Glu Gly Trp	
650 655 660	
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Ala His Asp Asn Leu Ile Ala Phe Leu Gln Glu Gln Glu Ser Thr	
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Thr Gly Met Asp Ala Gln Ala Val Ala Gly Asp Asp Gly Ile Val Leu	
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Ala	Leu	Phe	Ala	Ser	Arg	Phe	Arg	Glu	Cys	Ala	Ala	Arg	Ala	Leu	Leu	
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Glu Gln Gln Val Tyr Asn Gln Val Met Ser Ala Lys Ser Thr Ile Val	
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Phe Val Asn Ser Arg Arg Ser Ala Glu Arg Leu Thr Ser Arg Leu Asn	
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Glu Ile Trp Ala Met Glu His Asp Pro Glu Ser Leu Ser Pro Gln Leu	
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Arg Arg Asp Pro Ala Gln Ile Met Ser Ser Ala Asp Val Ala Gly Lys	
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Ala Pro Gln Val Ile Ala Arg Ala His His Gly Ser Val Ser Lys Asp	
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Glu Arg Ala Thr Thr Glu Thr Met Leu Lys Glu Gly Arg Leu Arg Ala	
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Val Ile Ser Thr Ser Ser Leu Glu Leu Gly Ile Asp Met Gly Ala Val	
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Asp Leu Val Ile Gln Val Glu Ser Pro Pro Ser Val Ala Ser Gly Leu	
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Gln Arg Val Gly Arg Ala Gly His Thr Val Gly Ala Thr Ser Ile Gly	
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Ser Phe Tyr Pro Lys His Arg Ser Asp Leu Val Gln Thr Ala Val Thr	
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Val Gln Arg Met Lys Glu Gly Leu Ile Glu Glu Ile His Val Pro Lys	
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Asn Ala Leu Asp Val Leu Ala Gln Gln Thr Val Ala Ala Val Ser Ile	
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Lys Asp Val Gln Val Asp Glu Trp Tyr Glu Thr Ile Arg Lys Ala Tyr	
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Pro Tyr Arg Asp Leu Ala Arg Glu Val Phe Asp Ser Val Ile Asp Leu	
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Val Ser Gly Val Tyr Pro Ser Thr Asp Phe Ala Glu Leu Lys Pro Arg	
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Gln Arg Val Ala Val Thr Ser Gly Gly Thr Ile Pro Asp Arg Gly Met	
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Phe Gly Val Phe Leu Val Gly Asp Gly Pro Arg Arg Val Gly Glu Leu	
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Gly Ala Ser Ser Trp Arg Ile Glu Glu Ile Thr Arg Asp Gln Val Leu	
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Val Thr Pro Ala Pro Gly His Thr Gly Arg Leu Pro Phe Trp Thr Gly	
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Asp Ala Ala Gly Arg Pro Ala Glu Leu Gly Lys Ala Leu Gly Ala Phe	
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Thr	Gly	Met	Asp	Ala	Gln	Ala	Val	Ala	Gly	Asp	Asp	Gly	Ile	Val	Leu	
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Gln	Arg	Ala	Ala	Gln	Leu	Leu	Asp	Val	Ala	Arg	Lys	Tyr	Pro	Ser	Phe	
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Pro	Ile	Ile	Leu	Glu	Thr	Val	Arg	Glu	Cys	Leu	Gln	Asp	Val	Tyr	Asp	
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ctc	gca	gag	aaa	cgt	gcc	gca	gcg	ttg	gcc	ctg	gat	ccg	gca	ctg	ttg	2803
Leu	Ala	Glu	Lys	Arg	Ala	Ala	Ala	Leu	Ala	Leu	Asp	Pro	Ala	Leu	Leu	

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Arg Asp Pro Trp Ile Ser Leu Leu Pro Val Asp Tyr Ala Ala Gln Leu	
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Glu Gln Thr Gly Gln Gln Val Leu Asp Thr Gly Thr Pro Val Pro Val
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 Glu Gly Asp Ser Pro Leu Ala Glu Lys Arg Ala Ala Ala Leu Ala Leu
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 Leu Leu Asp Pro Asp Ile Ile Ala Glu Val His Gln Gln Leu Arg Arg
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 Gln Gly Asp Arg Ala Ala Arg Asn Asn Glu Glu Leu Ala Asp Ser Leu
 930 935 940
 Arg Ile Leu Gly Pro Ile Pro Leu Asp Glu Leu Gly Glu His Ile Thr
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 Phe Glu Asn Pro Asp Leu Glu Asp Arg Ala Met Thr Val Arg Ile Asn
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 Gly Arg Glu His Leu Ala Gln Val Leu Asp Ala Pro Leu Leu Arg Asp
 980 985 990
 Ala Leu Gly Val Pro Val Pro Pro Gly Val Pro Ala Gln Val Glu Thr
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 Gly Pro Phe Thr Ala Asn Asp Leu Ala Glu Ala Phe Gly Leu Gly Ile
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 Ala Thr Ala Ile Thr Ala Leu Gln Ser Ala Pro Val Ile Glu Gly Arg
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 Tyr Arg Gln Gly Val Asp Val Gln Glu Tyr Cys Ala Thr Glu Val Leu

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Ser Ile Ile Arg Arg Arg Ser Leu Ala Ala Ala Arg Lys Gln Thr Arg 1075 1080 1085		
Pro Val Ser Gln Ser Ala Phe Ala Arg Phe Leu Leu Asp Trp Gln Gln 1090 1095 1100		
Ile Ala Pro Val Gly Ala Thr Pro Glu Leu Arg Gly Val Asp Gly Thr 1105 1110 1115 1120		
Tyr Thr Val Ile Glu Gln Leu Ala Gly Val Arg Leu Pro Ala Ser Ala 1125 1130 1135		
Trp Glu Asp Leu Val Leu Pro Arg Arg Val Ala Asp Tyr Ser Pro Ile 1140 1145 1150		
His Leu Asp Glu Leu Thr Ser Asn Gly Glu Val Leu Ile Val Gly Ala 1155 1160 1165		
Gly Gln Ala Gly Ser Arg Asp Pro Trp Ile Ser Leu Leu Pro Val Asp 1170 1175 1180		
Tyr Ala Ala Gln Leu Val Gly Glu Ala Ser Thr Ser Met Ser Pro Leu 1185 1190 1195 1200		
Gln Asp Ala Val Leu Asp Gln Leu Arg Ala Gly Gly Ala Phe Leu Phe 1205 1210 1215		
Ser Asp Ile Leu Glu Glu Asn Phe Gly Tyr Thr Thr Ala Gln Leu Gln 1220 1225 1230		
Glu Ala Met Trp Gly Leu Val Glu Ala Gly Leu Val Ser Pro Asp Ser 1235 1240 1245		
Phe Ala Pro Ile Arg Ala Arg Leu Ala Ser Gly Thr Thr Ala His Arg 1250 1255 1260		
Ala Lys Arg Arg Pro Ala Arg Ser Arg Leu Arg Thr Arg Thr Ser Phe 1265 1270 1275 1280		
Ala Ser Asp Val Pro Pro Asp Met Arg Gly Arg Trp Thr Leu Ser Val 1285 1290 1295		
Gln Pro Ala Asp Ala Thr Ser Arg Ser Val Ala His Gly Glu Gly Trp 1300 1305 1310		
Leu Asp Arg Tyr Gly Val Leu Thr Arg Gly Ser Val Val Ala Glu Asp 1315 1320 1325		
Ile Val Gly Gly Phe Ala Leu Ala Tyr Lys Val Leu Ser Gly Phe Glu 1330 1335 1340		
Glu Ser Gly Lys Ala Met Arg Gly Tyr Phe Ile Glu Gly Leu Gly Ala 1345 1350 1355 1360		
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Asp Ser Pro Asp Val Glu Gly Trp Pro Ser Gly Ala Thr Asp Pro Asp 1380 1385 1390		

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gcaaaatttg aaaaccagct taaggagcca tagagcgctt atg tcc tca ctc att																115
Met Ser Ser Leu Ile																
1 5																
cct gtc cat gcg gct ggc agc att caa gaa ggc atc acc gaa tat ttg	163															
Pro Val His Ala Ala Gly Ser Ile Gln Glu Gly Ile Thr Glu Tyr Leu																
10 15 20																
acc acc agt ttt tcc ctt gcg gat aag caa gtg gcc acc gag ctc aag	211															
Thr Thr Ser Phe Ser Leu Ala Asp Lys Gln Val Ala Thr Glu Leu Lys																
25 30 35																
cgg ttc ttg ggc cac ggt gat tcc ggc atg ttc cac ggg cct tat gtg	259															
Arg Phe Leu Gly His Gly Asp Ser Gly Met Phe His Gly Pro Tyr Val																
40 45 50																
cgt gca cgt ttg ccc tat gct cag gca cag gaa tgg gaa aat gtg ctg	307															
Arg Ala Arg Leu Pro Tyr Ala Gln Ala Gln Glu Trp Glu Asn Val Leu																
55 60 65																

agt tgg tta cct gag aac ttt gtg ccc tat cac cat caa aaa gcg gcg	355
Ser Trp Leu Pro Glu Asn Phe Val Pro Tyr His His Gln Lys Ala Ala	
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ttt cag cgg ctg agt tcc ctc gat aac cga ggt aaa gat cgc cgc ccc	403
Phe Gln Arg Leu Ser Ser Leu Asp Asn Arg Gly Lys Asp Arg Arg Pro	
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gat ccc acc ttg gtg gta act gga acg ggt tcc ggt aag acg gaa tct	451
Asp Pro Thr Leu Val Val Thr Gly Thr Gly Ser Gly Lys Thr Glu Ser	
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ttc ctc tac ccg att ctg gat cat gcc ctg cgc ctg cgg aaa cgt ggc	499
Phe Leu Tyr Pro Ile Leu Asp His Ala Leu Arg Leu Arg Lys Arg Gly	
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Gln Gln Gly Ile Lys Ala Leu Leu Leu Tyr Pro Met Asn Ala Leu Ala	
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Asn Asp Gln Ala Asp Arg Leu Ala Arg Leu Ile His Asn Asn Pro Ala	
150 155 160 165	
ctt aaa ggt gtt acc gcc ggt att tat acc ggt gaa gcc aag ggc aat	643
Leu Lys Gly Val Thr Ala Gly Ile Tyr Thr Gly Glu Ala Lys Gly Asn	
170 175 180	
cgc acg cag atg ggc gaa agg gag ctt att aat gat ccc caa gcc atg	691
Arg Thr Gln Met Gly Glu Arg Glu Leu Ile Asn Asp Pro Gln Ala Met	
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Arg Val Ser Pro Pro Asp Ile Leu Leu Thr Asn Tyr Lys Met Leu Asp	
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Gln Leu Leu Leu Arg Ser Val Asp Arg Glu Met Trp Gln Lys Ser Ala	
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Thr Ser Leu Gln Tyr Leu Val Leu Asp Glu Phe His Thr Tyr Asp Gly	
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Ala Gln Gly Thr Asp Val Ala Leu Leu Leu Arg Arg Leu Gly Leu Met	
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Leu Lys Ser Gln Gln Pro Ala Asn Phe Leu Asp Asp Ser Ala Met His	
265 270 275	
cgg cca ttg ggc att att acg cca gtg gct acc tca gca acc ttg ggt	979
Arg Pro Leu Gly Ile Ile Thr Pro Val Ala Thr Ser Ala Thr Leu Gly	
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Ser Gly Asp Ser Gly Ser Pro Met Leu Asp Phe Ala Tyr Thr Ile Phe	
295 300 305	

ggt gag cgt ttt cca gct gat gcc atc gtc ggg gaa act cgc ctg gag	1075
Gly Glu Arg Phe Pro Ala Asp Ala Ile Val Gly Glu Thr Arg Leu Glu	
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Leu Asp Gln Trp Arg Ala Glu Ile Ala Gln Asn Phe Gly Ala Pro Ala	
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Val Ser Glu Pro Arg Glu Leu Pro Thr Val Glu Asp Ile Glu Val Val	
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Leu Asp Thr Ile Ala Thr Ala Gln His Glu Asp Asp Tyr Ala Gln Leu	
360 365 370	
tgc ttc cgc gtt ttt tgt gag aaa gtg tgg ctg tgt gag gct gat ctg	1267
Cys Phe Arg Val Phe Cys Glu Lys Val Trp Leu Cys Glu Ala Asp Leu	
375 380 385	
cac gca gcg atc agt gct tat gcg gct cat gat tta act gct gcg att	1315
His Ala Ala Ile Ser Ala Tyr Ala Ala His Asp Leu Thr Ala Ala Ile	
390 395 400 405	
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Leu Gln His Ala Ala Asp Ser Thr Pro Leu Ser Arg Arg Asp Gln Asp	
410 415 420	
gag gtc act gcc ctt ccg gag ctg gta ttg ggg gct acc gcc cgc atc	1411
Glu Val Thr Ala Leu Pro Glu Leu Val Leu Gly Ala Thr Ala Arg Ile	
425 430 435	
tta ggt gag gtt aaa gct gcg gaa ttt atc agc cat gca ctg gct gcc	1459
Leu Gly Glu Val Lys Ala Ala Glu Phe Ile Ser His Ala Leu Ala Ala	
440 445 450	
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Met Ala Phe Val Arg Ala Glu Tyr Gly Lys Val Ala Ala Trp Gly Ala	
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Lys Arg Leu Pro Gly Val Glu Thr His Leu Trp Val Arg Glu Val Ser	
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Arg Ile Asp Arg Ala Leu Gly Val Gly Asp Glu Gln Ser Met Phe Arg	
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Trp Ser Asp Asp Gly Pro Ala Glu Asp Ala Asn Thr Gln Gln Trp Leu	
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Pro Ala Cys Tyr Cys Arg Ser Cys Gly Arg Ser Gly Trp Met Val Ser	
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Leu Glu Gln Gly Thr Asn Ile Pro Val Leu Glu Gln Gln Lys Ile Arg	
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Thr	Ser	Glu	Gln	Arg	Ala	Ala	Ile	Glu	Gln	Gly	Arg	Ser	Val	Ala	Gly		
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ccg	cga	gga	gtt	gat	ggc	acc	tca	gca	gtg	ctg	tgg	ttc	cat	agc	gcc	1891	
Pro	Arg	Gly	Val	Asp	Gly	Thr	Ser	Ala	Val	Leu	Trp	Phe	His	Ser	Ala		
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agc	aat	gaa	ctc	agc	acg	cgc	caa	ccc	agc	cca	gaa	gaa	gaa	caa	tca	1939	
Ser	Asn	Glu	Leu	Ser	Thr	Arg	Gln	Pro	Ser	Pro	Glu	Glu	Glu	Gln	Ser		
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ggg	tct	tct	atc	gca	gtg	ctc	acc	cac	ttt	ggc	cct	gag	gca	gac	gat	1987	
Gly	Ser	Ser	Ile	Ala	Val	Leu	Thr	His	Phe	Gly	Pro	Glu	Ala	Asp	Asp		
	615					620					625						
ctc	tcc	gcc	aaa	cag	acc	tgc	cct	tcc	tgt	ggg	gat	gtt	gat	tcc	atc	2035	
Leu	Ser	Ala	Lys	Gln	Thr	Cys	Pro	Ser	Cys	Gly	Asp	Val	Asp	Ser	Ile		
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cgt	tat	atc	gga	tcg	gga	atc	tct	acc	ctg	ctc	tct	gtc	tca	ctc	tcc	2083	
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aat	ctt	ttt	ggg	atg	gcc	gat	ttg	gat	agc	gct	gag	aaa	aag	acg	ctg	2131	
Asn	Leu	Phe	Gly	Met	Ala	Asp	Leu	Asp	Ser	Ala	Glu	Lys	Lys	Thr	Leu		
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gtc	ttt	gcc	gat	tcc	gtg	caa	gat	gcc	gcg	cac	cgc	gcc	ggg	tac	gtc	2179	
Val	Phe	Ala	Asp	Ser	Val	Gln	Asp	Ala	Ala	His	Arg	Ala	Gly	Tyr	Val		
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caa	gca	cgt	tcc	cgc	gct	ttt	gcc	ctt	cgt	acc	tat	acc	cgg	cgc	gca	2227	
Gln	Ala	Arg	Ser	Arg	Ala	Phe	Ala	Leu	Arg	Thr	Tyr	Thr	Arg	Arg	Ala		
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gtg	ggg	gat	aat	gaa	gtc	acc	ttg	cca	tca	atc	tcc	cgg	gcg	ctg	atg	2275	
Val	Gly	Asp	Asn	Glu	Val	Thr	Leu	Pro	Ser	Ile	Ser	Arg	Ala	Leu	Met		
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Asp	Asn	Ala	Thr	Ser	Gly	Arg	Thr	Arg	Tyr	Glu	Leu	Leu	Pro	Pro	Asp		
				730					735					740			
ctg	acc	gat	ctt	gat	att	tac	aaa	cct	tat	tgg	cac	ccc	gat	gcc	agc	2371	
Leu	Thr	Asp	Leu	Asp	Ile	Tyr	Lys	Pro	Tyr	Trp	His	Pro	Asp	Ala	Ser		
			745					750					755				
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Lys	Ala	Glu	Arg	Arg	Glu	Ala	Ser	Arg	Asn	Val	His	Lys	Arg	Leu	Ser		
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ttt	gat	ctc	gcc	ctc	gag	ttt	gga	caa	cgc	gct	gat	cta	ccc	cgt	tcc	2467	
Phe	Asp	Leu	Ala	Leu	Glu	Phe	Gly	Gln	Arg	Ala	Asp	Leu	Pro	Arg	Ser		
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ctt	gcg	ctg	acc	ggc	gct	ttg	agt	gct	ttt	gtg	gat	ttg	ccc	aaa	ggg	2515	
Leu	Ala	Leu	Thr	Gly	Ala	Leu	Ser	Ala	Phe	Val	Asp	Leu	Pro	Lys	Gly		

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Val Ala Leu Ser	Ala Ala Ala Glu Ala	Leu Tyr Ala Ile	Glu Val Pro	
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acc tta gat att gag gat gag aac ctg cga ctg cgc tgg gtg caa ggt				2611
Thr Leu Asp	Ile Glu Asp Glu Asn	Leu Arg Leu Arg Trp	Val Gln Gly	
	825	830	835	
gcc ctg gaa ctt ttg cgc gcc cgc ggg ggc atc aac cat gag tgg ttt				2659
Ala Leu Glu Leu Leu Arg Ala Arg Gly Gly Ile Asn His			Glu Trp Phe	
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ggc gcc tac ctg cgc acc gat ggc aac ccc tat atg ctt aac cgc cgc				2707
Gly Ala Tyr Leu Arg Thr Asp Gly Asn Pro Tyr Met Leu Asn Arg Arg				
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caa gcc cgc gct gag ggc att ccc ggt ttt gtc cgc ggt ggt gca cct				2755
Gln Ala Arg Ala Glu Gly Ile Pro Gly Phe Val Arg Gly Gly Ala Pro				
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gaa ttc cca cgt gta ggt tcc gca ctt tcc gga tcc ctg cgt tcc agc				2803
Glu Phe Pro Arg	Val Gly Ser Ala Leu	Ser Gly Ser Leu Arg	Ser Ser	
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acc ggc acc acc ccg ctt ggt agc ccg cgc gga cgt tat gcg tcc tgg				2851
Thr Gly Thr Thr Pro Leu Gly Ser Pro Arg Gly Arg Tyr Ala Ser Trp				
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acc tcg cag gtg ctt ggc atc agc acc cac gat gcc gcc acc gcc atc				2899
Thr Ser Gln Val Leu Gly Ile Ser Thr His Asp Ala Ala Thr Ala Ile				
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aca aag ctt ttc gac gct tta agc aac cgc agc att ctc tcc tca ata				2947
Thr Lys Leu Phe Asp Ala Leu Ser Asn Arg Ser Ile Leu Ser Ser Ile				
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Ser Thr Asp Ser Gly Gly Lys Ile Tyr Cys Leu Glu Ala Glu Arg Ile				
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cgt att ttt agc gaa gac cat ccc gaa gtt ctg gaa tgc agc gtg tgc				3043
Arg Ile Phe Ser Glu Asp His Pro Glu Val Leu Glu Cys Ser Val Cys				
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cat gcc caa act ggt gta act gat cat gtg cgt gac ttc ctt gat ggc				3091
His Ala Gln Thr Gly Val Thr Asp His Val Arg Asp Phe Leu Asp Gly				
	985	990	995	
gct ccg tgt ttt agc cct agt tgt ggg ggc gtt ctc cat atc gag gaa				3139
Ala Pro Cys Phe Ser Pro Ser Cys Gly Gly Val Leu His Ile Glu Glu				
	1000	1005	1010	
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Val Glu Asp Asn Tyr Tyr Arg Arg Leu Tyr Ser Ala Ile Glu Pro Arg				
	1015	1020	1025	
act gtc att gcc cgc gag cac acc agc atg ctc aag aaa aaa gac cgc				3235
Thr Val Ile Ala Arg Glu His Thr Ser Met Leu Lys Lys Lys Asp Arg				
	1030	1035	1040	1045

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Leu Ala Leu Glu Gln Ser Phe Arg Gly Gly Glu Gly Ser Ala Lys Gln	
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tcc ccc gat gcg ccc aat gtg ttg gta gct acg cca acg ctg gaa atg	3331
Ser Pro Asp Ala Pro Asn Val Leu Val Ala Thr Pro Thr Leu Glu Met	
1065 1070 1075	
ggg att gac atc ggc gat ctc tcc acc gtg atg ctt gcg tct ttg cca	3379
Gly Ile Asp Ile Gly Asp Leu Ser Thr Val Met Leu Ala Ser Leu Pro	
1080 1085 1090	
aca tca gtg gcc agt tat gta cag cgt gtt ggt cgt gcc ggg cgc ctc	3427
Thr Ser Val Ala Ser Tyr Val Gln Arg Val Gly Arg Ala Gly Arg Leu	
1095 1100 1105	
agc gga aac tcg ttg gta ctc gcc gtg gtg cgt ggc cgc ggt gtc aca	3475
Ser Gly Asn Ser Leu Val Leu Ala Val Val Arg Gly Arg Gly Val Thr	
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Leu Pro Arg Leu Asn Gln Pro Leu Ser Met Ile Lys Gly Ala Ile Thr	
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cca cca gtt gcg tat ctt tcc gcc agt gaa atc ttg cac cgc caa ttc	3571
Pro Pro Val Ala Tyr Leu Ser Ala Ser Glu Ile Leu His Arg Gln Phe	
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Leu Ala Tyr Val Ile Asp Cys Leu Asp Thr Arg Ala Glu Leu Pro Lys	
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Leu Glu Thr Ala Ile Asp Val Phe Asp Asn Ala Ala Gly Lys Thr Pro	
1175 1180 1185	
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Leu Val Ala Leu Leu Lys Ala Gln Ile His Ala Gly Leu Asp Pro Leu	
1190 1195 1200 1205	
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Leu Glu Glu Phe Val Arg Thr Leu Asn Met Gln Ile Ser Ile Asp Asn	
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Ile Phe Glu Leu Arg Thr Trp Ala Ser Gly Asn Ser Thr Asp Ser Leu	
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Ser Leu Thr Ala Arg Arg Gly Glu Leu Glu Lys Ile Phe Asp Lys Leu	
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Asp Ala Arg Asn Asp Ala His Asp Glu Glu Leu Lys Glu Glu Lys Arg	
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 Lys Thr Ala Ala Ser Leu Lys Ala Val Lys Leu Gln Ile Arg Asp Leu
 1290 1295 1300

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 Phe Tyr Ala Gln Gly Ile Ala Ala Lys Val Asp Ser Ile Glu Ile Gly
 1370 1375 1380

gaa cat ggc tct gcc att gag caa tgg cgg ttg tgc ccc gtg tgc tcg 4291
 Glu His Gly Ser Ala Ile Glu Gln Trp Arg Leu Cys Pro Val Cys Ser
 1385 1390 1395

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 His Ser Glu Ile Leu Gln Pro Gly Val Ser Thr Pro Gly Ser Cys Pro
 1400 1405 1410

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 Ile Ser Asp Asp Arg Glu Asp Arg Phe Ser Thr Arg Phe Asn Gln His
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 Val Ser Phe Val Val Pro Pro Asp Gly His Gly Lys Ser Trp Tyr Leu
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 Asn Asp Gly Phe Gly Ile Glu His Leu Pro Lys Val Glu Leu Arg Trp
 1480 1485 1490

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 Leu Asn Leu Gly Ile Gly Asn Gly Gln Lys Arg Arg Leu Gly Gly Phe
 1495 1500 1505

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 1510 1515 1520 1525

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Pro His Arg Tyr Glu Gln Lys Glu Asp Thr Val Ser Phe Ala Leu Gly	
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Arg Thr Leu Lys Thr Gln Gly Val Leu Met Leu Leu Pro Glu Tyr Phe	
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Gly Ser Glu Ala Asp Ser Met Val Val Thr Ser Leu Ile Ala Ala Ile	
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aaa tta gga ttt cgt gag gtg ttg ggt ggc gat cct gac cac ctg gat	4915
Lys Leu Gly Phe Arg Glu Val Leu Gly Gly Asp Pro Asp His Leu Asp	
1590 1595 1600 1605	
gtc acc agt gtg cag gtc ccc cgt act tct ggc gat ggt gca ctt gat	4963
Val Thr Ser Val Gln Val Pro Arg Thr Ser Gly Asp Gly Ala Leu Asp	
1610 1615 1620	
gcc ctt ttg ctg cac gat cag gtt cca gga ggc aca ggt tat ctt aac	5011
Ala Leu Leu Leu His Asp Gln Val Pro Gly Gly Thr Gly Tyr Leu Asn	
1625 1630 1635	
caa ttt gcc gat cct aca aag gtt cct gaa ctt att tcc cga gct tgg	5059
Gln Phe Ala Asp Pro Thr Lys Val Pro Glu Leu Ile Ser Arg Ala Trp	
1640 1645 1650	
gag cgg gtg tct agg tgc caa tgc cag tat gat gaa acg ctg gcc tgc	5107
Glu Arg Val Ser Arg Cys Gln Cys Gln Tyr Asp Glu Thr Leu Ala Cys	
1655 1660 1665	
cca gaa tgt ttg ttg cct tat acc cgc act gac acg ctc ctc cat act	5155
Pro Glu Cys Leu Leu Pro Tyr Thr Arg Thr Asp Thr Leu Leu His Thr	
1670 1675 1680 1685	
ttc cgc gca act gca gaa aaa tcc ttg cgc gca att ttg ctc aat agc	5203
Phe Arg Ala Thr Ala Glu Lys Ser Leu Arg Ala Ile Leu Leu Asn Ser	
1690 1695 1700	
tcg cgc ccc gaa gaa atc act gac ctt tct gca gta ccg gac tgg act	5251
Ser Arg Pro Glu Glu Ile Thr Asp Leu Ser Ala Val Pro Asp Trp Thr	
1705 1710 1715	
ttc ttg gaa aag cgc cca gag aac act ctt ggc tct cag ttg gaa ctg	5299
Phe Leu Glu Lys Arg Pro Glu Asn Thr Leu Gly Ser Gln Leu Glu Leu	
1720 1725 1730	
cgt ttc cgc gtg atg ctg cga cgc gcc tta aaa aat cgc cat gcc aaa	5347
Arg Phe Arg Val Met Leu Arg Arg Ala Leu Lys Asn Arg His Ala Lys	
1735 1740 1745	
ctt gtg gac cgc gtc aac ggc tca aac tct tat gtg gat att gag atg	5395
Leu Val Asp Arg Val Asn Gly Ser Asn Ser Tyr Val Asp Ile Glu Met	
1750 1755 1760 1765	
agc tcc ggt gtg cgc tgg cgg atg agc gaa caa gtt gat cgt gga tat	5443
Ser Ser Gly Val Arg Trp Arg Met Ser Glu Gln Val Asp Arg Gly Tyr	

1770										1775					1780					
aca cgc cct gat ttc tgg ttt gaa ccg ctc aac ggc aac tat ccc acc	5491																			
Thr Arg Pro Asp Phe Trp Phe Glu Pro Leu Asn Gly Asn Tyr Pro Thr																				
1785	1790	1795																		
gtg gct gtt ttt acc gat ggc gct gcg ttc cat atc tct tca gct aac	5539																			
Val Ala Val Phe Thr Asp Gly Ala Ala Phe His Ile Ser Ser Ala Asn																				
1800	1805	1810																		
tac cgt ctt gat ggc gat att cag aaa cgg atg aaa cta gcg ctc gat	5587																			
Tyr Arg Leu Asp Gly Asp Ile Gln Lys Arg Met Lys Leu Ala Leu Asp																				
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cca gac aat att ttg ccg tgg aat atc act agc tta gac ctc gac cgc	5635																			
Pro Asp Asn Ile Leu Pro Trp Asn Ile Thr Ser Leu Asp Leu Asp Arg																				
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Phe Ser Asn Pro Ala Ala Gln Gly Glu Glu Pro Ala Trp Phe Ser Pro																				
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atc ggc agg cag ctc agc aaa gca aat ttg att ctt gat cca caa tca	5731																			
Ile Gly Arg Gln Leu Ser Lys Ala Asn Leu Ile Leu Asp Pro Gln Ser																				
1865	1870	1875																		
act gca ctc ctg gca gca acg cct atg gat caa ctc ttg gca ttt tta	5779																			
Thr Ala Leu Leu Ala Ala Thr Pro Met Asp Gln Leu Leu Ala Phe Leu																				
1880	1885	1890																		
gat aat ccc gcg gca tcc tcg tgg aag gag ttt gct cat atc gct gct	5827																			
Asp Asn Pro Ala Ala Ser Ser Trp Lys Glu Phe Ala His Ile Ala Ala																				
1895	1900	1905																		
gct cac atg ctt ggg cat aat cca caa aaa aat ggc gac gga att gtt	5875																			
Ala His Met Leu Gly His Asn Pro Gln Lys Asn Gly Asp Gly Ile Val																				
1910	1915	1920	1925																	
ggt acc ttc cgc aat aag att tcc ttg ccg gcc acc atg gtt aat cgg	5923																			
Gly Thr Phe Arg Asn Lys Ile Ser Leu Arg Ala Thr Met Val Asn Arg																				
1930	1935	1940																		
gaa ctg cgc gcc cgc caa ttg tgg ctt gct ccc acc act cca gaa gag	5971																			
Glu Leu Arg Ala Arg Gln Leu Trp Leu Ala Pro Thr Thr Pro Glu Glu																				
1945	1950	1955																		
ctg gaa gtg gat acc tgg act gcc ttc ctc aat ttg gcc aac ctc atg	6019																			
Leu Glu Val Asp Thr Trp Thr Ala Phe Leu Asn Leu Ala Asn Leu Met																				
1960	1965	1970																		
tgg ctg gca ccg gaa tcc gta tac gta agc act aat ggt tca ccg cat	6067																			
Trp Leu Ala Pro Glu Ser Val Tyr Val Ser Thr Asn Gly Ser Pro His																				
1975	1980	1985																		
aaa att gat att gtg cct gct cca gca gct ccg ctt gtt gtt gaa gtt	6115																			
Lys Ile Asp Ile Val Pro Ala Pro Ala Ala Pro Leu Val Val Glu Val																				
1990	1995	2000	2005																	
cct gaa ttg tgg gct ccc atc ttg gat ggc ttt acc gcc gat gaa gat	6163																			
Pro Glu Leu Trp Ala Pro Ile Leu Asp Gly Phe Thr Ala Asp Glu Asp																				
2010	2015	2020																		

gaa gaa gcc gaa ggc gct ttg cag atc ttg gct aag gaa cat gcc ctg 6211
 Glu Glu Ala Glu Gly Ala Leu Gln Ile Leu Ala Lys Glu His Ala Leu
 2025 2030 2035
 gtt cca gag acc acc ggt gat gag ctc tcg agt att cct acg att gct 6259
 Val Pro Glu Thr Thr Gly Asp Glu Leu Ser Ser Ile Pro Thr Ile Ala
 2040 2045 2050
 acg tgg ccg agt gtc aag atc gct ttg ctc tat gaa tct gat ccc gat 6307
 Thr Trp Pro Ser Val Lys Ile Ala Leu Leu Tyr Glu Ser Asp Pro Asp
 2055 2060 2065
 gag cct ttg gag gat gat ctc aaa gct gaa ggt tgg acg ctg ctt ttt 6355
 Glu Pro Leu Glu Asp Asp Leu Lys Ala Glu Gly Trp Thr Leu Leu Phe
 2070 2075 2080 2085
 gca aat gac ctc gag acc tcc gat att ccc gct gcc ctt cgt ccc 6400
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<213> Corynebacterium glutamicum

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 20 25 30
 Ala Thr Glu Leu Lys Arg Phe Leu Gly His Gly Asp Ser Gly Met Phe
 35 40 45
 His Gly Pro Tyr Val Arg Ala Arg Leu Pro Tyr Ala Gln Ala Gln Glu
 50 55 60
 Trp Glu Asn Val Leu Ser Trp Leu Pro Glu Asn Phe Val Pro Tyr His
 65 70 75 80
 His Gln Lys Ala Ala Phe Gln Arg Leu Ser Ser Leu Asp Asn Arg Gly
 85 90 95
 Lys Asp Arg Arg Pro Asp Pro Thr Leu Val Val Thr Gly Thr Gly Ser
 100 105 110
 Gly Lys Thr Glu Ser Phe Leu Tyr Pro Ile Leu Asp His Ala Leu Arg
 115 120 125
 Leu Arg Lys Arg Gly Gln Gln Gly Ile Lys Ala Leu Leu Leu Tyr Pro
 130 135 140
 Met Asn Ala Leu Ala Asn Asp Gln Ala Asp Arg Leu Ala Arg Leu Ile
 145 150 155 160
 His Asn Asn Pro Ala Leu Lys Gly Val Thr Ala Gly Ile Tyr Thr Gly

165					170					175					
Glu	Ala	Lys	Gly	Asn	Arg	Thr	Gln	Met	Gly	Glu	Arg	Glu	Leu	Ile	Asn
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Asp	Pro	Gln	Ala	Met	Arg	Val	Ser	Pro	Pro	Asp	Ile	Leu	Leu	Thr	Asn
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Tyr	Lys	Met	Leu	Asp	Gln	Leu	Leu	Leu	Arg	Ser	Val	Asp	Arg	Glu	Met
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Trp	Gln	Lys	Ser	Ala	Thr	Ser	Leu	Gln	Tyr	Leu	Val	Leu	Asp	Glu	Phe
225						230					235				240
His	Thr	Tyr	Asp	Gly	Ala	Gln	Gly	Thr	Asp	Val	Ala	Leu	Leu	Leu	Arg
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Arg	Leu	Gly	Leu	Met	Leu	Lys	Ser	Gln	Gln	Pro	Ala	Asn	Phe	Leu	Asp
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Asp	Ser	Ala	Met	His	Arg	Pro	Leu	Gly	Ile	Ile	Thr	Pro	Val	Ala	Thr
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Ser	Ala	Thr	Leu	Gly	Ser	Gly	Asp	Ser	Gly	Ser	Pro	Met	Leu	Asp	Phe
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Ala	Tyr	Thr	Ile	Phe	Gly	Glu	Arg	Phe	Pro	Ala	Asp	Ala	Ile	Val	Gly
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Glu	Thr	Arg	Leu	Glu	Leu	Asp	Gln	Trp	Arg	Ala	Glu	Ile	Ala	Gln	Asn
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Phe	Gly	Ala	Pro	Ala	Val	Ser	Glu	Pro	Arg	Glu	Leu	Pro	Thr	Val	Glu
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Asp	Ile	Glu	Val	Val	Leu	Asp	Thr	Ile	Ala	Thr	Ala	Gln	His	Glu	Asp
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Asp	Tyr	Ala	Gln	Leu	Cys	Phe	Arg	Val	Phe	Cys	Glu	Lys	Val	Trp	Leu
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Cys	Glu	Ala	Asp	Leu	His	Ala	Ala	Ile	Ser	Ala	Tyr	Ala	Ala	His	Asp
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Leu	Thr	Ala	Ala	Ile	Leu	Gln	His	Ala	Ala	Asp	Ser	Thr	Pro	Leu	Ser
				405					410					415	
Arg	Arg	Asp	Gln	Asp	Glu	Val	Thr	Ala	Leu	Pro	Glu	Leu	Val	Leu	Gly
			420					425					430		
Ala	Thr	Ala	Arg	Ile	Leu	Gly	Glu	Val	Lys	Ala	Ala	Glu	Phe	Ile	Ser
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His	Ala	Leu	Ala	Ala	Met	Ala	Phe	Val	Arg	Ala	Glu	Tyr	Gly	Lys	Val
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Ala	Ala	Trp	Gly	Ala	Lys	Arg	Leu	Pro	Gly	Val	Glu	Thr	His	Leu	Trp
465						470					475				480
Val	Arg	Glu	Val	Ser	Arg	Ile	Asp	Arg	Ala	Leu	Gly	Val	Gly	Asp	Glu
				485					490					495	

Gln Ser Met Phe Arg Trp Ser Asp Asp Gly Pro Ala Glu Asp Ala Asn
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 Thr Gln Gln Trp Leu Pro Ala Cys Tyr Cys Arg Ser Cys Gly Arg Ser
 515 520 525
 Gly Trp Met Val Ser Leu Glu Gln Gly Thr Asn Ile Pro Val Leu Glu
 530 535 540
 Glu Gln Lys Ile Arg Leu Asn Ser Phe Glu Gln Pro His Lys Gln Arg
 545 550 555 560
 Ala Leu Leu Asp Ala Thr Ser Glu Gln Arg Ala Ala Ile Glu Gln Gly
 565 570 575
 Arg Ser Val Ala Gly Pro Arg Gly Val Asp Gly Thr Ser Ala Val Leu
 580 585 590
 Trp Phe His Ser Ala Ser Asn Glu Leu Ser Thr Arg Gln Pro Ser Pro
 595 600 605
 Glu Glu Glu Gln Ser Gly Ser Ser Ile Ala Val Leu Thr His Phe Gly
 610 615 620
 Pro Glu Ala Asp Asp Leu Ser Ala Lys Gln Thr Cys Pro Ser Cys Gly
 625 630 635 640
 Asp Val Asp Ser Ile Arg Tyr Ile Gly Ser Gly Ile Ser Thr Leu Leu
 645 650 655
 Ser Val Ser Leu Ser Asn Leu Phe Gly Met Ala Asp Leu Asp Ser Ala
 660 665 670
 Glu Lys Lys Thr Leu Val Phe Ala Asp Ser Val Gln Asp Ala Ala His
 675 680 685
 Arg Ala Gly Tyr Val Gln Ala Arg Ser Arg Ala Phe Ala Leu Arg Thr
 690 695 700
 Tyr Thr Arg Arg Ala Val Gly Asp Asn Glu Val Thr Leu Pro Ser Ile
 705 710 715 720
 Ser Arg Ala Leu Met Asp Asn Ala Thr Ser Gly Arg Thr Arg Tyr Glu
 725 730 735
 Leu Leu Pro Pro Asp Leu Thr Asp Leu Asp Ile Tyr Lys Pro Tyr Trp
 740 745 750
 His Pro Asp Ala Ser Lys Ala Glu Arg Arg Glu Ala Ser Arg Asn Val
 755 760 765
 His Lys Arg Leu Ser Phe Asp Leu Ala Leu Glu Phe Gly Gln Arg Ala
 770 775 780
 Asp Leu Pro Arg Ser Leu Ala Leu Thr Gly Ala Leu Ser Ala Phe Val
 785 790 795 800
 Asp Leu Pro Lys Gly Val Ala Leu Ser Ala Ala Ala Glu Ala Leu Tyr
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Ala Ile Glu Val Pro Thr Leu Asp Ile Glu Asp Glu Asn Leu Arg Leu
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 Arg Trp Val Gln Gly Ala Leu Glu Leu Leu Arg Ala Arg Gly Gly Ile
 835 840 845
 Asn His Glu Trp Phe Gly Ala Tyr Leu Arg Thr Asp Gly Asn Pro Tyr
 850 855 860
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 Arg Gly Gly Ala Pro Glu Phe Pro Arg Val Gly Ser Ala Leu Ser Gly
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 Ser Leu Arg Ser Ser Thr Gly Thr Thr Pro Leu Gly Ser Pro Arg Gly
 900 905 910
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 915 920 925
 Ala Ala Thr Ala Ile Thr Lys Leu Phe Asp Ala Leu Ser Asn Arg Ser
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 965 970 975
 Glu Cys Ser Val Cys His Ala Gln Thr Gly Val Thr Asp His Val Arg
 980 985 990
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 995 1000 1005
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 Lys Lys Lys Asp Arg Leu Ala Leu Glu Gln Ser Phe Arg Gly Gly Glu
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 Gly Ser Ala Lys Gln Ser Pro Asp Ala Pro Asn Val Leu Val Ala Thr
 1060 1065 1070
 Pro Thr Leu Glu Met Gly Ile Asp Ile Gly Asp Leu Ser Thr Val Met
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 Gly Arg Gly Val Thr Leu Pro Arg Leu Asn Gln Pro Leu Ser Met Ile
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 Lys Gly Ala Ile Thr Pro Pro Val Ala Tyr Leu Ser Ala Ser Glu Ile

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Ala Glu Leu Pro Lys Leu Glu Thr Ala Ile Asp Val Phe Asp Asn Ala 1170 1175 1180		
Ala Gly Lys Thr Pro Leu Val Ala Leu Leu Lys Ala Gln Ile His Ala 1185 1190 1195 1200		
Gly Leu Asp Pro Leu Leu Glu Glu Phe Val Arg Thr Leu Asn Met Gln 1205 1210 1215		
Ile Ser Ile Asp Asn Ile Phe Glu Leu Arg Thr Trp Ala Ser Gly Asn 1220 1225 1230		
Ser Thr Asp Ser Leu Leu Ala Leu Leu Glu Thr Ser Gln Lys Glu Trp 1235 1240 1245		
Met Glu Glu Arg Arg Ser Leu Thr Ala Arg Arg Gly Glu Leu Glu Lys 1250 1255 1260		
Ile Phe Asp Lys Leu Asp Ala Arg Asn Asp Ala His Asp Glu Glu Leu 1265 1270 1275 1280		
Lys Glu Glu Lys Arg Lys Thr Ala Ala Ser Leu Lys Ala Val Lys Leu 1285 1290 1295		
Gln Ile Arg Asp Leu Leu Gly Glu Phe Trp Ile Ala Ala Leu Glu Arg 1300 1305 1310		
Tyr Gly Leu Leu Pro Asn Phe Thr Leu Val Asp Asp Ser Val Glu Leu 1315 1320 1325		
Asn Val Ala Val Thr Ser Phe Asn Pro Gln Glu Val Glu Phe Asp Thr 1330 1335 1340		
Lys Asn His Ala Tyr Ser Arg Gly Ile Ser Ala Ala Leu Phe Glu Leu 1345 1350 1355 1360		
Ala Pro Gly Ala Thr Phe Tyr Ala Gln Gly Ile Ala Ala Lys Val Asp 1365 1370 1375		
Ser Ile Glu Ile Gly Glu His Gly Ser Ala Ile Glu Gln Trp Arg Leu 1380 1385 1390		
Cys Pro Val Cys Ser His Ser Glu Ile Leu Gln Pro Gly Val Ser Thr 1395 1400 1405		
Pro Gly Ser Cys Pro Thr Cys Gly Ser Pro Ala Phe Ala Asp Lys Gly 1410 1415 1420		
Gln Ile Leu Glu Val Val Gln Met Arg Lys Val Ser Ser Ala Val Glu 1425 1430 1435 1440		
Lys Thr Arg Ala Ala Ile Ser Asp Asp Arg Glu Asp Arg Phe Ser Thr 1445 1450 1455		
Arg Phe Asn Gln His Val Ser Phe Val Val Pro Pro Asp Gly His Gly 1460 1465 1470		

Lys Ser Trp Tyr Leu Asn Asp Gly Phe Gly Ile Glu His Leu Pro Lys
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 His Arg Pro Trp Cys Pro His Arg Tyr Glu Gln Lys Glu Asp Thr Val
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 Pro Asp His Leu Asp Val Thr Ser Val Gln Val Pro Arg Thr Ser Gly
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 Thr Gly Tyr Leu Asn Gln Phe Ala Asp Pro Thr Lys Val Pro Glu Leu
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 Ile Ser Arg Ala Trp Glu Arg Val Ser Arg Cys Gln Cys Gln Tyr Asp
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 Glu Thr Leu Ala Cys Pro Glu Cys Leu Leu Pro Tyr Thr Arg Thr Asp
 1665 1670 1675 1680
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 1685 1690 1695
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 Val Pro Asp Trp Thr Phe Leu Glu Lys Arg Pro Glu Asn Thr Leu Gly
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 Asn Arg His Ala Lys Leu Val Asp Arg Val Asn Gly Ser Asn Ser Tyr
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Gly Asn Tyr Pro Thr Val Ala Val Phe Thr Asp Gly Ala Ala Phe His
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 1845 1850 1855
 Ala Trp Phe Ser Pro Ile Gly Arg Gln Leu Ser Lys Ala Asn Leu Ile
 1860 1865 1870
 Leu Asp Pro Gln Ser Thr Ala Leu Leu Ala Ala Thr Pro Met Asp Gln
 1875 1880 1885
 Leu Leu Ala Phe Leu Asp Asn Pro Ala Ala Ser Ser Trp Lys Glu Phe
 1890 1895 1900
 Ala His Ile Ala Ala Ala His Met Leu Gly His Asn Pro Gln Lys Asn
 1905 1910 1915 1920
 Gly Asp Gly Ile Val Gly Thr Phe Arg Asn Lys Ile Ser Leu Arg Ala
 1925 1930 1935
 Thr Met Val Asn Arg Glu Leu Arg Ala Arg Gln Leu Trp Leu Ala Pro
 1940 1945 1950
 Thr Thr Pro Glu Glu Leu Glu Val Asp Thr Trp Thr Ala Phe Leu Asn
 1955 1960 1965
 Leu Ala Asn Leu Met Trp Leu Ala Pro Glu Ser Val Tyr Val Ser Thr
 1970 1975 1980
 Asn Gly Ser Pro His Lys Ile Asp Ile Val Pro Ala Pro Ala Ala Pro
 1985 1990 1995 2000
 Leu Val Val Glu Val Pro Glu Leu Trp Ala Pro Ile Leu Asp Gly Phe
 2005 2010 2015
 Thr Ala Asp Glu Asp Glu Glu Ala Glu Gly Ala Leu Gln Ile Leu Ala
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 Pro Val His Ala Ala Gly Ser Ile Gln Glu Gly Ile Thr Glu Tyr Leu
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 Thr Thr Ser Phe Ser Leu Ala Asp Lys Gln Val Ala Thr Glu Leu Lys
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 cgg ttc ttg ggc cac ggt gat tcc ggc atg ttc cac ggg cct tat gtg 259
 Arg Phe Leu Gly His Gly Asp Ser Gly Met Phe His Gly Pro Tyr Val
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 Arg Ala Arg Leu Pro Tyr Ala Gln Ala Gln Glu Trp Glu Asn Val Leu
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 Ser Trp Leu Pro Glu Asn Phe Val Pro Tyr His His Gln Lys Ala Ala
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 Phe Leu Tyr Pro Ile Leu Asp His Ala Leu Arg Leu Arg Lys Arg Gly
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 135 140 145
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 150 155 160 165
 ctt aaa ggt gtt acc gcc ggt att tat acc ggt gaa gcc aag ggc aat 643
 Leu Lys Gly Val Thr Ala Gly Ile Tyr Thr Gly Glu Ala Lys Gly Asn
 170 175 180

cgc acg cag atg ggc gaa agg gag ctt att aat gat ccc caa gcc atg 691
 Arg Thr Gln Met Gly Glu Arg Glu Leu Ile Asn Asp Pro Gln Ala Met
 185 190 195

cgg gtt agt ccc cca gat att ttg ctc acc aac tac aaa atg ttg gat 739
 Arg Val Ser Pro Pro Asp Ile Leu Leu Thr Asn Tyr Lys Met Leu Asp
 200 205 210

cag ctc ttg ctg cgc agc gtc gac cgc gaa atg tgg caa aaa tcc gcc 787
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 35 40 45

His Gly Pro Tyr Val Arg Ala Arg Leu Pro Tyr Ala Gln Ala Gln Glu
 50 55 60

Trp Glu Asn Val Leu Ser Trp Leu Pro Glu Asn Phe Val Pro Tyr His
 65 70 75 80

His Gln Lys Ala Ala Phe Gln Arg Leu Ser Ser Leu Asp Asn Arg Gly
 85 90 95

Lys Asp Arg Arg Pro Asp Pro Thr Leu Val Val Thr Gly Thr Gly Ser
 100 105 110

Gly Lys Thr Glu Ser Phe Leu Tyr Pro Ile Leu Asp His Ala Leu Arg
 115 120 125

Leu Arg Lys Arg Gly Gln Gln Gly Ile Lys Ala Leu Leu Leu Tyr Pro
 130 135 140

Met Asn Ala Leu Ala Asn Asp Gln Ala Asp Arg Leu Ala Arg Leu Ile
 145 150 155 160

His Asn Asn Pro Ala Leu Lys Gly Val Thr Ala Gly Ile Tyr Thr Gly
 165 170 175

Glu Ala Lys Gly Asn Arg Thr Gln Met Gly Glu Arg Glu Leu Ile Asn
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Asp Pro Gln Ala Met Arg Val Ser Pro Pro Asp Ile Leu Leu Thr Asn
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Trp Gln Lys Ser Ala Thr Ser Leu Gln
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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1203)

<223> FRXA02357

<400> 101

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tgg act ttc ttg gaa aag cgc cca gag aac act ctt ggc tct cag ttg 96
 Trp Thr Phe Leu Glu Lys Arg Pro Glu Asn Thr Leu Gly Ser Gln Leu
 20 25 30

gaa ctg cgt ttc cgc gtg atg ctg cga cgc gcc tta aaa aat cgc cat 144
 Glu Leu Arg Phe Arg Val Met Leu Arg Arg Ala Leu Lys Asn Arg His
 35 40 45

gcc aaa ctt gtg gac cgc gtc aac ggc tca aac tct tat gtg gat att 192
 Ala Lys Leu Val Asp Arg Val Asn Gly Ser Asn Ser Tyr Val Asp Ile
 50 55 60

gag atg agc tcc ggt gtg cgc tgg cgg atg agc gaa caa gtt gat cgt 240
 Glu Met Ser Ser Gly Val Arg Trp Arg Met Ser Glu Gln Val Asp Arg
 65 70 75 80

gga tat aca cgc cct gat ttc tgg ttt gaa ccg ctc aac ggc aac tat 288
 Gly Tyr Thr Arg Pro Asp Phe Trp Phe Glu Pro Leu Asn Gly Asn Tyr
 85 90 95

ccc acc gtg gct gtt ttt acc gat ggc gct gcg ttc cat atc tct tca 336
 Pro Thr Val Ala Val Phe Thr Asp Gly Ala Ala Phe His Ile Ser Ser
 100 105 110

gct aac tac cgt ctt gat ggc gat att cag aaa ccg atg aaa cta gcg 384
 Ala Asn Tyr Arg Leu Asp Gly Asp Ile Gln Lys Arg Met Lys Leu Ala
 115 120 125

ctc gat cca gac aat att ttg ccg tgg aat atc act agc tta gac ctc 432
 Leu Asp Pro Asp Asn Ile Leu Pro Trp Asn Ile Thr Ser Leu Asp Leu
 130 135 140

gac cgc ttt agt aat ccc gct gca caa ggt gag gaa cca gca tgg ttt 480
 Asp Arg Phe Ser Asn Pro Ala Ala Gln Gly Glu Glu Pro Ala Trp Phe
 145 150 155 160

agc ccc atc ggc agg cag ctc agc aaa gca aat ttg att ctt gat cca 528
 Ser Pro Ile Gly Arg Gln Leu Ser Lys Ala Asn Leu Ile Leu Asp Pro

				165				170				175					
caa	tca	act	gca	ctc	ctg	gca	gca	acg	cct	atg	gat	caa	ctc	ttg	gca	576	
Gln	Ser	Thr	Ala	Leu	Leu	Ala	Ala	Thr	Pro	Met	Asp	Gln	Leu	Leu	Ala		
			180					185					190				
ttt	tta	gat	aat	ccc	gcg	gca	tcc	tcg	tgg	aag	gag	ttt	gct	cat	atc	624	
Phe	Leu	Asp	Asn	Pro	Ala	Ala	Ser	Ser	Trp	Lys	Glu	Phe	Ala	His	Ile		
			195					200					205				
gct	gct	gct	cac	atg	ctt	ggg	cat	aat	cca	caa	aaa	aat	ggc	gac	gga	672	
Ala	Ala	Ala	His	Met	Leu	Gly	His	Asn	Pro	Gln	Lys	Asn	Gly	Asp	Gly		
			210					215					220				
att	gtt	ggg	acc	ttc	cg	aat	aag	att	tcc	ttg	cg	gcc	acc	atg	gtt	720	
Ile	Val	Gly	Thr	Phe	Arg	Asn	Lys	Ile	Ser	Leu	Arg	Ala	Thr	Met	Val		
			225					230					235		240		
aat	cg	gaa	ctg	cg	gcc	cg	caa	ttg	tgg	ctt	gct	ccc	acc	act	cca	768	
Asn	Arg	Glu	Leu	Arg	Ala	Arg	Gln	Leu	Trp	Leu	Ala	Pro	Thr	Thr	Pro		
			245					250					255				
gaa	gag	ctg	gaa	gtg	gat	acc	tgg	act	gcc	ttc	ctc	aat	ttg	gcc	aac	816	
Glu	Glu	Leu	Glu	Val	Asp	Thr	Trp	Thr	Ala	Phe	Leu	Asn	Leu	Ala	Asn		
			260					265					270				
ctc	atg	tgg	ctg	gca	ccg	gaa	tcc	gta	tac	gta	agc	act	aat	ggg	tca	864	
Leu	Met	Trp	Leu	Ala	Pro	Glu	Ser	Val	Tyr	Val	Ser	Thr	Asn	Gly	Ser		
			275					280					285				
ccg	cat	aaa	att	gat	att	gtg	cct	gct	cca	gca	gct	ccg	ctt	gtt	gtt	912	
Pro	His	Lys	Ile	Asp	Ile	Val	Pro	Ala	Pro	Ala	Ala	Pro	Leu	Val	Val		
			290					295					300				
gaa	gtt	cct	gaa	ttg	tgg	gct	ccc	atc	ttg	gat	ggc	ttt	acc	gcc	gat	960	
Glu	Val	Pro	Glu	Leu	Trp	Ala	Pro	Ile	Leu	Asp	Gly	Phe	Thr	Ala	Asp		
			305					310					315		320		
gaa	gat	gaa	gaa	gcc	gaa	ggc	gct	ttg	cag	atc	ttg	gct	aag	gaa	cat	1008	
Glu	Asp	Glu	Glu	Ala	Glu	Gly	Ala	Leu	Gln	Ile	Leu	Ala	Lys	Glu	His		
			325					330					335				
gcc	ctg	gtt	cca	gag	acc	acc	ggg	gat	gag	ctc	tcg	agt	att	cct	acg	1056	
Ala	Leu	Val	Pro	Glu	Thr	Thr	Gly	Asp	Glu	Leu	Ser	Ser	Ile	Pro	Thr		
			340					345					350				
att	gct	acg	tgg	ccg	agt	gtc	aag	atc	gct	ttg	ctc	tat	gaa	tct	gat	1104	
Ile	Ala	Thr	Trp	Pro	Ser	Val	Lys	Ile	Ala	Leu	Leu	Tyr	Glu	Ser	Asp		
			355					360					365				
ccc	gat	gag	cct	ttg	gag	gat	gat	ctc	aaa	gct	gaa	ggg	tgg	acg	ctg	1152	
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<211> 401

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 102

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Trp	Thr	Phe	Leu	Glu	Lys	Arg	Pro	Glu	Asn	Thr	Leu	Gly	Ser	Gln	Leu
			20					25					30		

Glu	Leu	Arg	Phe	Arg	Val	Met	Leu	Arg	Arg	Ala	Leu	Lys	Asn	Arg	His
		35					40					45			

Ala	Lys	Leu	Val	Asp	Arg	Val	Asn	Gly	Ser	Asn	Ser	Tyr	Val	Asp	Ile
	50					55					60				

Glu	Met	Ser	Ser	Gly	Val	Arg	Trp	Arg	Met	Ser	Glu	Gln	Val	Asp	Arg
65					70					75					80

Gly	Tyr	Thr	Arg	Pro	Asp	Phe	Trp	Phe	Glu	Pro	Leu	Asn	Gly	Asn	Tyr
				85					90					95	

Pro	Thr	Val	Ala	Val	Phe	Thr	Asp	Gly	Ala	Ala	Phe	His	Ile	Ser	Ser
		100						105					110		

Ala	Asn	Tyr	Arg	Leu	Asp	Gly	Asp	Ile	Gln	Lys	Arg	Met	Lys	Leu	Ala
	115					120						125			

Leu	Asp	Pro	Asp	Asn	Ile	Leu	Pro	Trp	Asn	Ile	Thr	Ser	Leu	Asp	Leu
130					135						140				

Asp	Arg	Phe	Ser	Asn	Pro	Ala	Ala	Gln	Gly	Glu	Glu	Pro	Ala	Trp	Phe
145				150						155					160

Ser	Pro	Ile	Gly	Arg	Gln	Leu	Ser	Lys	Ala	Asn	Leu	Ile	Leu	Asp	Pro
			165						170					175	

Gln	Ser	Thr	Ala	Leu	Leu	Ala	Ala	Thr	Pro	Met	Asp	Gln	Leu	Leu	Ala
		180						185					190		

Phe	Leu	Asp	Asn	Pro	Ala	Ala	Ser	Ser	Trp	Lys	Glu	Phe	Ala	His	Ile
	195						200					205			

Ala	Ala	Ala	His	Met	Leu	Gly	His	Asn	Pro	Gln	Lys	Asn	Gly	Asp	Gly
	210					215					220				

Ile	Val	Gly	Thr	Phe	Arg	Asn	Lys	Ile	Ser	Leu	Arg	Ala	Thr	Met	Val
225					230					235					240

Asn	Arg	Glu	Leu	Arg	Ala	Arg	Gln	Leu	Trp	Leu	Ala	Pro	Thr	Thr	Pro
			245						250					255	

Glu	Glu	Leu	Glu	Val	Asp	Thr	Trp	Thr	Ala	Phe	Leu	Asn	Leu	Ala	Asn
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Leu	Met	Trp	Leu	Ala	Pro	Glu	Ser	Val	Tyr	Val	Ser	Thr	Asn	Gly	Ser
	275						280						285		

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Pro His Lys Ile Asp Ile Val Pro Ala Pro Ala Ala Pro Leu Val Val
 290 295 300
 Glu Val Pro Glu Leu Trp Ala Pro Ile Leu Asp Gly Phe Thr Ala Asp
 305 310 315 320
 Glu Asp Glu Glu Ala Glu Gly Ala Leu Gln Ile Leu Ala Lys Glu His
 325 330 335
 Ala Leu Val Pro Glu Thr Thr Gly Asp Glu Leu Ser Ser Ile Pro Thr
 340 345 350
 Ile Ala Thr Trp Pro Ser Val Lys Ile Ala Leu Leu Tyr Glu Ser Asp
 355 360 365
 Pro Asp Glu Pro Leu Glu Asp Asp Leu Lys Ala Glu Gly Trp Thr Leu
 370 375 380
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Pro

<210> 103
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(3855)
 <223> FRXA02785

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 Ile Ala Thr Ala Gln His Glu Asp Asp Tyr Ala Gln Leu Cys Phe Arg
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 gtt ttt tgt gag aaa gtg tgg ctg tgt gag gct gat ctg cac gca gcg 144
 Val Phe Cys Glu Lys Val Trp Leu Cys Glu Ala Asp Leu His Ala Ala
 35 40 45
 atc agt gct tat gcg gct cat gat tta act gct gcg att ttg cag cat 192
 Ile Ser Ala Tyr Ala Ala His Asp Leu Thr Ala Ala Ile Leu Gln His
 50 55 60
 gct gct gat tcc acc ccg ctt agc agg cgt gat caa gat gag gtc act 240
 Ala Ala Asp Ser Thr Pro Leu Ser Arg Arg Asp Gln Asp Glu Val Thr
 65 70 75 80
 gcc ctt ccg gag ctg gta ttg ggg gct acc gcc cgc atc tta ggt gag 288
 Ala Leu Pro Glu Leu Val Leu Gly Ala Thr Ala Arg Ile Leu Gly Glu
 85 90 95

gtt aaa gct gcg gaa ttt atc agc cat gca ctg gct gcc atg gca ttt	336
Val Lys Ala Ala Glu Phe Ile Ser His Ala Leu Ala Ala Met Ala Phe	
100 105 110	
gtg cgc gcg gaa tac ggc aaa gtt gcc gcc tgg ggt gcc aag cgc cta	384
Val Arg Ala Glu Tyr Gly Lys Val Ala Ala Trp Gly Ala Lys Arg Leu	
115 120 125	
cct ggc gtc gaa acg cat ctt tgg gtg cgc gag gtc tcc cgc att gac	432
Pro Gly Val Glu Thr His Leu Trp Val Arg Glu Val Ser Arg Ile Asp	
130 135 140	
cgc gcc ctg ggg gtt ggg gat gaa caa tcc atg ttt cgc tgg tcc gat	480
Arg Ala Leu Gly Val Gly Asp Glu Gln Ser Met Phe Arg Trp Ser Asp	
145 150 155 160	
gat ggc ccg gca gaa gat gcc aat acc caa caa tgg ttg ccg gcg tgt	528
Asp Gly Pro Ala Glu Asp Ala Asn Thr Gln Gln Trp Leu Pro Ala Cys	
165 170 175	
tat tgc cgc agt tgt ggc cgt tcc ggc tgg atg gtc agc ctg gaa caa	576
Tyr Cys Arg Ser Cys Gly Arg Ser Gly Trp Met Val Ser Leu Glu Gln	
180 185 190	
ggc acc aat atc ccg gtg ttg gaa gaa caa aaa att cgc ctc aac tcc	624
Gly Thr Asn Ile Pro Val Leu Glu Glu Gln Lys Ile Arg Leu Asn Ser	
195 200 205	
ttt gaa caa ccc cat aaa caa aga gcg ctt ctc gac gcc acc tct gag	672
Phe Glu Gln Pro His Lys Gln Arg Ala Leu Leu Asp Ala Thr Ser Glu	
210 215 220	
cag cgc gca gcc att gag cag ggg cgc agc gtt gct ggg ccg cga gga	720
Gln Arg Ala Ala Ile Glu Gln Gly Arg Ser Val Ala Gly Pro Arg Gly	
225 230 235 240	
gtt gat ggc acc tca gca gtg ctg tgg ttc cat agc gcc agc aat gaa	768
Val Asp Gly Thr Ser Ala Val Leu Trp Phe His Ser Ala Ser Asn Glu	
245 250 255	
ctc agc acg cgc caa ccc agc cca gaa gaa gaa caa tca ggt tct tct	816
Leu Ser Thr Arg Gln Pro Ser Pro Glu Glu Glu Gln Ser Gly Ser Ser	
260 265 270	
atc gca gtg ctc acc cac ttt ggc cct gag gca gac gat ctc tcc gcc	864
Ile Ala Val Leu Thr His Phe Gly Pro Glu Ala Asp Asp Leu Ser Ala	
275 280 285	
aaa cag acc tgc cct tcc tgt ggt gat gtt gat tcc atc cgt tat atc	912
Lys Gln Thr Cys Pro Ser Cys Gly Asp Val Asp Ser Ile Arg Tyr Ile	
290 295 300	
gga tcg gga atc tct acc ctg ctc tct gtc tca ctc tcc aat ctt ttt	960
Gly Ser Gly Ile Ser Thr Leu Leu Ser Val Ser Leu Ser Asn Leu Phe	
305 310 315 320	
ggt atg gcc gat ttg gat agc gct gag aaa aag acg ctg gtc ttt gcc	1008
Gly Met Ala Asp Leu Asp Ser Ala Glu Lys Lys Thr Leu Val Phe Ala	
325 330 335	
gat tcc gtg caa gat gcc gcg cac cgc gcc ggg tac gtc caa gca cgt	1056

Asp	Ser	Val	Gln	Asp	Ala	Ala	His	Arg	Ala	Gly	Tyr	Val	Gln	Ala	Arg		
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tcc	cgc	gct	ttt	gcc	ctt	cgt	acc	tat	acc	cgg	cgc	gca	gtg	ggc	gat	1104	
Ser	Arg	Ala	Phe	Ala	Leu	Arg	Thr	Tyr	Thr	Arg	Arg	Ala	Val	Gly	Asp		
			355				360					365					
aat	gaa	gtc	acc	ttg	cca	tca	atc	tcc	cgg	gcg	ctg	atg	gat	aac	gcc	1152	
Asn	Glu	Val	Thr	Leu	Pro	Ser	Ile	Ser	Arg	Ala	Leu	Met	Asp	Asn	Ala		
			370				375					380					
acc	tct	ggg	cgc	acc	cgt	tat	gag	ctc	cta	ccc	cct	gac	ctg	acc	gat	1200	
Thr	Ser	Gly	Arg	Thr	Arg	Tyr	Glu	Leu	Leu	Pro	Pro	Asp	Leu	Thr	Asp		
			385				390				395				400		
ctt	gat	att	tac	aaa	cct	tat	tgg	cac	ccc	gat	gcc	agc	aag	gct	gag	1248	
Leu	Asp	Ile	Tyr	Lys	Pro	Tyr	Trp	His	Pro	Asp	Ala	Ser	Lys	Ala	Glu		
			405					410					415				
cgc	cgt	gag	gcc	tcc	cgc	aat	gtg	cat	aaa	cgt	tta	agt	ttt	gat	ctc	1296	
Arg	Arg	Glu	Ala	Ser	Arg	Asn	Val	His	Lys	Arg	Leu	Ser	Phe	Asp	Leu		
			420					425					430				
gcc	ctc	gag	ttt	gga	caa	cgc	gct	gat	cta	ccc	cgt	tcc	ctt	gcg	ctg	1344	
Ala	Leu	Glu	Phe	Gly	Gln	Arg	Ala	Asp	Leu	Pro	Arg	Ser	Leu	Ala	Leu		
			435				440					445					
acc	ggc	gct	ttg	agt	gct	ttt	gtg	gat	ttg	ccc	aaa	ggc	gtt	gca	ttg	1392	
Thr	Gly	Ala	Leu	Ser	Ala	Phe	Val	Asp	Leu	Pro	Lys	Gly	Val	Ala	Leu		
			450				455					460					
tcc	gcg	gct	gcc	gaa	gca	ctt	tat	gcc	atc	gaa	gtt	ccc	acc	tta	gat	1440	
Ser	Ala	Ala	Ala	Glu	Ala	Leu	Tyr	Ala	Ile	Glu	Val	Pro	Thr	Leu	Asp		
			465				470				475				480		
att	gag	gat	gag	aac	ctg	cga	ctg	cgc	tgg	gtg	caa	ggc	gcc	ctg	gaa	1488	
Ile	Glu	Asp	Glu	Asn	Leu	Arg	Leu	Arg	Trp	Val	Gln	Gly	Ala	Leu	Glu		
			485					490					495				
ctt	ttg	cgc	gcc	cgc	ggg	ggc	atc	aac	cat	gag	tgg	ttt	ggc	gcc	tac	1536	
Leu	Leu	Arg	Ala	Arg	Gly	Gly	Ile	Asn	His	Glu	Trp	Phe	Gly	Ala	Tyr		
			500					505					510				
ctg	cgc	acc	gat	ggc	aac	ccc	tat	atg	ctt	aac	cgc	cgc	caa	gcc	cgc	1584	
Leu	Arg	Thr	Asp	Gly	Asn	Pro	Tyr	Met	Leu	Asn	Arg	Arg	Gln	Ala	Arg		
			515				520					525					
gct	gag	ggc	att	ccc	ggc	ttt	gtc	cgc	ggc	ggc	gca	cct	gaa	ttc	cca	1632	
Ala	Glu	Gly	Ile	Pro	Gly	Phe	Val	Arg	Gly	Gly	Ala	Pro	Glu	Phe	Pro		
			530				535				540						
cgt	gta	ggc	tcc	gca	ctt	tcc	gga	tcc	ctg	cgt	tcc	agc	acc	ggc	acc	1680	
Arg	Val	Gly	Ser	Ala	Leu	Ser	Gly	Ser	Leu	Arg	Ser	Ser	Thr	Gly	Thr		
			545				550				555				560		
acc	ccg	ctt	ggc	agc	ccg	cgc	gga	cgt	tat	gcg	tcc	tgg	acc	tcg	cag	1728	

580					585					590						
ttc	gac	gct	tta	agc	aac	cgc	agc	att	ctc	tcc	tca	ata	tct	acc	gac	1824
Phe	Asp	Ala	Leu	Ser	Asn	Arg	Ser	Ile	Leu	Ser	Ser	Ile	Ser	Thr	Asp	
	595						600					605				
agc	ggc	gga	aaa	atc	tac	tgc	ctc	gag	gcc	gaa	cgc	atc	cgt	att	ttt	1872
Ser	Gly	Gly	Lys	Ile	Tyr	Cys	Leu	Glu	Ala	Glu	Arg	Ile	Arg	Ile	Phe	
	610					615					620					
agc	gaa	gac	cat	ccc	gaa	gtt	ctg	gaa	tgc	agc	gtg	tgc	cat	gcc	caa	1920
Ser	Glu	Asp	His	Pro	Glu	Val	Leu	Glu	Cys	Ser	Val	Cys	His	Ala	Gln	
	625				630					635					640	
act	ggt	gta	act	gat	cat	gtg	cgt	gac	ttc	ctt	gat	ggc	gct	ccg	tgt	1968
Thr	Gly	Val	Thr	Asp	His	Val	Arg	Asp	Phe	Leu	Asp	Gly	Ala	Pro	Cys	
				645					650					655		
ttt	agc	cct	agt	tgt	ggg	ggc	gtt	ctc	cat	atc	gag	gaa	gta	gaa	gac	2016
Phe	Ser	Pro	Ser	Cys	Gly	Gly	Val	Leu	His	Ile	Glu	Glu	Val	Glu	Asp	
			660					665					670			
aac	tac	tac	cgc	agg	ctt	tat	tcc	gca	att	gaa	ccg	cgc	act	gtc	att	2064
Asn	Tyr	Tyr	Arg	Arg	Leu	Tyr	Ser	Ala	Ile	Glu	Pro	Arg	Thr	Val	Ile	
		675					680					685				
gcc	cgc	gag	cac	acc	agc	atg	ctc	aag	aaa	aaa	gac	cgc	ctc	gca	ctc	2112
Ala	Arg	Glu	His	Thr	Ser	Met	Leu	Lys	Lys	Lys	Asp	Arg	Leu	Ala	Leu	
	690					695					700					
gaa	caa	tcc	ttt	aga	ggt	gga	gaa	ggc	tcg	gcc	aaa	caa	tcc	ccc	gat	2160
Glu	Gln	Ser	Phe	Arg	Gly	Gly	Glu	Gly	Ser	Ala	Lys	Gln	Ser	Pro	Asp	
	705				710					715					720	
gcg	ccc	aat	gtg	ttg	gta	gct	acg	cca	acg	ctg	gaa	atg	ggt	att	gac	2208
Ala	Pro	Asn	Val	Leu	Val	Ala	Thr	Pro	Thr	Leu	Glu	Met	Gly	Ile	Asp	
			725						730					735		
atc	ggc	gat	ctc	tcc	acc	gtg	atg	ctt	gcg	tct	ttg	cca	aca	tca	gtg	2256
Ile	Gly	Asp	Leu	Ser	Thr	Val	Met	Leu	Ala	Ser	Leu	Pro	Thr	Ser	Val	
			740					745					750			
gcc	agt	tat	gta	cag	cgt	gtt	ggt	cgt	gcc	ggg	cgc	ctc	agc	gga	aac	2304
Ala	Ser	Tyr	Val	Gln	Arg	Val	Gly	Arg	Ala	Gly	Arg	Leu	Ser	Gly	Asn	
	755					760						765				
tcg	ttg	gta	ctc	gcc	gtg	gtg	cgt	ggc	cgc	ggt	gtc	aca	ttg	cct	cgt	2352
Ser	Leu	Val	Leu	Ala	Val	Val	Arg	Gly	Arg	Gly	Val	Thr	Leu	Pro	Arg	
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gcg	tat	ctt	tcc	gcc	agt	gaa	atc	ttg	cac	cgc	caa	ttc	ttg	gca	tat	2448
Ala	Tyr	Leu	Ser	Ala	Ser	Glu	Ile	Leu	His	Arg	Gln	Phe	Leu	Ala	Tyr	
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Val	Ile	Asp	Cys	Leu	Asp	Thr	Arg	Ala	Glu	Leu	Pro	Lys	Leu	Glu	Thr	
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tta ctc aaa gcg cag att cac gca ggc cta gat cct ttg ctg gag gaa	2592
Leu Leu Lys Ala Gln Ile His Ala Gly Leu Asp Pro Leu Leu Glu Glu	
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Phe Val Arg Thr Leu Asn Met Gln Ile Ser Ile Asp Asn Ile Phe Glu	
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Leu Arg Thr Trp Ala Ser Gly Asn Ser Thr Asp Ser Leu Leu Ala Leu	
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Ala Arg Arg Gly Glu Leu Glu Lys Ile Phe Asp Lys Leu Asp Ala Arg	
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Asn Asp Ala His Asp Glu Glu Leu Lys Glu Glu Lys Arg Lys Thr Ala	
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Ala Ser Leu Lys Ala Val Lys Leu Gln Ile Arg Asp Leu Leu Gly Glu	
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Ile Ser Ala Ala Leu Phe Glu Leu Ala Pro Gly Ala Thr Phe Tyr Ala	
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Ile Leu Gln Pro Gly Val Ser Thr Pro Gly Ser Cys Pro Thr Cys Gly	
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Val Val Pro Pro Asp Gly His Gly Lys Ser Trp Tyr Leu Asn Asp Gly
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Phe Gly Ile Glu His Leu Pro Lys Val Glu Leu Arg Trp Leu Asn Leu
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tat gag caa aaa gaa gat acc gta tct ttc gct ttg ggt cgt act ctt 3648
Tyr Glu Gln Lys Glu Asp Thr Val Ser Phe Ala Leu Gly Arg Thr Leu
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Lys Thr Gln Gly Val Leu Met Leu Leu Pro Glu Tyr Phe Gly Ser Glu
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Val	Phe	Cys	Glu	Lys	Val	Trp	Leu	Cys	Glu	Ala	Asp	Leu	His	Ala	Ala
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Ile	Ser	Ala	Tyr	Ala	Ala	His	Asp	Leu	Thr	Ala	Ala	Ile	Leu	Gln	His
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Ala	Leu	Pro	Glu	Leu	Val	Leu	Gly	Ala	Thr	Ala	Arg	Ile	Leu	Gly	Glu
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Tyr	Cys	Arg	Ser	Cys	Gly	Arg	Ser	Gly	Trp	Met	Val	Ser	Leu	Glu	Gln
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Ile	Ala	Val	Leu	Thr	His	Phe	Gly	Pro	Glu	Ala	Asp	Asp	Leu	Ser	Ala
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Lys	Gln	Thr	Cys	Pro	Ser	Cys	Gly	Asp	Val	Asp	Ser	Ile	Arg	Tyr	Ile
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Gly Met Ala Asp Leu Asp Ser Ala Glu Lys Lys Thr Leu Val Phe Ala
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 Thr Pro Leu Gly Ser Pro Arg Gly Arg Tyr Ala Ser Trp Thr Ser Gln
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 Ser Gly Gly Lys Ile Tyr Cys Leu Glu Ala Glu Arg Ile Arg Ile Phe
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 Ser Glu Asp His Pro Glu Val Leu Glu Cys Ser Val Cys His Ala Gln
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Thr Gly Val Thr Asp His Val Arg Asp Phe Leu Asp Gly Ala Pro Cys
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 Phe Ser Pro Ser Cys Gly Gly Val Leu His Ile Glu Glu Val Glu Asp
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 Asn Tyr Tyr Arg Arg Leu Tyr Ser Ala Ile Glu Pro Arg Thr Val Ile
 675 680 685
 Ala Arg Glu His Thr Ser Met Leu Lys Lys Lys Asp Arg Leu Ala Leu
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 Glu Gln Ser Phe Arg Gly Gly Glu Gly Ser Ala Lys Gln Ser Pro Asp
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 Ala Pro Asn Val Leu Val Ala Thr Pro Thr Leu Glu Met Gly Ile Asp
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 945 950 955 960
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965

970

975

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Glu	Trp	Asp	Ala	Val	Phe	Leu	Val	Gly	Leu	Val	Asp	Ser	Thr	Leu	Pro
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Arg	Leu	Phe	Tyr	Val	Gly	Val	Thr	Arg	Ala	Arg	Glu	His	Leu	His	Cys
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Ser	Trp	Ala	Leu	Ala	Arg	Gln	Glu	Gly	Gly	Arg	Lys	Ser	Arg	Lys	Arg
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<222> (101)..(2668)

<223> RXN01683

<400> 107

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Tyr Ala Met Phe Asp Asn Gly Tyr Arg Pro Asp Arg Ser Tyr Val Lys
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Asn Asp Gly Pro Ala Ala Met Arg Tyr Thr Glu Cys Arg Met Thr Pro
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Leu Ala Met Glu Met Val Arg Asp Ile Arg Glu Asn Thr Val Asn Phe
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Met Ala Thr Asn Ile Pro Pro His Asn Leu Asn Glu Leu Ala Asp Ala
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Ile Phe Trp Leu Leu Glu Asn Pro Asp Ala Glu Glu Ser Glu Ala Leu
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Leu Ile Ile Gly Asp Lys Gly Ile His Asp Ala Tyr Thr Thr Gly Arg	
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Gly Ser Ile Arg Met Arg Gly Val Thr Ser Ile Glu Glu Glu Gly Asn	
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Arg Thr Val Ile Val Ile Thr Glu Leu Pro Tyr Gln Val Asn Pro Asp	
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Asn Leu Ile Ser Asn Ile Ala Glu Gln Val Arg Asp Gly Lys Leu Val	
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Gly Ile Ser Lys Ile Glu Asp Glu Ser Ser Asp Arg Val Gly Met Arg	
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Asn Leu Phe Lys His Ser Gln Leu Gln Ala Asn Phe Gly Ala Asn Met	
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Gln Tyr Arg Leu Asp Lys Ala Glu Glu Arg Ala His Leu Leu Arg Gly	
375 380 385	
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Asp Val Asp Glu Ala Gln Ala Asp Ala Ile Leu Ala Met Gln Leu Arg	
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Lys Arg Gly Gly Lys Gly Val Arg Gly Ala Glu Leu Lys Gln Asp Asp	
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Glu Ala Ser Arg Thr Ala Arg Gly Gln His Val Ala Asn Leu Leu Glu	
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Phe Gln Pro Gly Glu Gln Ile Ala Gln Val Ile Gln Leu Glu Ser Tyr	
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Gly	Gly	Leu	Gly	Val	Val	Thr	Phe	Lys	Tyr	Thr	Pro	Lys	Arg	Gly	Arg	
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Leu	Val	Ser	Ala	Ile	Ala	Val	Glu	Glu	Asp	Asp	Glu	Ile	Phe	Ala	Ile	
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Thr	Ser	Ala	Gly	Gly	Val	Val	Arg	Thr	Glu	Val	Lys	Gln	Ile	Arg	Pro	
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Ser	Ser	Arg	Ala	Thr	Met	Gly	Val	Arg	Leu	Val	Asn	Leu	Glu	Glu	Gly	
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gta	gaa	ctg	ctt	gcc	atc	gac	aag	aac	gtc	gaa	gac	cag	ggc	gaa	gca	2563
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Ser	Ala	Glu	Ala	Val	Ala	Lys	Gly	Ala	Val	Glu	Gly	Pro	Ala	Ser	Lys	
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Thr	Ala	Ala	Glu	Glu	Thr	Asp	Ser	Val	Asp	Asn	Gly	Ser	Asp	Glu	Asn	
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Gly	Glu	Glu														
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<213> Corynebacterium glutamicum

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Ile	Val	Gly	Arg	Ala	Leu	Pro	Glu	Val	Arg	Asp	Gly	Leu	Lys	Pro	Val	
		35					40					45				
His	Arg	Arg	Val	Leu	Tyr	Ala	Met	Phe	Asp	Asn	Gly	Tyr	Arg	Pro	Asp	
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 Phe Gly Ser Arg Gly Asn Asp Gly Pro Ala Ala Met Arg Tyr Thr Glu
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 Cys Arg Met Thr Pro Leu Ala Met Glu Met Val Arg Asp Ile Arg Glu
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 Asn Thr Val Asn Phe Ser Pro Asn Tyr Asp Gly Lys Thr Leu Glu Pro
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 Asp Val Leu Pro Ser Arg Val Pro Asn Leu Leu Met Asn Gly Ser Gly
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 Gly Ile Ala Val Gly Met Ala Thr Asn Ile Pro Pro His Asn Leu Asn
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 Glu Leu Ala Asp Ala Ile Phe Trp Leu Leu Glu Asn Pro Asp Ala Glu
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 Glu Ser Glu Ala Leu Glu Ala Cys Met Lys Phe Val Lys Gly Pro Asp
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 Phe Pro Thr Ala Gly Leu Ile Ile Gly Asp Lys Gly Ile His Asp Ala
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 Gln Val Asn Pro Asp Asn Leu Ile Ser Asn Ile Ala Glu Gln Val Arg
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 Asp Gly Lys Leu Val Gly Ile Ser Lys Ile Glu Asp Glu Ser Ser Asp
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 Arg Leu Asp Gln Met Leu Arg Tyr Tyr Val Ala His Gln Ile Glu Val
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 Ile Val Arg Arg Thr Gln Tyr Arg Leu Asp Lys Ala Glu Glu Arg Ala
 370 375 380

His Leu Leu Arg Gly Leu Val Lys Ala Leu Asp Met Leu Asp Glu Val
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 Ile Ala Leu Ile Arg Arg Ser Pro Thr Pro Asp Glu Ala Arg Thr Gly
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 420 425 430
 Ala Met Gln Leu Arg Arg Leu Ala Ala Leu Glu Arg Gln Lys Ile Ile
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 Asp Glu Leu Ala Glu Ile Glu Leu Glu Ile Ala Asp Leu Lys Ala Ile
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 Leu Ala Ser Pro Glu Arg Gln Arg Thr Ile Val Arg Asp Glu Leu Thr
 465 470 475 480
 Glu Ile Val Glu Lys Tyr Gly Asp Glu Arg Arg Ser Gln Ile Ile Ala
 485 490 495
 Ala Thr Gly Asp Val Ser Glu Glu Asp Leu Ile Ala Arg Glu Asn Val
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 Val Ile Thr Ile Thr Ser Thr Gly Tyr Ala Lys Arg Thr Lys Val Asp
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 Ala Tyr Lys Ser Gln Lys Arg Gly Gly Lys Gly Val Arg Gly Ala Glu
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 His Gly Arg Val Lys Lys Ser Arg Leu Leu Asp Tyr Glu Ser Ala Arg
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 660 665 670
 Phe Gly Gln Ser Ile Arg Phe Thr Ala Asp Asp Glu Gln Leu Arg Pro
 675 680 685
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 Asp Gln Leu Leu Ser Met Ser Val Val Arg Asp Gly Glu Phe Leu Leu

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Ser Thr Gln Gly Arg Gly Gly Leu Gly Val Val Thr Phe Lys Tyr Thr						
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Pro Lys Arg Gly Arg Leu Val Ser Ala Ile Ala Val Glu Glu Asp Asp						
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Glu Ile Phe Ala Ile Thr Ser Ala Gly Gly Val Val Arg Thr Glu Val						
	770			775		780
Lys Gln Ile Arg Pro Ser Ser Arg Ala Thr Met Gly Val Arg Leu Val						
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Asn Leu Glu Glu Gly Val Glu Leu Leu Ala Ile Asp Lys Asn Val Glu						
	805			810		815
Asp Gln Gly Glu Ala Ser Ala Glu Ala Val Ala Lys Gly Ala Val Glu						
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Val Ser Ser Thr His Asp Trp Ile Leu Phe Leu His Gln Leu Arg Ser	
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cgt gta ccg cct caa ggc att cga act tcc aga ggc atc ccg cac cgc	192
Arg Val Pro Pro Gln Gly Ile Arg Thr Ser Arg Gly Ile Pro His Arg	
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acg tgg aca gca cgt ggc caa cct tct gga att cca acc tgg	234
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Ala Asn Leu Leu Glu Phe Gln Pro Gly Glu Gln Ile Ala Gln Val Ile
25 30 35

cag ttg gaa agc tac aac gac ttc cca tac ctg gtg ctc gca acc gca 259
Gln Leu Glu Ser Tyr Asn Asp Phe Pro Tyr Leu Val Leu Ala Thr Ala
40 45 50

cac ggt cgc gtg aag aag tcc cgc ctg ctc gac tac gaa tca gca cgt 307
His Gly Arg Val Lys Lys Ser Arg Leu Leu Asp Tyr Glu Ser Ala Arg
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tcc ggt ggc ctc atc gcc atc aac ctg aac gag gac gat cgc ctc atc 355
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Phe Gly Gln Ser Ile Arg Phe Thr Ala Asp Asp Glu Gln Leu Arg Pro
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gac caa ctg ctg tcc atg tcc gtg gtc cgc gac ggc gaa ttc ctc ctc 547
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gtt gcc acc tcc ggc ggc tac ggc aag cgc acc cca ctt gag gat tac 595
Val Ala Thr Ser Gly Gly Tyr Gly Lys Arg Thr Pro Leu Glu Asp Tyr
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tcc acc cag ggc cgt ggt ggc ctc ggc gtg gtg acc ttc aag tac acc 643
Ser Thr Gln Gly Arg Gly Gly Leu Gly Val Val Thr Phe Lys Tyr Thr
          170                      175                      180

ccg aag cgc ggt cgc ctc gtc agc gcc atc gca gtt gag gaa gat gac 691
Pro Lys Arg Gly Arg Leu Val Ser Ala Ile Ala Val Glu Glu Asp Asp
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gag atc ttc gcc atc acc tcc gcc ggc ggc gtt gtt cgc acc gaa gtc 739
Glu Ile Phe Ala Ile Thr Ser Ala Gly Gly Val Val Arg Thr Glu Val
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Lys Gln Ile Arg Pro Ser Ser Arg Ala Thr Met Gly Val Arg Leu Val
          215                      220                      225

aac ttg gaa gaa ggt gta gaa ctg ctt gcc atc gac aag aac gtc gaa 835
Asn Leu Glu Glu Gly Val Glu Leu Leu Ala Ile Asp Lys Asn Val Glu
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Asp Gln Gly Glu Ala
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<213> Corynebacterium glutamicum

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      20              25              30

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Ile Ala Gln Val Ile Gln Leu Glu Ser Tyr Asn Asp Phe Pro Tyr Leu
  35              40              45

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Val Leu Ala Thr Ala His Gly Arg Val Lys Lys Ser Arg Leu Leu Asp
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 Tyr Glu Ser Ala Arg Ser Gly Gly Leu Ile Ala Ile Asn Leu Asn Glu
 65 70 75 80
 Asp Asp Arg Leu Ile Gly Ala Ala Leu Cys Gly Glu Glu Asp Asp Leu
 85 90 95
 Leu Leu Val Ser Glu Phe Gly Gln Ser Ile Arg Phe Thr Ala Asp Asp
 100 105 110
 Glu Gln Leu Arg Pro Met Gly Arg Ala Thr Ala Gly Val Lys Gly Met
 115 120 125
 Arg Phe Arg Asp Asn Asp Gln Leu Leu Ser Met Ser Val Val Arg Asp
 130 135 140
 Gly Glu Phe Leu Leu Val Ala Thr Ser Gly Gly Tyr Gly Lys Arg Thr
 145 150 155 160
 Pro Leu Glu Asp Tyr Ser Thr Gln Gly Arg Gly Gly Leu Gly Val Val
 165 170 175
 Thr Phe Lys Tyr Thr Pro Lys Arg Gly Arg Leu Val Ser Ala Ile Ala
 180 185 190
 Val Glu Glu Asp Asp Glu Ile Phe Ala Ile Thr Ser Ala Gly Gly Val
 195 200 205
 Val Arg Thr Glu Val Lys Gln Ile Arg Pro Ser Ser Arg Ala Thr Met
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 Ser Met Arg Tyr Pro Leu Val Asp Gly Gln Gly Asn Phe Gly Ser Arg
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 Gly Asn Asp Gly Pro Ala Ala Met Arg Tyr Thr Glu Cys Arg Met Thr

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Pro	Leu	Ala	Met	Glu	Met	Val	Arg	Asp	Ile	Arg	Glu	Asn	Thr	Val	Asn		
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Phe	Ser	Pro	Asn	Tyr	Asp	Gly	Lys	Thr	Leu	Glu	Pro	Asp	Val	Leu	Pro		
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Ser	Arg	Val	Pro	Asn	Leu	Leu	Met	Asn	Gly	Ser	Gly	Gly	Ile	Ala	Val		
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Gly	Met	Ala	Thr	Asn	Ile	Pro	Pro	His	Asn	Leu	Asn	Glu	Leu	Ala	Asp		
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Ala	Ile	Phe	Trp	Leu	Leu	Glu	Asn	Pro	Asp	Ala	Glu	Glu	Ser	Glu	Ala		
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Leu	Glu	Ala	Cys	Met	Lys	Phe	Val	Lys	Gly	Pro	Asp	Phe	Pro	Thr	Ala		
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Asn	Arg	Thr	Val	Ile	Val	Ile	Thr	Glu	Leu	Pro	Tyr	Gln	Val	Asn	Pro		
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Asp	Asn	Leu	Ile	Ser	Asn	Ile	Ala	Glu	Gln	Val	Arg	Asp	Gly	Lys	Leu		
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Val	Gly	Ile	Ser	Lys	Ile	Glu	Asp	Glu	Ser	Ser	Asp	Arg	Val	Gly	Met		
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Arg	Ile	Val	Val	Thr	Leu	Lys	Arg	Asp	Ala	Val	Ala	Arg	Val	Val	Leu		
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Asn	Asn	Leu	Phe	Lys	His	Ser	Gln	Leu	Gln	Ala	Asn	Phe	Gly	Ala	Asn		
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Met	Leu	Ser	Ile	Val	Asp	Gly	Val	Pro	Arg	Thr	Leu	Arg	Leu	Asp	Gln		
260					265					270							
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Met	Leu	Arg	Tyr	Tyr	Val	Ala	His	Gln	Ile	Glu	Val	Ile	Val	Arg	Arg		
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 Thr Gln Tyr
 290

873

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 Pro Leu Ala Met Glu Met Val Arg Asp Ile Arg Glu Asn Thr Val Asn
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 Phe Ser Pro Asn Tyr Asp Gly Lys Thr Leu Glu Pro Asp Val Leu Pro
 65 70 75 80
 Ser Arg Val Pro Asn Leu Leu Met Asn Gly Ser Gly Gly Ile Ala Val
 85 90 95
 Gly Met Ala Thr Asn Ile Pro Pro His Asn Leu Asn Glu Leu Ala Asp
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 Ala Ile Phe Trp Leu Leu Glu Asn Pro Asp Ala Glu Glu Ser Glu Ala
 115 120 125
 Leu Glu Ala Cys Met Lys Phe Val Lys Gly Pro Asp Phe Pro Thr Ala
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 Gly Leu Ile Ile Gly Asp Lys Gly Ile His Asp Ala Tyr Thr Thr Gly
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 Arg Gly Ser Ile Arg Met Arg Gly Val Thr Ser Ile Glu Glu Glu Gly
 165 170 175
 Asn Arg Thr Val Ile Val Ile Thr Glu Leu Pro Tyr Gln Val Asn Pro
 180 185 190
 Asp Asn Leu Ile Ser Asn Ile Ala Glu Gln Val Arg Asp Gly Lys Leu
 195 200 205
 Val Gly Ile Ser Lys Ile Glu Asp Glu Ser Ser Asp Arg Val Gly Met
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 Arg Ile Val Val Thr Leu Lys Arg Asp Ala Val Ala Arg Val Val Leu
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 245 250 255
 Met Leu Ser Ile Val Asp Gly Val Pro Arg Thr Leu Arg Leu Asp Gln

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Thr Gln Tyr			
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Ser Phe Val Gln Arg Met Ala Asn Glu His Ile Gly His Trp Leu Glu			
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35 40 45			
gcg cag gca cgc ctt gct gct cga aaa gcc cgt gac ctg gtc cga cgg			192
Ala Gln Ala Arg Leu Ala Ala Arg Lys Ala Arg Asp Leu Val Arg Arg			
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Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys			
65 70 75 80			
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Arg Ser Lys Asp Pro Glu Lys Ser Glu Leu Tyr Ile Val Glu Gly Asp			
85 90 95			
tcc gca ggt ggt tct gcg aag tcc ggc cgt gac tcc atg ttc cag gca			336
Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala			
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Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Arg Leu			
115 120 125			
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Asp Lys Val Leu Lys Asn Ala Glu Val Gln Ala Ile Ile Thr Ala Leu			
130 135 140			
ggt acc ggc atc cac gac gag ttc gac atc aac aag ctg cgc tac cac			480
Gly Thr Gly Ile His Asp Glu Phe Asp Ile Asn Lys Leu Arg Tyr His			
145 150 155 160			
aag atc gtg ctg atg gcc gac gcc gat gtt gac ggc cag cac atc gca			528

Lys Ile Val Leu Met Ala Asp Ala Asp Val Asp Gly Gln His Ile Ala
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 Thr Leu Leu Thr Leu Leu Phe Arg Phe Met Pro Asp Leu Val Ala
 180 185 190
 gaa ggc cac gtc tac ttg gca cag cca cct ttg tac aaa ctg aag tgg 624
 Glu Gly His Val Tyr Leu Ala Gln Pro Pro Leu Tyr Lys Leu Lys Trp
 195 200 205
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 Gln Arg Gly Glu Pro Gly Phe Ala Tyr Ser Asp Glu Glu Arg Asp Glu
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 225 230 235 240
 ggc atc cag cgc tac aag ggt ctc ggc gag atg aac gcc agc gag ctg 768
 Gly Ile Gln Arg Tyr Lys Gly Leu Gly Glu Met Asn Ala Ser Glu Leu
 245 250 255
 tgg gaa acc acc atg gac cca act gtt cgt att ctg cgc cgc gtg gac 816
 Trp Glu Thr Thr Met Asp Pro Thr Val Arg Ile Leu Arg Arg Val Asp
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 atc acc gat gct cag cgt gct gat gaa ctg ttc tcc atc ttg atg ggt 864
 Ile Thr Asp Ala Gln Arg Ala Asp Glu Leu Phe Ser Ile Leu Met Gly
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 Asp Asp Val Val Ala Arg Arg Ser Phe Ile Thr Arg Asn Ala Lys Asp
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 Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys
 65 70 75 80

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1 5 10 15

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 Ser Phe Val Gln Arg Met Ala Asn Glu His Ile Gly His Trp Leu Glu
 20 25 30
 gca aac cct gct gaa gcc aag gtc atc atc aac aag gct gtc ggt tcc 144
 Ala Asn Pro Ala Glu Ala Lys Val Ile Ile Asn Lys Ala Val Gly Ser
 35 40 45
 gcg cag gca cgc ctt gct gct cga aaa gcc cgt gac ctg gtc cga cgg 192
 Ala Gln Ala Arg Leu Ala Ala Arg Lys Ala Arg Asp Leu Val Arg Arg
 50 55 60
 aag tca gca acc gat ctg ggt gga ctg ccc ggt aag ctt gcc gac tgc 240
 Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys
 65 70 75 80
 cgt tcc aag gat cca gaa aag tcc gaa ctt tac atc gtg gag ggc gac 288
 Arg Ser Lys Asp Pro Glu Lys Ser Glu Leu Tyr Ile Val Glu Gly Asp
 85 90 95
 tcc gca ggt ggt tct gcg aag tcc ggc cgt gac tcc atg ttc cag gca 336
 Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala
 100 105 110
 atc ctt cca ctg cga ggc aag atc ctc aac gtg gaa aag gcc cgc cta 384
 Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Arg Leu
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 gac aag gtt ctg aag aac gcc gaa gtc caa gcg atc atc acc gca ctg 432
 Asp Lys Val Leu Lys Asn Ala Glu Val Gln Ala Ile Ile Thr Ala Leu
 130 135 140
 ggt acc ggc atc cac gac gag ttc gac atc aac aag ctg cgc tac cac 480
 Gly Thr Gly Ile His Asp Glu Phe Asp Ile Asn Lys Leu Arg Tyr His
 145 150 155 160
 aag atc gtg ctg atg gcc gac gcc gat gtt gac ggc cag cac atc gca 528
 Lys Ile Val Leu Met Ala Asp Ala Asp Val Asp Gly Gln His Ile Ala
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<211> 188

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<213> Corynebacterium glutamicum

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																			Val	Ala	Asn	Thr	Glu	5								
																			1													
cac	aat	tat	gac	gct	tca	tcg	atc	acc	atc	ctt	gaa	ggg	ctt	gag	gcg	163																
His	Asn	Tyr	Asp	Ala	Ser	Ser	Ile	Thr	Ile	Leu	Glu	Gly	Leu	Glu	Ala																	
																10	15	20														
gta																cgt	aag	cgc	ccg	ggc	atg	tac	atc	ggg	tca	act	gga	ccg	cgt	gga	211	
Val																Arg	Lys	Arg	Pro	Gly	Met	Tyr	Ile	Gly	Ser	Thr	Gly	Pro	Arg	Gly		
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ctg																cac	cac	ctg	att	tgg	gaa	gtc	gtt	gac	aac	tca	gtg	gat	gag	gcc	259	
Leu																His	His	Leu	Ile	Trp	Glu	Val	Val	Asp	Asn	Ser	Val	Asp	Glu	Ala		
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atg																gct	ggc	cac	gcc	acc	aag	gtt	gaa	gtg	acc	ctt	ctg	gaa	gat	ggg	307	
Met																Ala	Gly	His	Ala	Thr	Lys	Val	Glu	Val	Thr	Leu	Leu	Glu	Asp	Gly		
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ggc																gtt	caa	gtt	gtc	gat	gac	ggg	cga	gga	att	ccc	gtc	gat	atg	cac	355	

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Pro	Ser	Gly	Ala	Pro 90	Thr	Val	Gln	Val	Val 95	Met	Thr	Gln	Leu	His	Ala 100	
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Gly	Gly	Lys	Phe 105	Asp	Ser	Asp	Ser	Tyr 110	Ala	Val	Ser	Gly	Gly	Leu	His	
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Gly	Val	Gly 120	Ile	Ser	Val	Val	Asn 125	Ala	Leu	Ser	Thr	Arg 130	Val	Glu	Ala	
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Val	Pro	Asp	Glu	Leu	Ile 155	Glu	Gly	Gly	Asn 160	Ala	Arg	Gly	Thr	Gly	Thr 165	
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Lys	Gly	Leu 200	Thr	Ile	Thr	Leu	Thr 205	Asp	Asn	Arg	Ala	Thr 210	Asp	Glu	Glu	
ctc	gag	ctc	gaa	gca	ctc	gct	gag	cag	ggc	gaa	acc	gca	acg	gaa	cta	787
Leu	Glu	Leu	Glu	Ala	Leu 215	Ala	Glu 220	Gln	Gly	Glu	Thr 225	Ala	Thr	Glu	Leu	
tcc	ctc	gat	gag	atc	gac	aac	gaa	acc	gaa	ctc	gtt	gaa	gag	acc	acc	835
Ser	Leu	Asp	Glu	Ile 230	Asp 235	Asn	Glu	Thr	Glu	Leu 240	Val	Glu	Glu	Thr	Thr 245	
gat	gct	cca	aag	aag	cca	aaa	aag	cgt	gag	aag	aag	aaa	atc	ttc	cac	883
Asp	Ala	Pro	Lys	Lys 250	Pro	Lys	Lys	Arg	Glu	Lys 255	Lys	Lys	Ile	Phe	His 260	
tac	ccc	aat	ggc	ctc	gag	gac	tac	gtt	cac	tac	ctc	aac	cgc	agc	aag	931
Tyr	Pro	Asn 265	Gly	Leu	Glu	Asp	Tyr 270	Val	His	Tyr	Leu	Asn 275	Arg	Ser	Lys	
acc	aac	atc	cac	cct	tca	atc	gtg	tca	ttc	gag	gca	aag	gga	gat	gac	979
Thr	Asn	Ile 280	His	Pro	Ser	Ile	Val 285	Ser	Phe	Glu	Ala	Lys 290	Gly	Asp	Asp	
cac	gag	gtt	gag	gtg	gca	atg	cag	tgg	aac	tcc	tcc	tac	aag	gaa	tcc	1027
His	Glu	Val	Glu	Val	Ala 295	Met	Gln 300	Trp	Asn	Ser	Ser 305	Tyr	Lys	Glu	Ser	
gtc	cac	acc	ttc	gcc	aac	acc	att	aac	acc	cgc	gaa	ggc	ggc	acc	cac	1075
Val	His	Thr	Phe	Ala	Asn	Thr	Ile	Asn	Thr	Arg	Glu	Gly	Gly	Thr	His	

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 Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Leu Met Asn Arg Tyr Ala
 330 335 340

cgt gag cac aag ctt ctg aaa gaa aag gaa gca aac ctt acc ggt gac 1171
 Arg Glu His Lys Leu Leu Lys Glu Lys Glu Ala Asn Leu Thr Gly Asp
 345 350 355

gac tgt cgt gaa ggc ctg tcc gcg gtt att ttc cgt gcg cgt tgg 1216
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tgacccacag ttcgaaggcc aga 1239

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<400> 120

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 20 25 30

Thr Gly Pro Arg Gly Leu His His Leu Ile Trp Glu Val Val Asp Asn
 35 40 45

Ser Val Asp Glu Ala Met Ala Gly His Ala Thr Lys Val Glu Val Thr
 50 55 60

Leu Leu Glu Asp Gly Gly Val Gln Val Val Asp Asp Gly Arg Gly Ile
 65 70 75 80

Pro Val Asp Met His Pro Ser Gly Ala Pro Thr Val Gln Val Val Met
 85 90 95

Thr Gln Leu His Ala Gly Gly Lys Phe Asp Ser Asp Ser Tyr Ala Val
 100 105 110

Ser Gly Gly Leu His Gly Val Gly Ile Ser Val Val Asn Ala Leu Ser
 115 120 125

Thr Arg Val Glu Ala Asp Ile Lys Leu His Gly Lys His Trp Tyr Gln
 130 135 140

Asn Phe Glu Lys Ser Val Pro Asp Glu Leu Ile Glu Gly Gly Asn Ala
 145 150 155 160

Arg Gly Thr Gly Thr Thr Ile Arg Phe Trp Pro Asp Ala Glu Ile Phe
 165 170 175

Glu Thr Thr Glu Phe Asp Phe Glu Thr Ile Ser Arg Arg Leu Gln Glu
 180 185 190

Met Ala Phe Leu Asn Lys Gly Leu Thr Ile Thr Leu Thr Asp Asn Arg
 195 200 205

Ala Thr Asp Glu Glu Leu Glu Leu Glu Ala Leu Ala Glu Gln Gly Glu
 210 215 220

Thr Ala Thr Glu Leu Ser Leu Asp Glu Ile Asp Asn Glu Thr Glu Leu
 225 230 235 240

Val Glu Glu Thr Thr Asp Ala Pro Lys Lys Pro Lys Lys Arg Glu Lys
 245 250 255

Lys Lys Ile Phe His Tyr Pro Asn Gly Leu Glu Asp Tyr Val His Tyr
 260 265 270

Leu Asn Arg Ser Lys Thr Asn Ile His Pro Ser Ile Val Ser Phe Glu
 275 280 285

Ala Lys Gly Asp Asp His Glu Val Glu Val Ala Met Gln Trp Asn Ser
 290 295 300

Ser Tyr Lys Glu Ser Val His Thr Phe Ala Asn Thr Ile Asn Thr Arg
 305 310 315 320

Glu Gly Gly Thr His Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Leu
 325 330 335

Met Asn Arg Tyr Ala Arg Glu His Lys Leu Leu Lys Glu Lys Glu Ala
 340 345 350

Asn Leu Thr Gly Asp Asp Cys Arg Glu Gly Leu Ser Ala Val Ile Phe
 355 360 365

Arg Ala Arg Trp
 370

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 <211> 726
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(726)
 <223> FRXA01689

<400> 121
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 1 5 10 15

att tct gtg gtg aac gcc ctg tcc acc cgc gtg gaa gcc gac atc aag 96
 Ile Ser Val Val Asn Ala Leu Ser Thr Arg Val Glu Ala Asp Ile Lys
 20 25 30

ttg cac ggc aag cac tgg tac caa aac ttt gaa aag tct gtt cca gac 144
 Leu His Gly Lys His Trp Tyr Gln Asn Phe Glu Lys Ser Val Pro Asp
 35 40 45

gag ttg atc gaa ggc ggc aac gct cgc ggc acc ggt acc acc att cgt 192
 Glu Leu Ile Glu Gly Gly Asn Ala Arg Gly Thr Gly Thr Thr Ile Arg
 50 55 60

ttt tgg cca gac gct gaa att ttc gaa acc acc gag ttt gat ttc gaa	240
Phe Trp Pro Asp Ala Glu Ile Phe Glu Thr Thr Glu Phe Asp Phe Glu	
65 70 75 80	
acg att tct cga cgt ctg cag gaa atg gca ttc ctt aac aag ggt ctg	288
Thr Ile Ser Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu	
85 90 95	
acc atc acc ttg acg gac aac cgc gcc acc gac gag gaa ctc gag ctc	336
Thr Ile Thr Leu Thr Asp Asn Arg Ala Thr Asp Glu Glu Leu Glu Leu	
100 105 110	
gaa gca ctc gct gag cag ggc gaa acc gca acg gaa cta tcc ctc gat	384
Glu Ala Leu Ala Glu Gln Gly Glu Thr Ala Thr Glu Leu Ser Leu Asp	
115 120 125	
gag atc gac aac gaa acc gaa ctc gtt gaa gag acc acc gat gct cca	432
Glu Ile Asp Asn Glu Thr Glu Leu Val Glu Glu Thr Thr Asp Ala Pro	
130 135 140	
aag aag cca aaa aag cgt gag aag aag aaa atc ttc cac tac ccc aat	480
Lys Lys Pro Lys Lys Arg Glu Lys Lys Lys Ile Phe His Tyr Pro Asn	
145 150 155 160	
ggc ctc gag gac tac gtt cac tac ctc aac cgc agc aag acc aac atc	528
Gly Leu Glu Asp Tyr Val His Tyr Leu Asn Arg Ser Lys Thr Asn Ile	
165 170 175	
cac cct tca atc gtg tca ttc gag gca aag gga gat gac cac gag gtt	576
His Pro Ser Ile Val Ser Phe Glu Ala Lys Gly Asp Asp His Glu Val	
180 185 190	
gag gtg gca atg cag tgg aac tcc tcc tac aag gaa tcc gtc cac acc	624
Glu Val Ala Met Gln Trp Asn Ser Ser Tyr Lys Glu Ser Val His Thr	
195 200 205	
ttc gcc aac acc att aac acc cgc gaa ggc ggc acc cac gag gaa ggt	672
Phe Ala Asn Thr Ile Asn Thr Arg Glu Gly Gly Thr His Glu Glu Gly	
210 215 220	
ttc cgc tct gcg ctg acc tcc ctg atg aac cgc tac gca cgt gag cac	720
Phe Arg Ser Ala Leu Thr Ser Leu Met Asn Arg Tyr Ala Arg Glu His	
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aag ctt	726
Lys Leu	

<210> 122

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 122

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Ile Ser Val Val Asn Ala Leu Ser Thr Arg Val Glu Ala Asp Ile Lys	
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<222> (101)..(382)
<223> FRXA01735
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<400> 123
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acgtctgtat cggataagta gcgaggagtg ttcgttaaaa gtg gca aac act gaa 115
                               Val Ala Asn Thr Glu
                               1           5

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cac aat tat gac gct tca tcg atc acc atc ctt gaa ggt ctt gag gcg 163
 His Asn Tyr Asp Ala Ser Ser Ile Thr Ile Leu Glu Gly Leu Glu Ala
 10 15 20

gta cgt aag cgc ccg ggc atg tac atc ggt tca act gga ccg cgt gga 211
 Val Arg Lys Arg Pro Gly Met Tyr Ile Gly Ser Thr Gly Pro Arg Gly
 25 30 35

ctg cac cac ctg att tgg gaa gtc gtt gac aac tca gtg gat gag gcc 259
 Leu His His Leu Ile Trp Glu Val Val Asp Asn Ser Val Asp Glu Ala
 40 45 50

atg gct ggc cac gcc acc aag gtt gaa gtg acc ctt ctg gaa gat ggt 307
 Met Ala Gly His Ala Thr Lys Val Glu Val Thr Leu Leu Glu Asp Gly
 55 60 65

ggc gtt caa gtt gtc gat gac ggt cga gga att ccc gtc gat atg cac 355
 Gly Val Gln Val Val Asp Asp Gly Arg Gly Ile Pro Val Asp Met His
 70 75 80 85

cca tcc ggt gca cca acc gtg cag gtt 382
 Pro Ser Gly Ala Pro Thr Val Gln Val
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<210> 124

<211> 94

<212> PRT

<213> Corynebacterium glutamicum

<400> 124

Val Ala Asn Thr Glu His Asn Tyr Asp Ala Ser Ser Ile Thr Ile Leu
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Glu Gly Leu Glu Ala Val Arg Lys Arg Pro Gly Met Tyr Ile Gly Ser
 20 25 30

Thr Gly Pro Arg Gly Leu His His Leu Ile Trp Glu Val Val Asp Asn
 35 40 45

Ser Val Asp Glu Ala Met Ala Gly His Ala Thr Lys Val Glu Val Thr
 50 55 60

Leu Leu Glu Asp Gly Gly Val Gln Val Val Asp Asp Gly Arg Gly Ile
 65 70 75 80

Pro Val Asp Met His Pro Ser Gly Ala Pro Thr Val Gln Val
 85 90

<210> 125

<211> 1962

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1939)

<223> RXN03093

<400> 125

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Val Ala Asp Thr Ala 5

ggc acc aca gga tcg aaa aag aag tac ttg gtg atc gtc gag tcg gcg 163
Gly Thr Thr Gly Ser Lys Lys Lys Tyr Leu Val Ile Val Glu Ser Ala 20

acc aag gct aaa aag att cag cct tac ctt ggc aac gac tac atc gtc 211
Thr Lys Ala Lys Lys Ile Gln Pro Tyr Leu Gly Asn Asp Tyr Ile Val 35

gag gcc tcc gtt ggt cat att cgt gat ctg cca cgt ggc gct gct gac 259
Glu Ala Ser Val Gly His Ile Arg Asp Leu Pro Arg Gly Ala Ala Asp 50

atc cct gca aag tac aag aag gag cct tgg gct cgt ctt ggt gtg gac 307
Ile Pro Ala Lys Tyr Lys Lys Glu Pro Trp Ala Arg Leu Gly Val Asp 65

acc gat cgc ggt ttc gcg ccg ctt tat gtg gtg agc ccc gat aaa aag 355
Thr Asp Arg Gly Phe Ala Pro Leu Tyr Val Val Ser Pro Asp Lys Lys 85

aag aag gtc gct gac ctc aag gcg aag ctc aag ctc gtt gat gag ttg 403
Lys Lys Val Ala Asp Leu Lys Ala Lys Leu Lys Leu Val Asp Glu Leu 100

ctg ctg gca aca gac ccc gac cgt gag ggc gag gcg att gcg tgg cat 451
Leu Leu Ala Thr Asp Pro Asp Arg Glu Gly Glu Ala Ile Ala Trp His 115

ttg ctt gag gtg ttg aag ccg act gtt cct gtg cgt cgc atg gtg ttc 499
Leu Leu Glu Val Leu Lys Pro Thr Val Pro Val Arg Arg Met Val Phe 130

aat gag atc acg aag cct gcc att ttg gct gcg gcg gaa aac act cgt 547
Asn Glu Ile Thr Lys Pro Ala Ile Leu Ala Ala Ala Glu Asn Thr Arg 145

gag ctg gat gag aac ctg gtg gat gcg cag gaa act cgt cgt att ctg 595
Glu Leu Asp Glu Asn Leu Val Asp Ala Gln Glu Thr Arg Arg Ile Leu 165

gac cgt ttg tac ggc tat gaa gtc tct cct gtg ctg tgg aaa aag gtc 643
Asp Arg Leu Tyr Gly Tyr Glu Val Ser Pro Val Leu Trp Lys Lys Val 180

atg ccg agg ttg tcg gcg ggc cgt gtg cag tcg gtg gca acc cgt gtg 691
Met Pro Arg Leu Ser Ala Gly Arg Val Gln Ser Val Ala Thr Arg Val 195

att gtt gag cgg gag cgc gag cgc atg gcg ttc gtg tcg gcg gat tat 739
Ile Val Glu Arg Glu Arg Glu Arg Met Ala Phe Val Ser Ala Asp Tyr 210

tgg gat ctg tcg gcg gag ttt aat gcg cgt gaa aac ggc aag gcg gat 787
Trp Asp Leu Ser Ala Glu Phe Asn Ala Arg Glu Asn Gly Lys Ala Asp 225

tcg gat aac ccg tcg tcg ttt act gcg cgt ttg tcc acg att gat gga	835
Ser Asp Asn Pro Ser Ser Phe Thr Ala Arg Leu Ser Thr Ile Asp Gly	
230 235 240 245	
aac cgt gtt gct caa ggc cgt gat ttt aat gat cgg gga gag ctg acc	883
Asn Arg Val Ala Gln Gly Arg Asp Phe Asn Asp Arg Gly Glu Leu Thr	
250 255 260	
tcg gag gct gtc gtc gtc gat aag cag cgt gct gag gcg tta gcc gag	931
Ser Glu Ala Val Val Val Asp Lys Gln Arg Ala Glu Ala Leu Ala Glu	
265 270 275	
gct ttg gaa ggc cag gaa atg gcc gtc gtt ggg gtc gag gaa aag ccg	979
Ala Leu Glu Gly Gln Glu Met Ala Val Val Gly Val Glu Glu Lys Pro	
280 285 290	
tac acc cgt cgc cct tat gcg ccg ttt atg acc tct acg ctg cag caa	1027
Tyr Thr Arg Arg Pro Tyr Ala Pro Phe Met Thr Ser Thr Leu Gln Gln	
295 300 305	
gag tct ggc cgc aag ctg cat tac act tct gag cgc acg atg cgt att	1075
Glu Ser Gly Arg Lys Leu His Tyr Thr Ser Glu Arg Thr Met Arg Ile	
310 315 320 325	
gcg cag cgc ttg tat gaa aac ggc cat atc act tat atg cgt act gac	1123
Ala Gln Arg Leu Tyr Glu Asn Gly His Ile Thr Tyr Met Arg Thr Asp	
330 335 340	
tcg acc tcg ttg tcg gag cag ggc atg aag gct gcg cgc gat cag gcg	1171
Ser Thr Ser Leu Ser Glu Gln Gly Met Lys Ala Ala Arg Asp Gln Ala	
345 350 355	
ttg gag ctg tac ggt gcg gaa tat gtt tcg ccg agc cca cgt acc tat	1219
Leu Glu Leu Tyr Gly Ala Glu Tyr Val Ser Pro Ser Pro Arg Thr Tyr	
360 365 370	
gac cgc aag gtg aag aac tcc cag gag gcc cac gag gcg att cgc cca	1267
Asp Arg Lys Val Lys Asn Ser Gln Glu Ala His Glu Ala Ile Arg Pro	
375 380 385	
gct ggt gaa act ttt gcg acc ccg ggc cag ctg cat ggc cag ttg gat	1315
Ala Gly Glu Thr Phe Ala Thr Pro Gly Gln Leu His Gly Gln Leu Asp	
390 395 400 405	
gcg gaa gaa ttt aag ctc tat gag ctg att tgg cag cgc act gtg gcc	1363
Ala Glu Glu Phe Lys Leu Tyr Glu Leu Ile Trp Gln Arg Thr Val Ala	
410 415 420	
tcc cag atg gcc gat gcc aag ggc acg tcc atg aag gtc acc atc ggt	1411
Ser Gln Met Ala Asp Ala Lys Gly Thr Ser Met Lys Val Thr Ile Gly	
425 430 435	
ggc acc gcg aag acc ggc gag aag act gag ttc aac gcg acc ggc cgc	1459
Gly Thr Ala Lys Thr Gly Glu Lys Thr Glu Phe Asn Ala Thr Gly Arg	
440 445 450	
acg ctg act ttc cct ggc ttc ctg cgc gct tac gtg gaa acc acc cgc	1507
Thr Leu Thr Phe Pro Gly Phe Leu Arg Ala Tyr Val Glu Thr Thr Arg	
455 460 465	

acc gcc gat ggc cgc gac gta gct gac aac gcc gaa aag cgt ctg cca 1555
 Thr Ala Asp Gly Arg Asp Val Ala Asp Asn Ala Glu Lys Arg Leu Pro
 470 475 480 485

ctg ctg tct gag ggc gat ctg ctc aag gtt ttg agc atc gaa gcc gat 1603
 Leu Leu Ser Glu Gly Asp Leu Leu Lys Val Leu Ser Ile Glu Ala Asp
 490 495 500

ggt cac agc acc aat cca cct gcg cgc tac aca gag gcg tcg ctg gtg 1651
 Gly His Ser Thr Asn Pro Pro Ala Arg Tyr Thr Glu Ala Ser Leu Val
 505 510 515

aag aag atg gaa gat ctg ggc atc ggc cgt cct tcc act tat gca tcg 1699
 Lys Lys Met Glu Asp Leu Gly Ile Gly Arg Pro Ser Thr Tyr Ala Ser
 520 525 530

atc att aag acg att cag gat cga ggc tac gtt tat tcg cgt ggc aat 1747
 Ile Ile Lys Thr Ile Gln Asp Arg Gly Tyr Val Tyr Ser Arg Gly Asn
 535 540 545

gcg ctg gtg ccg tcc tgg gtc gcg ttc gcc gtg gtc gga ttg ctt gaa 1795
 Ala Leu Val Pro Ser Trp Val Ala Phe Ala Val Val Gly Leu Leu Glu
 550 555 560 565

gcc aac ttc acc tcg ctg gtg gat tac gat ttc acc tcc tcc atg gaa 1843
 Ala Asn Phe Thr Ser Leu Val Asp Tyr Asp Phe Thr Ser Ser Met Glu
 570 575 580

gat gag ctg gac aac atc gcc gca ggt cgc gag ggc cgc acg gag tgg 1891
 Asp Glu Leu Asp Asn Ile Ala Ala Gly Arg Glu Gly Arg Thr Glu Trp
 585 590 595

ctc aac ggt ttc tac ttc ggg cga tgc cga agc gga tca gtc cat ggc 1939
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 600 605 610

tgaatcagtt gcccgccagg gcg 1962

<210> 126

<211> 613

<212> PRT

<213> Corynebacterium glutamicum

<400> 126

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Ile Val Glu Ser Ala Thr Lys Ala Lys Lys Ile Gln Pro Tyr Leu Gly
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Asn Asp Tyr Ile Val Glu Ala Ser Val Gly His Ile Arg Asp Leu Pro
 35 40 45

Arg Gly Ala Ala Asp Ile Pro Ala Lys Tyr Lys Lys Glu Pro Trp Ala
 50 55 60

Arg Leu Gly Val Asp Thr Asp Arg Gly Phe Ala Pro Leu Tyr Val Val
 65 70 75 80

Ser Pro Asp Lys Lys Lys Lys Val Ala Asp Leu Lys Ala Lys Leu Lys

[illegible]

Gln Arg Thr Val Ala Ser Gln Met Ala Asp Ala Lys Gly Thr Ser Met
 420 425 430
 Lys Val Thr Ile Gly Gly Thr Ala Lys Thr Gly Glu Lys Thr Glu Phe
 435 440 445
 Asn Ala Thr Gly Arg Thr Leu Thr Phe Pro Gly Phe Leu Arg Ala Tyr
 450 455 460
 Val Glu Thr Thr Arg Thr Ala Asp Gly Arg Asp Val Ala Asp Asn Ala
 465 470 475 480
 Glu Lys Arg Leu Pro Leu Leu Ser Glu Gly Asp Leu Leu Lys Val Leu
 485 490 495
 Ser Ile Glu Ala Asp Gly His Ser Thr Asn Pro Pro Ala Arg Tyr Thr
 500 505 510
 Glu Ala Ser Leu Val Lys Lys Met Glu Asp Leu Gly Ile Gly Arg Pro
 515 520 525
 Ser Thr Tyr Ala Ser Ile Ile Lys Thr Ile Gln Asp Arg Gly Tyr Val
 530 535 540
 Tyr Ser Arg Gly Asn Ala Leu Val Pro Ser Trp Val Ala Phe Ala Val
 545 550 555 560
 Val Gly Leu Leu Glu Ala Asn Phe Thr Ser Leu Val Asp Tyr Asp Phe
 565 570 575
 Thr Ser Ser Met Glu Asp Glu Leu Asp Asn Ile Ala Ala Gly Arg Glu
 580 585 590
 Gly Arg Thr Glu Trp Leu Asn Gly Phe Tyr Phe Gly Arg Cys Arg Ser
 595 600 605
 Gly Ser Val His Gly
 610

<210> 127

<211> 2378

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(2355)

<223> FRXA00798

<400> 127

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gcg gat tcg gat aac ccg tcg tcg ttt act gcg cgt ttg tcc acg att 96
 Ala Asp Ser Asp Asn Pro Ser Ser Phe Thr Ala Arg Leu Ser Thr Ile
 20 25 30

gat gga aac cgt gtt gct caa ggc cgt gat ttt aat gat cgg gga gag 144

Asp	Gly	Asn	Arg	Val	Ala	Gln	Gly	Arg	Asp	Phe	Asn	Asp	Arg	Gly	Glu	
		35					40					45				
ctg	acc	tcg	gag	gct	gtc	gtc	gtc	gat	aag	cag	cgt	gct	gag	gcg	tta	192
Leu	Thr	Ser	Glu	Ala	Val	Val	Val	Asp	Lys	Gln	Arg	Ala	Glu	Ala	Leu	
	50					55					60					
gcc	gag	gct	ttg	gaa	ggc	cag	gaa	atg	gcc	gtc	gtt	ggg	gtc	gag	gaa	240
Ala	Glu	Ala	Leu	Glu	Gly	Gln	Glu	Met	Ala	Val	Val	Gly	Val	Glu	Glu	
	65				70					75					80	
aag	ccg	tac	acc	cgt	cgc	cct	tat	gcg	ccg	ttt	atg	acc	tct	acg	ctg	288
Lys	Pro	Tyr	Thr	Arg	Arg	Pro	Tyr	Ala	Pro	Phe	Met	Thr	Ser	Thr	Leu	
				85					90					95		
cag	caa	gag	tct	ggc	cgc	aag	ctg	cat	tac	act	tct	gag	cgc	acg	atg	336
Gln	Gln	Glu	Ser	Gly	Arg	Lys	Leu	His	Tyr	Thr	Ser	Glu	Arg	Thr	Met	
			100					105						110		
cgt	att	gcg	cag	cgc	ttg	tat	gaa	aac	ggc	cat	atc	act	tat	atg	cgt	384
Arg	Ile	Ala	Gln	Arg	Leu	Tyr	Glu	Asn	Gly	His	Ile	Thr	Tyr	Met	Arg	
		115					120						125			
act	gac	tcg	acc	tcg	ttg	tcg	gag	cag	ggc	atg	aag	gct	gcg	cgc	gat	432
Thr	Asp	Ser	Thr	Ser	Leu	Ser	Glu	Gln	Gly	Met	Lys	Ala	Ala	Arg	Asp	
	130					135					140					
cag	gcg	ttg	gag	ctg	tac	ggc	gcg	gaa	tat	gtt	tcg	ccg	agc	cca	cgt	480
Gln	Ala	Leu	Glu	Leu	Tyr	Gly	Ala	Glu	Tyr	Val	Ser	Pro	Ser	Pro	Arg	
	145				150					155					160	
acc	tat	gac	cgc	aag	gtg	aag	aac	tcc	cag	gag	gcc	cac	gag	gcg	att	528
Thr	Tyr	Asp	Arg	Lys	Val	Lys	Asn	Ser	Gln	Glu	Ala	His	Glu	Ala	Ile	
				165					170					175		
cgc	cca	gct	ggt	gaa	act	ttt	gcg	acc	ccg	ggc	cag	ctg	cat	ggc	cag	576
Arg	Pro	Ala	Gly	Glu	Thr	Phe	Ala	Thr	Pro	Gly	Gln	Leu	His	Gly	Gln	
			180					185					190			
ttg	gat	gcg	gaa	gaa	ttt	aag	ctc	tat	gag	ctg	att	tgg	cag	cgc	act	624
Leu	Asp	Ala	Glu	Glu	Phe	Lys	Leu	Tyr	Glu	Leu	Ile	Trp	Gln	Arg	Thr	
		195					200					205				
gtg	gcc	tcc	cag	atg	gcc	gat	gcc	aag	ggc	acg	tcc	atg	aag	gtc	acc	672
Val	Ala	Ser	Gln	Met	Ala	Asp	Ala	Lys	Gly	Thr	Ser	Met	Lys	Val	Thr	
	210					215					220					
atc	ggt	ggc	acc	gcg	aag	acc	ggc	gag	aag	act	gag	ttc	aac	gcg	acc	720
Ile	Gly	Gly	Thr	Ala	Lys	Thr	Gly	Glu	Lys	Thr	Glu	Phe	Asn	Ala	Thr	
	225				230					235					240	
ggc	cgc	acg	ctg	act	ttc	cct	ggc	ttc	ctg	cgc	gct	tac	gtg	gaa	acc	768
Gly	Arg	Thr	Leu	Thr	Phe	Pro	Gly	Phe	Leu	Arg	Ala	Tyr	Val	Glu	Thr	
				245					250					255		
acc	cgc	acc	gcc	gat	ggc	cgc	gac	gta	gct	gac	aac	gcc	gaa	aag	cgt	816
Thr	Arg	Thr	Ala	Asp	Gly	Arg	Asp	Val	Ala	Asp	Asn	Ala	Glu	Lys	Arg	
			260					265					270			
ctg	cca	ctg	ctg	tct	gag	ggc	gat	ctg	ctc	aag	gtt	ttg	agc	atc	gaa	864
Leu	Pro	Leu	Leu	Ser	Glu	Gly	Asp	Leu	Leu	Lys	Val	Leu	Ser	Ile	Glu	

275	280	285	
gcc gat ggt cac agc acc aat cca cct gcg cgc tac aca gag gcg tcg Ala Asp Gly His Ser Thr Asn Pro Pro Ala Arg Tyr Thr Glu Ala Ser 290 295 300			912
ctg gtg aag aag atg gaa gat ctg ggc atc ggc cgt cct tcc act tat Leu Val Lys Lys Met Glu Asp Leu Gly Ile Gly Arg Pro Ser Thr Tyr 305 310 315 320			960
gca tcg atc att aag acg att cag gat cga ggc tac gtt tat tcg cgt Ala Ser Ile Ile Lys Thr Ile Gln Asp Arg Gly Tyr Val Tyr Ser Arg 325 330 335			1008
ggc aat gcg ctg gtg ccg tcc tgg gtc gcg ttc gcc gtg gtc gga ttg Gly Asn Ala Leu Val Pro Ser Trp Val Ala Phe Ala Val Val Gly Leu 340 345 350			1056
ctt gaa gcc aac ttc acc tcg ctg gtg gat tac gat ttc acc tcc tcc Leu Glu Ala Asn Phe Thr Ser Leu Val Asp Tyr Asp Phe Thr Ser Ser 355 360 365			1104
atg gaa gat gag ctg gac aac atc gcc gca ggt cgc gag ggc cgc acg Met Glu Asp Glu Leu Asp Asn Ile Ala Ala Gly Arg Glu Gly Arg Thr 370 375 380			1152
gag tgg ctc aac ggt ttc tac ttc ggc gat gcc gaa gcg gat cag tcc Glu Trp Leu Asn Gly Phe Tyr Phe Gly Asp Ala Glu Ala Asp Gln Ser 385 390 395 400			1200
atg gct gaa tca gtt gcc cgc cag ggc ggt ttg aag gcg ctt gtc gac Met Ala Glu Ser Val Ala Arg Gln Gly Gly Leu Lys Ala Leu Val Asp 405 410 415			1248
gcg aac ctg gag cac atc gac gcg cgt tca gta aac tca ctc aag ctt Ala Asn Leu Glu His Ile Asp Ala Arg Ser Val Asn Ser Leu Lys Leu 420 425 430			1296
ttc gac gac gcc gaa ggc cgt gcc gtg aac gtt cga gtc gga cgc tac Phe Asp Asp Ala Glu Gly Arg Ala Val Asn Val Arg Val Gly Arg Tyr 435 440 445			1344
ggt ccg tac atc gag cgc atc gtg ggc acc acc gcg gaa ggc gag cca Gly Pro Tyr Ile Glu Arg Ile Val Gly Thr Thr Ala Glu Gly Glu Pro 450 455 460			1392
gaa ttt cag cgc gcc aac cta cct gag gaa acc acg cct gat gag ctg Glu Phe Gln Arg Ala Asn Leu Pro Glu Glu Thr Thr Pro Asp Glu Leu 465 470 475 480			1440
acc ctc gag gtc gct gag aag ctt ttc gct acc cca caa ggt gga cgt Thr Leu Glu Val Ala Glu Lys Leu Phe Ala Thr Pro Gln Gly Gly Arg 485 490 495			1488
gaa ctg ggc att aac cca gca aac ggt cgc atg gtg gtg gct aag gaa Glu Leu Gly Ile Asn Pro Ala Asn Gly Arg Met Val Val Ala Lys Glu 500 505 510			1536
ggc cgc ttt ggt cca tac gtg atc gag cag gtc acg gac tca gag cgc Gly Arg Phe Gly Pro Tyr Val Ile Glu Gln Val Thr Asp Ser Glu Arg 515 520 525			1584

gct ggc gcc gaa gcc caa gca gaa gaa gtc gtt gca gcg gaa cga aaa	1632
Ala Gly Ala Glu Ala Gln Ala Glu Glu Val Val Ala Ala Glu Arg Lys	
530 535 540	
gct gaa gac gaa caa cgt gcc acc gat gga atg cga ccc aag aac tgg	1680
Ala Glu Asp Glu Gln Arg Ala Thr Asp Gly Met Arg Pro Lys Asn Trp	
545 550 555 560	
gaa acc aag act gcc gca aac cag aag gaa aag cgc atc aac cag ctg	1728
Glu Thr Lys Thr Ala Ala Asn Gln Lys Glu Lys Arg Ile Asn Gln Leu	
565 570 575	
gtt gag gaa aac ctc aag cca gcg acc gca tcc ctg ttc agc ggc atg	1776
Val Glu Glu Asn Leu Lys Pro Ala Thr Ala Ser Leu Phe Ser Gly Met	
580 585 590	
gaa cct gca gcc gtg acc ctg gaa gaa gcc ctc aag ctg ctg tcc ctg	1824
Glu Pro Ala Ala Val Thr Leu Glu Glu Ala Leu Lys Leu Leu Ser Leu	
595 600 605	
cca cgc gaa gta ggt gtc gat cct tcc gac aac gaa gtg atc acc gct	1872
Pro Arg Glu Val Gly Val Asp Pro Ser Asp Asn Glu Val Ile Thr Ala	
610 615 620	
caa aac gga cga tac ggc cct tat ctg aag aag ggt agc gac tcc cgt	1920
Gln Asn Gly Arg Tyr Gly Pro Tyr Leu Lys Lys Gly Ser Asp Ser Arg	
625 630 635 640	
tcc ctc aac agc gaa gag cag atc ttc acc gtc act ttg gat gag gct	1968
Ser Leu Asn Ser Glu Glu Gln Ile Phe Thr Val Thr Leu Asp Glu Ala	
645 650 655	
cgc cgc atc tac gcc gaa cca aag cgt cgt gga cgc gcc gct gct cag	2016
Arg Arg Ile Tyr Ala Glu Pro Lys Arg Arg Gly Arg Ala Ala Ala Gln	
660 665 670	
cca cca ctg aag caa ctt ggc gac aat gac gtt tcc ggc aaa cca atg	2064
Pro Pro Leu Lys Gln Leu Gly Asp Asn Asp Val Ser Gly Lys Pro Met	
675 680 685	
acc gtc aag gac gga cgt ttc ggc cca tac gtc acc gac ggc acc acc	2112
Thr Val Lys Asp Gly Arg Phe Gly Pro Tyr Val Thr Asp Gly Thr Thr	
690 695 700	
aac gcg tca ctg cgc aag ggc gat gtt cca gag tcc ctg acc gat gcg	2160
Asn Ala Ser Leu Arg Lys Gly Asp Val Pro Glu Ser Leu Thr Asp Ala	
705 710 715 720	
cgt gcc aac gag tta ctt tcc gag cgt cgt gcc aag gaa gca gca gat	2208
Arg Ala Asn Glu Leu Leu Ser Glu Arg Arg Ala Lys Glu Ala Ala Asp	
725 730 735	
ggc gga gct cct gcg aag aag acg tcc act aaa aag act gca gcc aag	2256
Gly Gly Ala Pro Ala Lys Lys Thr Ser Thr Lys Lys Thr Ala Ala Lys	
740 745 750	
aag acc acg gct aaa aag aca aca gct aag aaa acc gtg agg aag gct	2304
Lys Thr Thr Ala Lys Lys Thr Thr Ala Lys Lys Thr Val Arg Lys Ala	
755 760 765	

ccg ccg aaa acc acc aaa aac gtg gtg aag gcc ggc gct aag aag aag 2352
 Pro Pro Lys Thr Thr Lys Asn Val Val Lys Ala Gly Ala Lys Lys Lys
 770 775 780

tcc taaaacatgc tgaacgggtt cgt 2378
 Ser
 785

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<211> 785

<212> PRT

<213> Corynebacterium glutamicum

<400> 128

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 1 5 10 15

Ala Asp Ser Asp Asn Pro Ser Ser Phe Thr Ala Arg Leu Ser Thr Ile
 20 25 30

Asp Gly Asn Arg Val Ala Gln Gly Arg Asp Phe Asn Asp Arg Gly Glu
 35 40 45

Leu Thr Ser Glu Ala Val Val Val Asp Lys Gln Arg Ala Glu Ala Leu
 50 55 60

Ala Glu Ala Leu Glu Gly Gln Glu Met Ala Val Val Gly Val Glu Glu
 65 70 75 80

Lys Pro Tyr Thr Arg Arg Pro Tyr Ala Pro Phe Met Thr Ser Thr Leu
 85 90 95

Gln Gln Glu Ser Gly Arg Lys Leu His Tyr Thr Ser Glu Arg Thr Met
 100 105 110

Arg Ile Ala Gln Arg Leu Tyr Glu Asn Gly His Ile Thr Tyr Met Arg
 115 120 125

Thr Asp Ser Thr Ser Leu Ser Glu Gln Gly Met Lys Ala Ala Arg Asp
 130 135 140

Gln Ala Leu Glu Leu Tyr Gly Ala Glu Tyr Val Ser Pro Ser Pro Arg
 145 150 155 160

Thr Tyr Asp Arg Lys Val Lys Asn Ser Gln Glu Ala His Glu Ala Ile
 165 170 175

Arg Pro Ala Gly Glu Thr Phe Ala Thr Pro Gly Gln Leu His Gly Gln
 180 185 190

Leu Asp Ala Glu Glu Phe Lys Leu Tyr Glu Leu Ile Trp Gln Arg Thr
 195 200 205

Val Ala Ser Gln Met Ala Asp Ala Lys Gly Thr Ser Met Lys Val Thr
 210 215 220

Ile Gly Gly Thr Ala Lys Thr Gly Glu Lys Thr Glu Phe Asn Ala Thr
 225 230 235 240

Gly Arg Thr Leu Thr Phe Pro Gly Phe Leu Arg Ala Tyr Val Glu Thr

					245						250						255
Thr	Arg	Thr	Ala	Asp	Gly	Arg	Asp	Val	Ala	Asp	Asn	Ala	Glu	Lys	Arg		
			260				265						270				
Leu	Pro	Leu	Leu	Ser	Glu	Gly	Asp	Leu	Leu	Lys	Val	Leu	Ser	Ile	Glu		
			275				280						285				
Ala	Asp	Gly	His	Ser	Thr	Asn	Pro	Pro	Ala	Arg	Tyr	Thr	Glu	Ala	Ser		
			290				295						300				
Leu	Val	Lys	Lys	Met	Glu	Asp	Leu	Gly	Ile	Gly	Arg	Pro	Ser	Thr	Tyr		
305						310						315	320				
Ala	Ser	Ile	Ile	Lys	Thr	Ile	Gln	Asp	Arg	Gly	Tyr	Val	Tyr	Ser	Arg		
			325						330			335					
Gly	Asn	Ala	Leu	Val	Pro	Ser	Trp	Val	Ala	Phe	Ala	Val	Val	Gly	Leu		
			340						345			350					
Leu	Glu	Ala	Asn	Phe	Thr	Ser	Leu	Val	Asp	Tyr	Asp	Phe	Thr	Ser	Ser		
			355									365					
Met	Glu	Asp	Glu	Leu	Asp	Asn	Ile	Ala	Ala	Gly	Arg	Glu	Gly	Arg	Thr		
370						375						380					
Glu	Trp	Leu	Asn	Gly	Phe	Tyr	Phe	Gly	Asp	Ala	Glu	Ala	Asp	Gln	Ser		
385						390						395					
Met	Ala	Glu	Ser	Val	Ala	Arg	Gln	Gly	Gly	Leu	Lys	Ala	Leu	Val	Asp		
			405						410			415					
Ala	Asn	Leu	Glu	His	Ile	Asp	Ala	Arg	Ser	Val	Asn	Ser	Leu	Lys	Leu		
			420						425			430					
Phe	Asp	Asp	Ala	Glu	Gly	Arg	Ala	Val	Asn	Val	Arg	Val	Gly	Arg	Tyr		
			435						440			445					
Gly	Pro	Tyr	Ile	Glu	Arg	Ile	Val	Gly	Thr	Thr	Ala	Glu	Gly	Glu	Pro		
450						455						460					
Glu	Phe	Gln	Arg	Ala	Asn	Leu	Pro	Glu	Glu	Thr	Thr	Pro	Asp	Glu	Leu		
465						470						475					
Thr	Leu	Glu	Val	Ala	Glu	Lys	Leu	Phe	Ala	Thr	Pro	Gln	Gly	Gly	Arg		
			485						490			495					
Glu	Leu	Gly	Ile	Asn	Pro	Ala	Asn	Gly	Arg	Met	Val	Val	Ala	Lys	Glu		
			500						505			510					
Gly	Arg	Phe	Gly	Pro	Tyr	Val	Ile	Glu	Gln	Val	Thr	Asp	Ser	Glu	Arg		
			515						520			525					
Ala	Gly	Ala	Glu	Ala	Gln	Ala	Glu	Glu	Val	Val	Ala	Ala	Glu	Arg	Lys		
530						535						540					
Ala	Glu	Asp	Glu	Gln	Arg	Ala	Thr	Asp	Gly	Met	Arg	Pro	Lys	Asn	Trp		
545						550						555					
Glu	Thr	Lys	Thr	Ala	Ala	Asn	Gln	Lys	Glu	Lys	Arg	Ile	Asn	Gln	Leu		
			565						570			575					

Val Glu Glu Asn Leu Lys Pro Ala Thr Ala Ser Leu Phe Ser Gly Met
580 585 590

Glu Pro Ala Ala Val Thr Leu Glu Glu Ala Leu Lys Leu Leu Ser Leu
595 600 605

Pro Arg Glu Val Gly Val Asp Pro Ser Asp Asn Glu Val Ile Thr Ala
610 615 620

Gln Asn Gly Arg Tyr Gly Pro Tyr Leu Lys Lys Gly Ser Asp Ser Arg
625 630 635 640

Ser Leu Asn Ser Glu Glu Gln Ile Phe Thr Val Thr Leu Asp Glu Ala
645 650 655

Arg Arg Ile Tyr Ala Glu Pro Lys Arg Arg Gly Arg Ala Ala Ala Gln
660 665 670

Pro Pro Leu Lys Gln Leu Gly Asp Asn Asp Val Ser Gly Lys Pro Met
675 680 685

Thr Val Lys Asp Gly Arg Phe Gly Pro Tyr Val Thr Asp Gly Thr Thr
690 695 700

Asn Ala Ser Leu Arg Lys Gly Asp Val Pro Glu Ser Leu Thr Asp Ala
705 710 715 720

Arg Ala Asn Glu Leu Leu Ser Glu Arg Arg Ala Lys Glu Ala Ala Asp
725 730 735

Gly Gly Ala Pro Ala Lys Lys Thr Ser Thr Lys Lys Thr Ala Ala Lys
740 745 750

Lys Thr Thr Ala Lys Lys Thr Thr Ala Lys Lys Thr Val Arg Lys Ala
755 760 765

Pro Pro Lys Thr Thr Lys Asn Val Val Lys Ala Gly Ala Lys Lys Lys
770 775 780

Ser
785

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<211> 488
<212> DNA
<213> Corynebacterium glutamicum

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<222> (1)..(465)
<223> RXN00990

<400> 129
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Ile Pro Val Leu Val Ala Thr Asp Ile Ala Ala Arg Gly Ile Asp Val
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gat gac gtc tcg ctt gtt gtg cac gtt gat ccc cca gca gaa cac aaa 96
Asp Asp Val Ser Leu Val Val His Val Asp Pro Pro Ala Glu His Lys

	20	25	30	
gcg tat ttg cac cgc gct ggt cgt act gca cga gcc gga act tcc ggt				144
Ala Tyr Leu His Arg Ala Gly Arg Thr Ala Arg Ala Gly Thr Ser Gly				
	35	40	45	
aca gtt gtg act cta gta atg gac gaa caa atc aag gaa gtc cgt gaa				192
Thr Val Val Thr Leu Val Met Asp Glu Gln Ile Lys Glu Val Arg Glu				
	50	55	60	
ctt ttc caa aaa gca ggc gtg aca gcc gct gag gta aaa gtc aac gaa				240
Leu Phe Gln Lys Ala Gly Val Thr Ala Ala Glu Val Lys Val Asn Glu				
	65	70	75	80
aac tca cct gaa ttg gct aaa att act ggt gca cga cgc ccg tca ggc				288
Asn Ser Pro Glu Leu Ala Lys Ile Thr Gly Ala Arg Arg Pro Ser Gly				
	85	90	95	
gtt gct ctt cca gca cct gga cag cag cag cca aag cgg gaa caa aaa				336
Val Ala Leu Pro Ala Pro Gly Gln Gln Gln Pro Lys Arg Glu Gln Lys				
	100	105	110	
aat acc cat aat cgt tct gat tcc aga ggt tcc agc cgg aat cca cgc				384
Asn Thr His Asn Arg Ser Asp Ser Arg Gly Ser Ser Arg Asn Pro Arg				
	115	120	125	
agg cgc gga caa agc gga tcc aga tca acg ggc cgc tcc aac ccg agg				432
Arg Arg Gly Gln Ser Gly Ser Arg Ser Thr Gly Arg Ser Asn Pro Arg				
	130	135	140	
cgt cag act tca agg aaa gac ggt ccc aag agc taaaactccc ccacggcacg				485
Arg Gln Thr Ser Arg Lys Asp Gly Pro Lys Ser				
	145	150	155	
cga				488
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<400> 130				
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Asp Asp Val Ser Leu Val Val His Val Asp Pro Pro Ala Glu His Lys				
	20	25	30	
Ala Tyr Leu His Arg Ala Gly Arg Thr Ala Arg Ala Gly Thr Ser Gly				
	35	40	45	
Thr Val Val Thr Leu Val Met Asp Glu Gln Ile Lys Glu Val Arg Glu				
	50	55	60	
Leu Phe Gln Lys Ala Gly Val Thr Ala Ala Glu Val Lys Val Asn Glu				
	65	70	75	80
Asn Ser Pro Glu Leu Ala Lys Ile Thr Gly Ala Arg Arg Pro Ser Gly				
	85	90	95	

Val Ala Leu Pro Ala Pro Gly Gln Gln Gln Pro Lys Arg Glu Gln Lys
 100 105 110

Asn Thr His Asn Arg Ser Asp Ser Arg Gly Ser Ser Arg Asn Pro Arg
 115 120 125

Arg Arg Gly Gln Ser Gly Ser Arg Ser Thr Gly Arg Ser Asn Pro Arg
 130 135 140

Arg Gln Thr Ser Arg Lys Asp Gly Pro Lys Ser
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<212> DNA

<213> Corynebacterium glutamicum

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<222> (1) .. (453)

<223> FRXA00990

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Leu Val Val His Val Asp Pro Pro Ala Glu His Lys Ala Tyr Leu His	
20 25 30	
cgc gct ggt cgt act gca cga gcc gga act tcc ggt aca gtt gtg act	144
Arg Ala Gly Arg Thr Ala Arg Ala Gly Thr Ser Gly Thr Val Val Thr	
35 40 45	
cta gta atg gac gaa caa atc aag gaa gtc cgt gaa ctt ttc caa aaa	192
Leu Val Met Asp Glu Gln Ile Lys Glu Val Arg Glu Leu Phe Gln Lys	
50 55 60	
gca ggc gtg aca gcc gct gag gta aaa gtc aac gaa aac tca cct gaa	240
Ala Gly Val Thr Ala Ala Glu Val Lys Val Asn Glu Asn Ser Pro Glu	
65 70 75 80	
ttg gct aaa att act ggt gca cga cgc ccg tca ggc gtt gct ctt cca	288
Leu Ala Lys Ile Thr Gly Ala Arg Arg Pro Ser Gly Val Ala Leu Pro	
85 90 95	
gca cct gga cag cag cag cca aag cgg gaa caa aaa aat acc cat aat	336
Ala Pro Gly Gln Gln Gln Pro Lys Arg Glu Gln Lys Asn Thr His Asn	
100 105 110	
cgt tct gat tcc aga ggt tcc agc cgg aat cca cgc agg cgc gga caa	384
Arg Ser Asp Ser Arg Gly Ser Ser Arg Asn Pro Arg Arg Arg Gly Gln	
115 120 125	
agc gga tcc aga tca acg ggc cgc tcc aac ccg agg cgt cag act tca	432
Ser Gly Ser Arg Ser Thr Gly Arg Ser Asn Pro Arg Arg Gln Thr Ser	
130 135 140	
agg aaa gac ggt ccc aag agc taaaactccc ccacggcacg cga	476

Arg Lys Asp Gly Pro Lys Ser
145 150

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<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 132
Val Ala Thr Asp Ile Ala Ala Arg Gly Ile Asp Val Asp Asp Val Ser
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Leu Val Val His Val Asp Pro Pro Ala Glu His Lys Ala Tyr Leu His
20 25 30
Arg Ala Gly Arg Thr Ala Arg Ala Gly Thr Ser Gly Thr Val Val Thr
35 40 45
Leu Val Met Asp Glu Gln Ile Lys Glu Val Arg Glu Leu Phe Gln Lys
50 55 60
Ala Gly Val Thr Ala Ala Glu Val Lys Val Asn Glu Asn Ser Pro Glu
65 70 75 80
Leu Ala Lys Ile Thr Gly Ala Arg Arg Pro Ser Gly Val Ala Leu Pro
85 90 95
Ala Pro Gly Gln Gln Gln Pro Lys Arg Glu Gln Lys Asn Thr His Asn
100 105 110
Arg Ser Asp Ser Arg Gly Ser Ser Arg Asn Pro Arg Arg Arg Gly Gln
115 120 125
Ser Gly Ser Arg Ser Thr Gly Arg Ser Asn Pro Arg Arg Gln Thr Ser
130 135 140
Arg Lys Asp Gly Pro Lys Ser
145 150

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tgatcacttt tcaaccagca ccgactagag ttagtgggca atg act acc ttt cta 115
Met Thr Thr Phe Leu
1 5
gaa ctc aag ctt ccc gac gag att gtg cgc gaa ctt cgc agt cag gga 163
Glu Leu Lys Leu Pro Asp Glu Ile Val Arg Glu Leu Arg Ser Gln Gly
10 15 20

atc acc gag gca ttc ccc atc caa gaa gca gcc atc ccc gat gcg ctc 211
 Ile Thr Glu Ala Phe Pro Ile Gln Glu Ala Ala Ile Pro Asp Ala Leu
 25 30 35

gct ggc aaa gat gtc ctc ggc cgt gga ccc acc ggc tct ggt aaa acc 259
 Ala Gly Lys Asp Val Leu Gly Arg Gly Pro Thr Gly Ser Gly Lys Thr
 40 45 50

ttc acc ttt ggg ctt ccc atg atc acc cga ctc gcg cgc tcg ggc gcc 307
 Phe Thr Phe Gly Leu Pro Met Ile Thr Arg Leu Ala Arg Ser Gly Ala
 55 60 65

tcc aaa cca ggt cgc ccc cgc ggg ctt gtc ctg gtt ccc acc cgt gaa 355
 Ser Lys Pro Gly Arg Pro Arg Gly Leu Val Leu Val Pro Thr Arg Glu
 70 75 80 85

cta gca gct cag gtg cgt gaa cgc ctc gac gat ccc gcc cgc gtt atg 403
 Leu Ala Ala Gln Val Arg Glu Arg Leu Asp Asp Pro Ala Arg Val Met
 90 95 100

ggt ctg cgc gtc ctc gag gtg gtc ggt ggc gtc aac atc aac cgc aac 451
 Gly Leu Arg Val Leu Glu Val Val Gly Gly Val Asn Ile Asn Arg Asn
 105 110 115

<210> 134

<211> 117

<212> PRT

<213> Corynebacterium glutamicum

<400> 134

Met Thr Thr Phe Leu Glu Leu Lys Leu Pro Asp Glu Ile Val Arg Glu
 1 5 10 15

Leu Arg Ser Gln Gly Ile Thr Glu Ala Phe Pro Ile Gln Glu Ala Ala
 20 25 30

Ile Pro Asp Ala Leu Ala Gly Lys Asp Val Leu Gly Arg Gly Pro Thr
 35 40 45

Gly Ser Gly Lys Thr Phe Thr Phe Gly Leu Pro Met Ile Thr Arg Leu
 50 55 60

Ala Arg Ser Gly Ala Ser Lys Pro Gly Arg Pro Arg Gly Leu Val Leu
 65 70 75 80

Val Pro Thr Arg Glu Leu Ala Ala Gln Val Arg Glu Arg Leu Asp Asp
 85 90 95

Pro Ala Arg Val Met Gly Leu Arg Val Leu Glu Val Val Gly Gly Val
 100 105 110

Asn Ile Asn Arg Asn
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<210> 135

<211> 442

<212> DNA

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<222> (101)..(442)

<223> FRXA00994

<400> 135

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				Met	Thr	Thr	Phe	Leu	
				1				5	

gaa	ctc	aag	ctt	ccc	gac	gag	att	gtg	cgc	gaa	ctt	cgc	agt	cag	gga	163
Glu	Leu	Lys	Leu	Pro	Asp	Glu	Ile	Val	Arg	Glu	Leu	Arg	Ser	Gln	Gly	
			10					15						20		

atc	acc	gag	gca	ttc	ccc	atc	caa	gaa	gca	gcc	atc	ccc	gat	gcg	ctc	211
Ile	Thr	Glu	Ala	Phe	Pro	Ile	Gln	Glu	Ala	Ala	Ile	Pro	Asp	Ala	Leu	
		25					30						35			

gct	ggc	aaa	gat	gtc	ctc	ggc	cgt	gga	ccc	acc	ggc	tct	ggg	aaa	acc	259
Ala	Gly	Lys	Asp	Val	Leu	Gly	Arg	Gly	Pro	Thr	Gly	Ser	Gly	Lys	Thr	
		40				45					50					

ttc	acc	ttt	ggg	ctt	ccc	atg	atc	acc	cga	ctc	gcg	cgc	tcg	ggc	gcc	307
Phe	Thr	Phe	Gly	Leu	Pro	Met	Ile	Thr	Arg	Leu	Ala	Arg	Ser	Gly	Ala	
		55				60					65					

tcc	aaa	cca	ggg	cgc	ccc	cgc	ggg	ctt	gtc	ctg	gtt	ccc	acc	cgt	gaa	355
Ser	Lys	Pro	Gly	Arg	Pro	Arg	Gly	Leu	Val	Leu	Val	Pro	Thr	Arg	Glu	
	70				75				80						85	

cta	gca	gct	cag	gtg	cgt	gaa	cgc	ctc	gac	gat	ccc	gcc	cgc	gtt	atg	403
Leu	Ala	Ala	Gln	Val	Arg	Glu	Arg	Leu	Asp	Asp	Pro	Ala	Arg	Val	Met	
			90					95						100		

ggg	ctg	cgc	gtc	ctc	gag	gtg	gtc	ggg	ggc	gtc	aac	atc				442
Gly	Leu	Arg	Val	Leu	Glu	Val	Val	Gly	Gly	Val	Asn	Ile				
		105					110									

<210> 136

<211> 114

<212> PRT

<213> Corynebacterium glutamicum

<400> 136

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Leu	Arg	Ser	Gln	Gly	Ile	Thr	Glu	Ala	Phe	Pro	Ile	Gln	Glu	Ala	Ala	
			20					25					30			

Ile	Pro	Asp	Ala	Leu	Ala	Gly	Lys	Asp	Val	Leu	Gly	Arg	Gly	Pro	Thr	
		35					40					45				

Gly	Ser	Gly	Lys	Thr	Phe	Thr	Phe	Gly	Leu	Pro	Met	Ile	Thr	Arg	Leu	
	50					55					60					

Ala	Arg	Ser	Gly	Ala	Ser	Lys	Pro	Gly	Arg	Pro	Arg	Gly	Leu	Val	Leu	
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Asn Ile

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<222> (101) .. (1324)
<223> RXN02468
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Val Glu Ile Thr Asp 5															
gca ctc gaa gcc ctc ggc atc aac cga act ttc gcg atc cag gag tac 163															
Ala Leu Glu Ala Leu Gly Ile Asn Arg Thr Phe Ala Ile Gln Glu Tyr 20															
aca ctt ccc atc gcg ctc gac ggc cac gac ttc atc ggc caa gcc cgc 211															
Thr Leu Pro Ile Ala Leu Asp Gly His Asp Phe Ile Gly Gln Ala Arg 35															
acc ggc atg ggc aaa acc tac gga ttc ggt gtc cca ctc ctc gat aga 259															
Thr Gly Met Gly Lys Thr Tyr Gly Phe Gly Val Pro Leu Leu Asp Arg 50															
gtc ttc gac tca gcc gac gtc gca gaa acc gac ggt acc ccc cga gcc 307															
Val Phe Asp Ser Ala Asp Val Ala Glu Thr Asp Gly Thr Pro Arg Ala 65															
ctc gtc atc gtg ccc acc cga gaa ctc gca gtc caa gtc ggc gac gac 355															
Leu Val Ile Val Pro Thr Arg Glu Leu Ala Val Gln Val Gly Asp Asp 85															
ctc caa cgc gca gca acc aac ctg ccg cta aag atc ttc acc ttc tac 403															
Leu Gln Arg Ala Ala Thr Asn Leu Pro Leu Lys Ile Phe Thr Phe Tyr 100															
ggc ggc acc ccc tac gaa gaa cag atc gac gca ctc aaa gtc ggc gtc 451															
Gly Gly Thr Pro Tyr Glu Glu Gln Ile Asp Ala Leu Lys Val Gly Val 115															
gac gtt gtc gta ggc aca ccc gga cga tta ctc gac ctg cac aaa cga 499															
Asp Val Val Val Gly Thr Pro Gly Arg Leu Leu Asp Leu His Lys Arg 125															

ggc gcg cta tcg ctc gac aaa gta gcg atc tta gtc ctc gat gaa gcc	547
Gly Ala Leu Ser Leu Asp Lys Val Ala Ile Leu Val Leu Asp Glu Ala	
135 140 145	
gac gaa atg ctc gat ctg ggc ttt ctg ccc gac atc gaa aaa atc ctc	595
Asp Glu Met Leu Asp Leu Gly Phe Leu Pro Asp Ile Glu Lys Ile Leu	
150 155 160 165	
cgt gcc ctc acc cac cag cat caa acc atg ctg ttc tct gcc acg atg	643
Arg Ala Leu Thr His Gln His Gln Thr Met Leu Phe Ser Ala Thr Met	
170 175 180	
ccc ggc gcg atc ctc aca ctc gca cgc agc ttc ctg aac aaa cca gtg	691
Pro Gly Ala Ile Leu Thr Leu Ala Arg Ser Phe Leu Asn Lys Pro Val	
185 190 195	
cac atc cga gcc gag aca tcg gac gcc tca gca aca cac aaa acc acc	739
His Ile Arg Ala Glu Thr Ser Asp Ala Ser Ala Thr His Lys Thr Thr	
200 205 210	
aga caa gtg gtt ttt cag gca cac aaa atg gac aag gaa gcc atc acc	787
Arg Gln Val Val Phe Gln Ala His Lys Met Asp Lys Glu Ala Ile Thr	
215 220 225	
gcg aaa att ctg cag tcg aaa gat cgc ggc aaa acg atc atc ttc gcc	835
Ala Lys Ile Leu Gln Ser Lys Asp Arg Gly Lys Thr Ile Ile Phe Ala	
230 235 240 245	
cgc acg aaa cgc acc gca gcg caa gtt gcc gaa gac cta gcc tcc aga	883
Arg Thr Lys Arg Thr Ala Ala Gln Val Ala Glu Asp Leu Ala Ser Arg	
250 255 260	
gga ttc tcc gtc gga tca gtg cac ggc gac atg ggc caa cca gcc cgc	931
Gly Phe Ser Val Gly Ser Val His Gly Asp Met Gly Gln Pro Ala Arg	
265 270 275	
gag aaa tca ctc aac gca ttc cgc aca gga aaa att gac atc ctt gta	979
Glu Lys Ser Leu Asn Ala Phe Arg Thr Gly Lys Ile Asp Ile Leu Val	
280 285 290	
gcc aca gac gta gcc gcc cga ggc atc gat gtt gat gac gtc acc cac	1027
Ala Thr Asp Val Ala Ala Arg Gly Ile Asp Val Asp Asp Val Thr His	
295 300 305	
gtg atc aac tac caa acc ccc gac gat cct atg acc tac gtc cat cgt	1075
Val Ile Asn Tyr Gln Thr Pro Asp Asp Pro Met Thr Tyr Val His Arg	
310 315 320 325	
atc gga cgc acg gga cgc gca ggg cac aac gga aca gcc gtc act ctt	1123
Ile Gly Arg Thr Gly Arg Ala Gly His Asn Gly Thr Ala Val Thr Leu	
330 335 340	
gtc ggg tac gac gaa acc ctc aaa tgg act gtc atc gac aac gaa ctc	1171
Val Gly Tyr Asp Glu Thr Leu Lys Trp Thr Val Ile Asp Asn Glu Leu	
345 350 355	
gaa ctc ggc caa cca aac cca cca caa tgg ttc tcc acc tca cca gag	1219
Glu Leu Gly Gln Pro Asn Pro Pro Gln Trp Phe Ser Thr Ser Pro Glu	
360 365 370	
ctg ctt gaa aca ctc gac atc cca gaa ggt gtc acc gaa cga gtc gga	1267

Leu Leu Glu Thr Leu Asp Ile Pro Glu Gly Val Thr Glu Arg Val Gly
375 380 385

cca cca acc aaa gtt cta ggc gga aca gcc cca cga cca cca cgc cgc 1315
Pro Pro Thr Lys Val Leu Gly Gly Thr Ala Pro Arg Pro Pro Arg Arg
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Thr Arg Lys

<210> 138

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 138

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Ile Gly Gln Ala Arg Thr Gly Met Gly Lys Thr Tyr Gly Phe Gly Val
35 40 45

Pro Leu Leu Asp Arg Val Phe Asp Ser Ala Asp Val Ala Glu Thr Asp
50 55 60

Gly Thr Pro Arg Ala Leu Val Ile Val Pro Thr Arg Glu Leu Ala Val
65 70 75 80

Gln Val Gly Asp Asp Leu Gln Arg Ala Ala Thr Asn Leu Pro Leu Lys
85 90 95

Ile Phe Thr Phe Tyr Gly Gly Thr Pro Tyr Glu Glu Gln Ile Asp Ala
100 105 110

Leu Lys Val Gly Val Asp Val Val Val Gly Thr Pro Gly Arg Leu Leu
115 120 125

Asp Leu His Lys Arg Gly Ala Leu Ser Leu Asp Lys Val Ala Ile Leu
130 135 140

Val Leu Asp Glu Ala Asp Glu Met Leu Asp Leu Gly Phe Leu Pro Asp
145 150 155 160

Ile Glu Lys Ile Leu Arg Ala Leu Thr His Gln His Gln Thr Met Leu
165 170 175

Phe Ser Ala Thr Met Pro Gly Ala Ile Leu Thr Leu Ala Arg Ser Phe
180 185 190

Leu Asn Lys Pro Val His Ile Arg Ala Glu Thr Ser Asp Ala Ser Ala
195 200 205

Thr His Lys Thr Thr Arg Gln Val Val Phe Gln Ala His Lys Met Asp
210 215 220

Lys Glu Ala Ile Thr Ala Lys Ile Leu Gln Ser Lys Asp Arg Gly Lys

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Thr Ile Ile Phe	Ala Arg Thr Lys Arg	Thr Ala Ala Gln Val	Ala Glu			
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Asp Leu Ala Ser	Arg Gly Phe Ser Val	Gly Ser Val His	Gly Asp Met			
	260	265	270			
Gly Gln Pro Ala	Arg Glu Lys Ser Leu Asn	Ala Phe Arg Thr	Gly Lys			
	275	280	285			
Ile Asp Ile Leu	Val Ala Thr Asp Val	Ala Ala Arg Gly	Ile Asp Val			
	290	295	300			
Asp Asp Val Thr	His Val Ile Asn Tyr	Gln Thr Pro Asp	Asp Pro Met			
305		310	315		320	
Thr Tyr Val His	Arg Ile Gly Arg Thr	Gly Arg Ala Gly	His Asn Gly			
	325	330	335			
Thr Ala Val Thr	Leu Val Gly Tyr Asp	Glu Thr Leu Lys	Trp Thr Val			
	340	345	350			
Ile Asp Asn Glu	Leu Glu Leu Gly Gln	Pro Asn Pro Pro	Gln Trp Phe			
	355	360	365			
Ser Thr Ser Pro	Glu Leu Leu Glu Thr	Leu Asp Ile Pro	Glu Gly Val			
	370	375	380			
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Arg Pro Pro Arg	Arg Thr Arg Lys					
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 <223> FRXA02463

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		Met Thr Tyr Val His	
		1 5	

tgt atn gga cgc acg gga cgc gca ggg cac aac gga	aca gcc gtc act	163
Cys Xaa Gly Arg Thr Gly Arg Ala Gly His Asn Gly	Thr Ala Val Thr	
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Leu Val Gly Phe Xaa Glu Thr Leu Lys Trp Thr	Xaa Xaa Asp Asn Glu	
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Val Glu Ile Thr Asp
1 5
gca ctc gaa gcc ctc ggc atc aac cga act ttc gcg atc cag gag tac 163
Ala Leu Glu Ala Leu Gly Ile Asn Arg Thr Phe Ala Ile Gln Glu Tyr
10 15 20
aca ctt ccc atc gcg ctc gac ggc cac gac ttc atc ggc caa gcc cgc 211
Thr Leu Pro Ile Ala Leu Asp Gly His Asp Phe Ile Gly Gln Ala Arg
25 30 35
acc ggc atg ggc aaa acc tac gga ttc ggt gtc cca ctc ctc gat aga 259
Thr Gly Met Gly Lys Thr Tyr Gly Phe Gly Val Pro Leu Leu Asp Arg
40 45 50
gtc ttc gac tca gcc gac gtc gca gaa acc gac ggt acc ccc cga gcc 307
Val Phe Asp Ser Ala Asp Val Ala Glu Thr Asp Gly Thr Pro Arg Ala
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ctc gtc atc gtg ccc acc cga gaa ctc gca gtc caa gtc ggc gac gac 355
Leu Val Ile Val Pro Thr Arg Glu Leu Ala Val Gln Val Gly Asp Asp
70 75 80 85
ctc caa cgc gca gca acc aac ctg ccg cta aag atc ttc acc ttc tac 403
Leu Gln Arg Ala Ala Thr Asn Leu Pro Leu Lys Ile Phe Thr Phe Tyr
90 95 100

ggc ggc acc ccc tac gaa gaa cag atc gac gca ctc aaa gtc ggc gtc 451
 Gly Gly Thr Pro Tyr Glu Glu Gln Ile Asp Ala Leu Lys Val Gly Val
 105 110 115
 gac gtt gtc gta ggc aca ccc gga cga tta ctc gac ctg cac aaa cga 499
 Asp Val Val Val Gly Thr Pro Gly Arg Leu Leu Asp Leu His Lys Arg
 120 125 130
 ggc gcg cta tcg ctc gac aaa gta gcg atc tta gtc ctc gat gaa gcc 547
 Gly Ala Leu Ser Leu Asp Lys Val Ala Ile Leu Val Leu Asp Glu Ala
 135 140 145
 gac gaa atg ctc gat ctg ggc ttt ctg ccc gac atc gaa aaa atc ctc 595
 Asp Glu Met Leu Asp Leu Gly Phe Leu Pro Asp Ile Glu Lys Ile Leu
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 35 40 45
 Pro Leu Leu Asp Arg Val Phe Asp Ser Ala Asp Val Ala Glu Thr Asp
 50 55 60
 Gly Thr Pro Arg Ala Leu Val Ile Val Pro Thr Arg Glu Leu Ala Val
 65 70 75 80
 Gln Val Gly Asp Asp Leu Gln Arg Ala Ala Thr Asn Leu Pro Leu Lys
 85 90 95
 Ile Phe Thr Phe Tyr Gly Gly Thr Pro Tyr Glu Glu Gln Ile Asp Ala
 100 105 110
 Leu Lys Val Gly Val Asp Val Val Val Gly Thr Pro Gly Arg Leu Leu
 115 120 125
 Asp Leu His Lys Arg Gly Ala Leu Ser Leu Asp Lys Val Ala Ile Leu
 130 135 140
 Val Leu Asp Glu Ala Asp Glu Met Leu Asp Leu Gly Phe Leu Pro Asp
 145 150 155 160
 Ile Glu Lys Ile Leu Arg Ala Leu Thr His Gln His Gln Thr Met Leu
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Met Ser Asn Thr Glu 1 5																
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Asn Val Asn Gly Asp Val Glu Gln Pro Asn Asn Val Ile Ser Ser Glu 10 15 20																
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Glu Thr Pro Thr Asn Thr Val Glu Asp Ala Pro Ala Ser Glu Gly Ser 40 45 50																
gaa gag atc acc agg gtt gcg gat act tct gag gac gcc gac tct gca 307																
Glu Glu Ile Thr Arg Val Ala Asp Thr Ser Glu Asp Ala Asp Ser Ala 55 60 65																
gat gca gac aac gcg agc aat gta atc aat gag aat gag gac tcc tcg 355																
Asp Ala Asp Asn Ala Ser Asn Val Ile Asn Glu Asn Glu Asp Ser Ser 70 75 80 85																
gaa ggt gct aac cag cct tca aac gag tca tcc tct acg gaa gcc aaa 403																
Glu Gly Ala Asn Gln Pro Ser Asn Glu Ser Ser Ser Thr Glu Ala Lys 90 95 100																
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Ser Gly Phe Asp Ala Leu Gly Leu Pro Glu Arg Val Leu Asp Ala Val 105 110 115																
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Arg Lys Val Gly Tyr Glu Thr Pro Ser Pro Ile Gln Ala Gln Thr Ile 120 125 130																
cca atc ctc atg gag ggc cag gat gtt gtt ggt cta gca cag acc ggt 547																
Pro Ile Leu Met Glu Gly Gln Asp Val Val Gly Leu Ala Gln Thr Gly 135 140 145																
acc ggt aag act gca gct ttc gcg ctg cca atc ctt gcc cgt att gac 595																
Thr Gly Lys Thr Ala Ala Phe Ala Leu Pro Ile Leu Ala Arg Ile Asp 150 155 160 165																

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Lys Ser Val Arg Ser Pro Gln Ala Leu Val Leu Ala Pro Thr Arg Glu	
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Leu Ala Leu Gln Val Ala Asp Ser Phe Gln Ser Phe Ala Asp His Val	
185 190 195	
ggg ggc ctg aac gtt ctg cca atc tat ggt gga cag gct tac ggc att	739
Gly Gly Leu Asn Val Leu Pro Ile Tyr Gly Gly Gln Ala Tyr Gly Ile	
200 205 210	
cag ctc tct ggc ctg cgt cgt ggc gct cac atc gtc gtg ggt acc cca	787
Gln Leu Ser Gly Leu Arg Arg Gly Ala His Ile Val Val Gly Thr Pro	
215 220 225	
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Gly Arg Ile Ile Asp His Leu Glu Lys Gly Ser Leu Asp Ile Ser Gly	
230 235 240 245	
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Leu Arg Phe Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Met Gly	
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Phe Gln Glu Asp Val Glu Arg Ile Leu Glu Asp Thr Pro Asp Glu Lys	
265 270 275	
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Gln Val Ala Leu Phe Ser Ala Thr Met Pro Asn Gly Ile Arg Arg Leu	
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acc agg act aac acc aac atc acc cag cgc ttc ctc aac gtt gca cac	1075
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Arg Asn Lys Met Asp Ala Leu Thr Arg Ile Leu Glu Val Thr Glu Phe	
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Glu Ala Met Ile Met Phe Val Arg Thr Lys His Glu Thr Glu Glu Val	
345 350 355	
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Ala Glu Lys Leu Arg Ala Arg Gly Phe Ser Ala Ala Ala Ile Asn Gly	
360 365 370	
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375 380 385	
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Gly Arg Leu Asp Ile Leu Val Ala Thr Asp Val Ala Ala Arg Gly Leu	
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gac gtt gag cgc atc tcc cac gtg ctt aac ttc gac att cca aac gac	1363

Asp	Val	Glu	Arg	Ile	Ser	His	Val	Leu	Asn	Phe	Asp	Ile	Pro	Asn	Asp		
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Thr	Glu	Ser	Tyr	Val	His	Arg	Ile	Gly	Arg	Thr	Gly	Arg	Ala	Gly	Arg		
			425					430					435				
acc	ggc	gag	gca	atc	ctg	ttc	gtg	acc	cca	cgt	gag	cgt	cgt	atg	ctt	1459	
Thr.	Gly	Glu	Ala	Ile	Leu	Phe	Val	Thr	Pro	Arg	Glu	Arg	Arg	Met	Leu		
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cgc	tcc	atc	gag	cgc	gca	acc	aac	gca	cca	ctg	cac	gaa	atg	gaa	ctg	1507	
Arg	Ser	Ile	Glu	Arg	Ala	Thr	Asn	Ala	Pro	Leu	His	Glu	Met	Glu	Leu		
	455					460					465						
cca	acc	gtc	gat	cag	gtc	aac	gac	ttc	cgc	aag	gtc	aag	ttc	gct	gac	1555	
Pro	Thr	Val	Asp	Gln	Val	Asn	Asp	Phe	Arg	Lys	Val	Lys	Phe	Ala	Asp		
470					475					480					485		
tcc	atc	acc	aag	tcc	ctc	gag	gac	aag	cag	atg	gac	ctg	ttc	cgc	acc	1603	
Ser	Ile	Thr	Lys	Ser	Leu	Glu	Asp	Lys	Gln	Met	Asp	Leu	Phe	Arg	Thr		
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ctg	gtc	aag	gaa	tac	tcc	cag	gcc	aac	gac	gtt	cct	cta	gag	gac	atc	1651	
Leu	Val	Lys	Glu	Tyr	Ser	Gln	Ala	Asn	Asp	Val	Pro	Leu	Glu	Asp	Ile		
			505					510					515				
gca	gcg	gca	ctg	gca	acc	cag	gca	cag	tcc	ggc	gac	ttc	ctg	ctc	aag	1699	
Ala	Ala	Ala	Leu	Ala	Thr	Gln	Ala	Gln	Ser	Gly	Asp	Phe	Leu	Leu	Lys		
		520					525					530					
gag	ctc	cca	cca	gag	cgc	cgt	gag	cgc	aac	gac	cgc	cgt	cgt	gac	cgt	1747	
Glu	Leu	Pro	Pro	Glu	Arg	Arg	Glu	Arg	Asn	Asp	Arg	Arg	Arg	Asp	Arg		
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gac	ttc	gac	gac	cgt	ggt	gga	cgt	gga	cgc	gac	cgt	gac	cgt	ggc	gac	1795	
Asp	Phe	Asp	Asp	Arg	Gly	Gly	Arg	Gly	Arg	Asp	Arg	Asp	Arg	Gly	Asp		
	550				555					560					565		
cgc	gga	gat	cgt	ggc	tca	cgc	ttc	gac	cgc	gac	gac	gag	aac	ctg	gca	1843	
Arg	Gly	Asp	Arg	Gly	Ser	Arg	Phe	Asp	Arg	Asp	Asp	Glu	Asn	Leu	Ala		
				570					575					580			
acc	tac	cgc	ctc	gca	gtg	ggc	aag	cgc	cag	cac	atc	cgc	cca	ggc	gca	1891	
Thr	Tyr	Arg	Leu	Ala	Val	Gly	Lys	Arg	Gln	His	Ile	Arg	Pro	Gly	Ala		
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atc	gtt	ggt	gca	ctt	gcc	aac	gaa	ggt	ggc	ctg	aac	tcc	aag	gac	ttc	1939	
Ile	Val	Gly	Ala	Leu	Ala	Asn	Glu	Gly	Gly	Leu	Asn	Ser	Lys	Asp	Phe		
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ggc	cgc	atc	acc	atc	gca	gcc	gac	cac	acc	ctg	gtt	gaa	ctg	cca	aag	1987	
Gly	Arg	Ile	Thr	Ile	Ala	Ala	Asp	His	Thr	Leu	Val	Glu	Leu	Pro	Lys		
	615					620					625						
gat	ctc	cca	cag	agc	gtt	ctt	gac	aac	ctg	cgc	gac	acc	cgc	atc	tcc	2035	
Asp	Leu	Pro	Gln	Ser	Val	Leu	Asp	Asn	Leu	Arg	Asp	Thr	Arg	Ile	Ser		
	630				635					640					645		
ggc	cag	ctc	atc	aac	ata	gaa	cgc	gac	tcc	ggt	gga	cgc	cca	cca	cgc	2083	
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Arg Phe Glu Arg Asp Asp Arg Gly Gly Arg Gly Gly Phe Arg Gly Asp			
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cgt gat gac cgc ggt gga cgt gga cgt gac cgt gac gat cgt gga agc			2179
Arg Asp Asp Arg Gly Gly Arg Gly Arg Asp Arg Asp Asp Arg Gly Ser			
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Gly Gly Phe Arg Gly Arg Asp Asp Arg Gly Asp Arg Gly Gly Arg Gly			
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35 40 45

Ala Ser Glu Gly Ser Glu Glu Ile Thr Arg Val Ala Asp Thr Ser Glu
50 55 60

Asp Ala Asp Ser Ala Asp Ala Asp Asn Ala Ser Asn Val Ile Asn Glu
65 70 75 80

Asn Glu Asp Ser Ser Glu Gly Ala Asn Gln Pro Ser Asn Glu Ser Ser
85 90 95

Ser Thr Glu Ala Lys Ser Gly Phe Asp Ala Leu Gly Leu Pro Glu Arg
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Val Leu Asp Ala Val Arg Lys Val Gly Tyr Glu Thr Pro Ser Pro Ile
115 120 125

Gln Ala Gln Thr Ile Pro Ile Leu Met Glu Gly Gln Asp Val Val Gly
130 135 140

Leu Ala Gln Thr Gly Thr Gly Lys Thr Ala Ala Phe Ala Leu Pro Ile
145 150 155 160

Leu Ala Arg Ile Asp Lys Ser Val Arg Ser Pro Gln Ala Leu Val Leu
165 170 175

Ala Pro Thr Arg Glu Leu Ala Leu Gln Val Ala Asp Ser Phe Gln Ser
 180 185 190
 Phe Ala Asp His Val Gly Gly Leu Asn Val Leu Pro Ile Tyr Gly Gly
 195 200 205
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 Val Val Gly Thr Pro Gly Arg Ile Ile Asp His Leu Glu Lys Gly Ser
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 385 390 395 400
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 Asp Ile Pro Asn Asp Thr Glu Ser Tyr Val His Arg Ile Gly Arg Thr
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 Gly Arg Ala Gly Arg Thr Gly Glu Ala Ile Leu Phe Val Thr Pro Arg
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 450 455 460
 His Glu Met Glu Leu Pro Thr Val Asp Gln Val Asn Asp Phe Arg Lys
 465 470 475 480
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 485 490 495

Asp Leu Phe Arg Thr Leu Val Lys Glu Tyr Ser Gln Ala Asn Asp Val
500 505 510

Pro Leu Glu Asp Ile Ala Ala Ala Leu Ala Thr Gln Ala Gln Ser Gly
515 520 525

Asp Phe Leu Leu Lys Glu Leu Pro Pro Glu Arg Arg Glu Arg Asn Asp
530 535 540

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Arg Asp Arg Gly Asp Arg Gly Asp Arg Gly Ser Arg Phe Asp Arg Asp
565 570 575

Asp Glu Asn Leu Ala Thr Tyr Arg Leu Ala Val Gly Lys Arg Gln His
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Ile Arg Pro Gly Ala Ile Val Gly Ala Leu Ala Asn Glu Gly Gly Leu
595 600 605

Asn Ser Lys Asp Phe Gly Arg Ile Thr Ile Ala Ala Asp His Thr Leu
610 615 620

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625 630 635 640

Asp Thr Arg Ile Ser Gly Gln Leu Ile Asn Ile Glu Arg Asp Ser Gly
645 650 655

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660 665 670

Gly Phe Arg Gly Asp Arg Asp Asp Arg Gly Gly Arg Gly Arg Asp Arg
675 680 685

Asp Asp Arg Gly Ser Arg Gly Gly Phe Arg Gly Gly Arg Asp Arg Asp
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Arg Gly Gly Arg Gly Gly Tyr Arg Gly Gly Arg Asp
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<223> RXA02682

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Met Ser Tyr His Asp

1

5

cac agc gac atc gaa tac ctc aag aag atc ggc gcc aac tcc cct gac 163
 His Ser Asp Ile Glu Tyr Leu Lys Lys Ile Gly Ala Asn Ser Pro Asp
 10 15 20

gcc ttc aaa gct ttt gtc cat ttt gat gag gca gct ctc cgc ggc ccg 211
 Ala Phe Lys Ala Phe Val His Phe Asp Glu Ala Ala Leu Arg Gly Pro
 25 30 35

aac aag aaa atc cca cgc aac tac acc gaa atg atc gca ctt gcg gtc 259
 Asn Lys Lys Ile Pro Arg Asn Tyr Thr Glu Met Ile Ala Leu Ala Val
 40 45 50

gca ttc aca acc caa tgc gcc tac tgc atc gac atc cac act gcc gct 307
 Ala Phe Thr Thr Gln Cys Ala Tyr Cys Ile Asp Ile His Thr Ala Ala
 55 60 65

gcg aag aag gaa ggt gtc acc acc gag gag ctc gct gag gtt gcg ctc 355
 Ala Lys Lys Glu Gly Val Thr Thr Glu Glu Leu Ala Glu Val Ala Leu
 70 75 80 85

atc gcc gca gca ctt cgg gca ggc ggc gcc atg acg cac ggc gca ctt 403
 Ile Ala Ala Ala Leu Arg Ala Gly Gly Ala Met Thr His Gly Ala Leu
 90 95 100

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<210> 146

<211> 109

<212> PRT

<213> Corynebacterium glutamicum

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 20 25 30

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 35 40 45

Ile Ala Leu Ala Val Ala Phe Thr Thr Gln Cys Ala Tyr Cys Ile Asp
 50 55 60

Ile His Thr Ala Ala Ala Lys Lys Glu Gly Val Thr Thr Glu Glu Leu
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Thr His Gly Ala Leu Ala Met Lys Leu Tyr Asp Glu Asn
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<210> 147

<211> 798

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<221> CDS

<222> (101)..(775)

<223> RXN00542

<400> 147

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              Met Ala Ile Gly Asp
              1              5

act aac atc acc gtc gtt ggc aac att gtt gct gac ccg gaa ctc cgc 163
Thr Asn Ile Thr Val Val Gly Asn Ile Val Ala Asp Pro Glu Leu Arg
              10              15              20

ttc acc cca tgc ggt gca gca gtg gct aac ttc cgc att gca tca act 211
Phe Thr Pro Ser Gly Ala Ala Val Ala Asn Phe Arg Ile Ala Ser Thr
              25              30              35

ccc cgc tgc ttc aac cgc caa acc aac cag tgg gaa gac ggc gaa gcc 259
Pro Arg Ser Phe Asn Arg Gln Thr Asn Gln Trp Glu Asp Gly Glu Ala
              40              45              50

ctc ttt ctc acc gtt aac gtt tgg cgt cag gca gct gaa aac gtt gca 307
Leu Phe Leu Thr Val Asn Val Trp Arg Gln Ala Ala Glu Asn Val Ala
              55              60              65

gag tcc ctg tcc aag ggt atg cgc gtt atc gtc acc ggt cgc ctc aag 355
Glu Ser Leu Ser Lys Gly Met Arg Val Ile Val Thr Gly Arg Leu Lys
              70              75              80              85

cag cgc tcc tat gaa acc cgt gag ggc gaa aag cgc agc gtt ttt gag 403
Gln Arg Ser Tyr Glu Thr Arg Glu Gly Glu Lys Arg Ser Val Phe Glu
              90              95              100

gtc gaa gcg gat gaa gtc gga cca tca cta aca ttt gcc aag gca gat 451
Val Glu Ala Asp Glu Val Gly Pro Ser Leu Thr Phe Ala Lys Ala Asp
              105              110              115

gtc cag cgc aca ccg cgc ggt gga aac tct ggc gga aac tac ggt ggc 499
Val Gln Arg Thr Pro Arg Gly Gly Asn Ser Gly Gly Asn Tyr Gly Gly
              120              125              130

ggc aac caa ggt ggt ggc ctc ggt gga aac caa ggc aac cag caa ggt 547
Gly Asn Gln Gly Gly Gly Leu Gly Gly Asn Gln Gly Asn Gln Gln Gly
              135              140              145

gga ttc agc aac cag aac tct ggc ggc ttc ggt gga aac caa ggc aac 595
Gly Phe Ser Asn Gln Asn Ser Gly Gly Phe Gly Gly Asn Gln Gly Asn
              150              155              160              165

cag cag caa agc aac cag ggc gga ttt ggt gga aac caa aac cag tcc 643
Gln Gln Gln Ser Asn Gln Gly Gly Phe Gly Gly Asn Gln Asn Gln Ser
              170              175              180

cag ggt aac aac ttc aac caa ggt gga ttt ggc gga ggc agc cca cag 691
Gln Gly Asn Asn Phe Asn Gln Gly Gly Phe Gly Gly Gly Ser Pro Gln

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185	190	195	
gca gca ccg gac aat gac cct tgg aat tct gca cca cca gct ggc tcc			739
Ala Ala Pro Asp Asn Asp Pro Trp Asn Ser Ala Pro Pro Ala Gly Ser			
200	205	210	
ggc ggg ttc ggc ggc gca gac gat gag cca ccg ttc taaagctttt			785
Gly Gly Phe Gly Gly Ala Asp Asp Glu Pro Pro Phe			
215	220	225	
cttttctaaa aca			798

<210> 148

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 148

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Asp	Pro	Glu	Leu	Arg	Phe	Thr	Pro	Ser	Gly	Ala	Ala	Val	Ala	Asn	Phe
			20					25						30	

Arg	Ile	Ala	Ser	Thr	Pro	Arg	Ser	Phe	Asn	Arg	Gln	Thr	Asn	Gln	Trp
		35					40					45			

Glu	Asp	Gly	Glu	Ala	Leu	Phe	Leu	Thr	Val	Asn	Val	Trp	Arg	Gln	Ala
	50					55					60				

Ala	Glu	Asn	Val	Ala	Glu	Ser	Leu	Ser	Lys	Gly	Met	Arg	Val	Ile	Val
65					70					75					80

Thr	Gly	Arg	Leu	Lys	Gln	Arg	Ser	Tyr	Glu	Thr	Arg	Glu	Gly	Glu	Lys
				85					90					95	

Arg	Ser	Val	Phe	Glu	Val	Glu	Ala	Asp	Glu	Val	Gly	Pro	Ser	Leu	Thr
			100					105					110		

Phe	Ala	Lys	Ala	Asp	Val	Gln	Arg	Thr	Pro	Arg	Gly	Gly	Asn	Ser	Gly
		115					120					125			

Gly	Asn	Tyr	Gly	Gly	Gly	Asn	Gln	Gly	Gly	Gly	Leu	Gly	Gly	Asn	Gln
	130					135					140				

Gly	Asn	Gln	Gln	Gly	Gly	Phe	Ser	Asn	Gln	Asn	Ser	Gly	Gly	Phe	Gly
145					150					155					160

Gly	Asn	Gln	Gly	Asn	Gln	Gln	Gln	Ser	Asn	Gln	Gly	Gly	Phe	Gly	Gly
				165					170					175	

Asn	Gln	Asn	Gln	Ser	Gln	Gly	Asn	Asn	Phe	Asn	Gln	Gly	Gly	Phe	Gly
			180					185					190		

Gly	Gly	Ser	Pro	Gln	Ala	Ala	Pro	Asp	Asn	Asp	Pro	Trp	Asn	Ser	Ala
		195					200					205			

Pro	Pro	Ala	Gly	Ser	Gly	Gly	Phe	Gly	Gly	Ala	Asp	Asp	Glu	Pro	Pro
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Phe
225

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<211> 542
<212> DNA
<213> *Corynebacterium glutamicum*

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<223> FRXA00542

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gca gag tcc ctg tcc aag ggt atg cgc gtt atc gtc acc ggt cgc ctc 96
Ala Glu Ser Leu Ser Lys Gly Met Arg Val Ile Val Thr Gly Arg Leu
20 25 30
aag cag cgc tcc tat gaa acc cgt gag ggc gaa aag cgc agc gtt ttt 144
Lys Gln Arg Ser Tyr Glu Thr Arg Glu Gly Glu Lys Arg Ser Val Phe
35 40 45
gag gtc gaa gcg gat gaa gtc gga cca tca cta aca ttt gcc aag gca 192
Glu Val Glu Ala Asp Glu Val Gly Pro Ser Leu Thr Phe Ala Lys Ala
50 55 60
gat gtc cag cgc aca ccg cgc ggt gga aac tct ggc gga aac tac ggt 240
Asp Val Gln Arg Thr Pro Arg Gly Gly Asn Ser Gly Gly Asn Tyr Gly
65 70 75 80
ggc ggc aac caa ggt ggt ggc ctc ggt gga aac caa ggc aac cag caa 288
Gly Gly Asn Gln Gly Gly Gly Leu Gly Gly Asn Gln Gly Asn Gln Gln
85 90 95
ggt gga ttc agc aac cag aac tct ggc ggc ttc ggt gga aac caa ggc 336
Gly Gly Phe Ser Asn Gln Asn Ser Gly Gly Phe Gly Gly Asn Gln Gly
100 105 110
aac cag cag caa agc aac cag ggc gga ttt ggt gga aac caa aac cag 384
Asn Gln Gln Gln Ser Asn Gln Gly Gly Phe Gly Gly Asn Gln Asn Gln
115 120 125
tcc cag ggt aac aac ttc aac caa ggt gga ttt ggc gga ggc agc cca 432
Ser Gln Gly Asn Asn Phe Asn Gln Gly Gly Phe Gly Gly Gly Ser Pro
130 135 140
cag gca gca ccg gac aat gac cct tgg aat tct gca cca cca gct ggc 480
Gln Ala Ala Pro Asp Asn Asp Pro Trp Asn Ser Ala Pro Pro Ala Gly
145 150 155 160
tcc ggc ggg ttc ggc ggc gca gac gat gag cca ccg ttc taaagctttt 529
Ser Gly Gly Phe Gly Gly Ala Asp Asp Glu Pro Pro Phe
165 170
cttttctaaa aca 542

<210> 150
 <211> 173
 <212> PRT
 <213> Corynebacterium glutamicum

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 20 25 30
 Lys Gln Arg Ser Tyr Glu Thr Arg Glu Gly Glu Lys Arg Ser Val Phe
 35 40 45
 Glu Val Glu Ala Asp Glu Val Gly Pro Ser Leu Thr Phe Ala Lys Ala
 50 55 60
 Asp Val Gln Arg Thr Pro Arg Gly Gly Asn Ser Gly Gly Asn Tyr Gly
 65 70 75 80
 Gly Gly Asn Gln Gly Gly Gly Leu Gly Gly Asn Gln Gly Asn Gln Gln
 85 90 95
 Gly Gly Phe Ser Asn Gln Asn Ser Gly Gly Phe Gly Gly Asn Gln Gly
 100 105 110
 Asn Gln Gln Gln Ser Asn Gln Gly Gly Phe Gly Gly Asn Gln Asn Gln
 115 120 125
 Ser Gln Gly Asn Asn Phe Asn Gln Gly Gly Phe Gly Gly Gly Ser Pro
 130 135 140
 Gln Ala Ala Pro Asp Asn Asp Pro Trp Asn Ser Ala Pro Pro Ala Gly
 145 150 155 160
 Ser Gly Gly Phe Gly Gly Ala Asp Asp Glu Pro Pro Phe
 165 170

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> RXN02833

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 Leu Leu Glu Thr Trp
 1 5
 cgc caa gtt gtt gcc gat ctc aca act ttg agc cag caa gcg gac agt 163
 Arg Gln Val Val Ala Asp Leu Thr Thr Leu Ser Gln Gln Ala Asp Ser
 10 15 20

gga ttc gac cca ttg acg cca act caa cgt gca tat ttg aac ctg acg	211
Gly Phe Asp Pro Leu Thr Pro Thr Gln Arg Ala Tyr Leu Asn Leu Thr	
25 30 35	
aag ccg att gcc atc gtc gat ggc tac gcc gtg ctg tcc aca ccc aac	259
Lys Pro Ile Ala Ile Val Asp Gly Tyr Ala Val Leu Ser Thr Pro Asn	
40 45 50	
gcg atg gca aaa aat gtc att gaa aac gat ttg ggc gat gct ttg acc	307
Ala Met Ala Lys Asn Val Ile Glu Asn Asp Leu Gly Asp Ala Leu Thr	
55 60 65	
cgt gtg ttg tcg ctg cgc atg ggc cga tca ttc agc ttg gct gtc agt	355
Arg Val Leu Ser Leu Arg Met Gly Arg Ser Phe Ser Leu Ala Val Ser	
70 75 80 85	
gtg gag cct gag cag gaa att cca gaa acc cca gct cag cag gag ttt	403
Val Glu Pro Glu Gln Glu Ile Pro Glu Thr Pro Ala Gln Gln Glu Phe	
90 95 100	
aaa tat cag cct gac gca cct gtg atc tct tcc aac aag gcg cca aag	451
Lys Tyr Gln Pro Asp Ala Pro Val Ile Ser Ser Asn Lys Ala Pro Lys	
105 110 115	
cag tat gaa gtt ggt ggt cgg gga gag gcg tcg aca agc gac ggc tgg	499
Gln Tyr Glu Val Gly Gly Arg Gly Glu Ala Ser Thr Ser Asp Gly Trp	
120 125 130	
gaa cgt acc cac tct gca ccg gct ccc gag ccg cac ccg gca cct atc	547
Glu Arg Thr His Ser Ala Pro Ala Pro Glu Pro His Pro Ala Pro Ile	
135 140 145	
gcc gat cgt gag cca gag ctg gcc acc ccg cag cgc att ccg cgc gaa	595
Ala Asp Arg Glu Pro Glu Leu Ala Thr Pro Gln Arg Ile Pro Arg Glu	
150 155 160 165	
acc cca gct cac aac cct aat cgg gaa gtg tcc ctc aac ccg aaa tac	643
Thr Pro Ala His Asn Pro Asn Arg Glu Val Ser Leu Asn Pro Lys Tyr	
170 175 180	
act ttt gaa agc ttc gtg atc ggg ccg ttc aac cgt ttc gcc aat gca	691
Thr Phe Glu Ser Phe Val Ile Gly Pro Phe Asn Arg Phe Ala Asn Ala	
185 190 195	
gcc gca gtt gct gtg gcg gaa agc cca gcg aaa gct ttc aac ccg ctg	739
Ala Ala Val Ala Val Ala Glu Ser Pro Ala Lys Ala Phe Asn Pro Leu	
200 205 210	
ttt att tcc ggc ggt tcc ggc ttg ggc aaa act cac ctg ctg cac gca	787
Phe Ile Ser Gly Gly Ser Gly Leu Gly Lys Thr His Leu Leu His Ala	
215 220 225	
gta gga aat tat gct caa gaa ttg cag cct ggc ccg cgg att aag tac	835
Val Gly Asn Tyr Ala Gln Glu Leu Gln Pro Gly Pro Arg Ile Lys Tyr	
230 235 240 245	
gtc tca agt gag gaa tat cac caa cga cta cat caa ctc cgt gcg aga	883
Val Ser Ser Glu Glu Tyr His Gln Arg Leu His Gln Leu Arg Ala Arg	
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906

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<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 152

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 35 40 45

Leu Ser Thr Pro Asn Ala Met Ala Lys Asn Val Ile Glu Asn Asp Leu
 50 55 60

Gly Asp Ala Leu Thr Arg Val Leu Ser Leu Arg Met Gly Arg Ser Phe
 65 70 75 80

Ser Leu Ala Val Ser Val Glu Pro Glu Gln Glu Ile Pro Glu Thr Pro
 85 90 95

Ala Gln Gln Glu Phe Lys Tyr Gln Pro Asp Ala Pro Val Ile Ser Ser
 100 105 110

Asn Lys Ala Pro Lys Gln Tyr Glu Val Gly Gly Arg Gly Glu Ala Ser
 115 120 125

Thr Ser Asp Gly Trp Glu Arg Thr His Ser Ala Pro Ala Pro Glu Pro
 130 135 140

His Pro Ala Pro Ile Ala Asp Arg Glu Pro Glu Leu Ala Thr Pro Gln
 145 150 155 160

Arg Ile Pro Arg Glu Thr Pro Ala His Asn Pro Asn Arg Glu Val Ser
 165 170 175

Leu Asn Pro Lys Tyr Thr Phe Glu Ser Phe Val Ile Gly Pro Phe Asn
 180 185 190

Arg Phe Ala Asn Ala Ala Ala Val Ala Val Ala Glu Ser Pro Ala Lys
 195 200 205

Ala Phe Asn Pro Leu Phe Ile Ser Gly Gly Ser Gly Leu Gly Lys Thr
 210 215 220

His Leu Leu His Ala Val Gly Asn Tyr Ala Gln Glu Leu Gln Pro Gly
 225 230 235 240

Pro Arg Ile Lys Tyr Val Ser Ser Glu Glu Tyr His Gln Arg Leu His
 245 250 255

Gln Leu Arg Ala Arg
 260

0123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899

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 <223> FRXA02833

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 agt gtg gag cct gag cag gaa att cca aaa ccc cag ctc aag cag gag 96
 Ser Val Glu Pro Glu Gln Glu Ile Pro Lys Pro Gln Leu Lys Gln Glu
 20 25 30
 ttt aaa tat cag cct gac gca ctt gtg ttt tct tcc aac aag gcg cca 144
 Phe Lys Tyr Gln Pro Asp Ala Leu Val Phe Ser Ser Asn Lys Ala Pro
 35 40 45
 aag cag tat gaa gtt ggt ggt cgg gga gag gcg tcg aca agc gac ggt 192
 Lys Gln Tyr Glu Val Gly Gly Arg Gly Glu Ala Ser Thr Ser Asp Gly
 50 55 60
 tgg gaa ggt acc cac tct gca ccg gct ccc gag ccg cac ccg gca cct 240
 Trp Glu Gly Thr His Ser Ala Pro Ala Pro Glu Pro His Pro Ala Pro
 65 70 75 80
 atc gcc gat cgt gag cca gag ctg gcc acc ccg cag cgc att ccg cgc 288
 Ile Ala Asp Arg Glu Pro Glu Leu Ala Thr Pro Gln Arg Ile Pro Arg
 85 90 95
 gaa acc cca gct cac aac cct aat cgg gaa gtg tcc ctc aac ccg aaa 336
 Glu Thr Pro Ala His Asn Pro Asn Arg Glu Val Ser Leu Asn Pro Lys
 100 105 110
 tac act ttt gaa agc ttc gtg atc ggg ccg ttc aac cgt ttc gcc aat 384
 Tyr Thr Phe Glu Ser Phe Val Ile Gly Pro Phe Asn Arg Phe Ala Asn
 115 120 125
 gca gcc gca gtt gct gtg gcg gaa agc cca gcg aaa gct ttc aac ccg 432
 Ala Ala Ala Val Ala Val Ala Glu Ser Pro Ala Lys Ala Phe Asn Pro
 130 135 140
 ctg ttt att tcc ggc ggt tcc ggc ttg ggc aaa act cac ctg ctg cac 480
 Leu Phe Ile Ser Gly Gly Ser Gly Leu Gly Lys Thr His Leu Leu His
 145 150 155 160
 gca gta gga aat tat gct caa gaa ttg cag cct ggc ccg cgg att aag 528
 Ala Val Gly Asn Tyr Ala Gln Glu Leu Gln Pro Gly Pro Arg Ile Lys
 165 170 175
 tac gtc tca agt gag gaa tat cac caa cga cta cat caa ctc cgt gcg 576
 Tyr Val Ser Ser Glu Glu Tyr His Gln Arg Leu His Gln Leu Arg Ala
 180 185 190
 aga tgaccgccag gaaaccttca agc 602
 Arg

<210> 154
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 154
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Ser Val Glu Pro Glu Gln Glu Ile Pro Lys Pro Gln Leu Lys Gln Glu
20 25 30
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35 40 45
Lys Gln Tyr Glu Val Gly Gly Arg Gly Glu Ala Ser Thr Ser Asp Gly
50 55 60
Trp Glu Gly Thr His Ser Ala Pro Ala Pro Glu Pro His Pro Ala Pro
65 70 75 80
Ile Ala Asp Arg Glu Pro Glu Leu Ala Thr Pro Gln Arg Ile Pro Arg
85 90 95
Glu Thr Pro Ala His Asn Pro Asn Arg Glu Val Ser Leu Asn Pro Lys
100 105 110
Tyr Thr Phe Glu Ser Phe Val Ile Gly Pro Phe Asn Arg Phe Ala Asn
115 120 125
Ala Ala Ala Val Ala Val Ala Glu Ser Pro Ala Lys Ala Phe Asn Pro
130 135 140
Leu Phe Ile Ser Gly Gly Ser Gly Leu Gly Lys Thr His Leu Leu His
145 150 155 160
Ala Val Gly Asn Tyr Ala Gln Glu Leu Gln Pro Gly Pro Arg Ile Lys
165 170 175
Tyr Val Ser Ser Glu Glu Tyr His Gln Arg Leu His Gln Leu Arg Ala
180 185 190

Arg

<210> 155
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<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1993)
<223> RXA01480

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	Met Ala Lys Gly Arg	
	1 5	
att ccg gaa agt gac att cag gca atc cgc gag cgc acc ccg atc gag		163
Ile Pro Glu Ser Asp Ile Gln Ala Ile Arg Glu Arg Thr Pro Ile Glu		
	10 15 20	
gag atc gtg ggt gat tat gtg cag ctg aaa tcg gca ggt gct gat tcg		211
Glu Ile Val Gly Asp Tyr Val Gln Leu Lys Ser Ala Gly Ala Asp Ser		
	25 30 35	
ctc aag ggg ctt tct ccc ttt aaa gat gaa aaa aca cca tcg ttc cat		259
Leu Lys Gly Leu Ser Pro Phe Lys Asp Glu Lys Thr Pro Ser Phe His		
	40 45 50	
gtg cgc ccc aac cgt ggt tac tac cac tgt ttc tcc acc ggc aaa ggt		307
Val Arg Pro Asn Arg Gly Tyr Tyr His Cys Phe Ser Thr Gly Lys Gly		
	55 60 65	
gga gat gtg ttc tcc ttc ctc atg gag atg gaa cac atc tct ttc cct		355
Gly Asp Val Phe Ser Phe Leu Met Glu Met Glu His Ile Ser Phe Pro		
	70 75 80 85	
gag gct gtg gaa gtg tgt gcg gag aaa att ggt tat cag atc aat tac		403
Glu Ala Val Glu Val Cys Ala Glu Lys Ile Gly Tyr Gln Ile Asn Tyr		
	90 95 100	
caa ggt ggt ggc ccg ggg cgc cgt gag gaa cct gga act cgc cag cgc		451
Gln Gly Gly Gly Pro Gly Arg Arg Glu Glu Pro Gly Thr Arg Gln Arg		
	105 110 115	
ctt att ttg gct aat aag gct gcg cac cag ttt tat cgc gag caa tta		499
Leu Ile Leu Ala Asn Lys Ala Ala His Gln Phe Tyr Arg Glu Gln Leu		
	120 125 130	
gaa acc ccc gaa gca caa cct ggc agg gag ttt ttg ctg cag cgt gga		547
Glu Thr Pro Glu Ala Gln Pro Gly Arg Glu Phe Leu Leu Gln Arg Gly		
	135 140 145	
ttc gga cag cag cac att tat cat ttc gaa tgt ggc tat gcg cct gcc		595
Phe Gly Gln Gln His Ile Tyr His Phe Glu Cys Gly Tyr Ala Pro Ala		
	150 155 160 165	
ggc tgg gat acc ttg acc aag cat ttg ctg aag aag ggc ttt gag ttc		643
Gly Trp Asp Thr Leu Thr Lys His Leu Leu Lys Lys Gly Phe Glu Phe		
	170 175 180	
aag gaa tta gaa gct gcc ggt cta agc aag atg ggt aag cgc ggt ccg		691
Lys Glu Leu Glu Ala Ala Gly Leu Ser Lys Met Gly Lys Arg Gly Pro		
	185 190 195	
att gat cag ttc cag cgc agg ttg ctg tgg ccg atc aag aac ctg tct		739
Ile Asp Gln Phe Gln Arg Arg Leu Leu Trp Pro Ile Lys Asn Leu Ser		
	200 205 210	
ggt gat gtc att ggt ttt ggc gcc cgc aag ctt ttc gat gac gac aaa		787
Gly Asp Val Ile Gly Phe Gly Ala Arg Lys Leu Phe Asp Asp Asp Lys		
	215 220 225	

atg ggc aag tac atg aat acg cct gag acg ttg ttg tac aaa aag tcc	835
Met Gly Lys Tyr Met Asn Thr Pro Glu Thr Leu Leu Tyr Lys Lys Ser	
230 235 240 245	
aag gtg ctc ttt ggt cta gat tct gca aag aag gcc att gca gct ggc	883
Lys Val Leu Phe Gly Leu Asp Ser Ala Lys Lys Ala Ile Ala Ala Gly	
250 255 260	
cac caa gca gta gtg gtg gaa ggc tac acc gat gtg atg gcc atg cat	931
His Gln Ala Val Val Glu Gly Tyr Thr Asp Val Met Ala Met His	
265 270 275	
gcc gcg ggc att gat aca gcc gtg gca tcg tgt ggc act gcg ttt ggt	979
Ala Ala Gly Ile Asp Thr Ala Val Ala Ser Cys Gly Thr Ala Phe Gly	
280 285 290	
gaa gaa cac ttg cag atg ctt cgt cga ctc atg ctg gat gat aac tac	1027
Glu Glu His Leu Gln Met Leu Arg Arg Leu Met Leu Asp Asp Asn Tyr	
295 300 305	
ttc cgc ggt gaa ctg att tac acc ttc gat ggt gat gag gcc ggc cag	1075
Phe Arg Gly Glu Leu Ile Tyr Thr Phe Asp Gly Asp Glu Ala Gly Gln	
310 315 320 325	
aag gcc gcc atg cgt gcc ttt gag ggc gat cag aag ttc aca gga caa	1123
Lys Ala Ala Met Arg Ala Phe Glu Gly Asp Gln Lys Phe Thr Gly Gln	
330 335 340	
tca ttt gtg tct gtg gca ccc aac ggc atg gat ccg tgt gat ctg cgc	1171
Ser Phe Val Ser Val Ala Pro Asn Gly Met Asp Pro Cys Asp Leu Arg	
345 350 355	
ctt gag cgt ggc gat gcg gcg gtg cgt gat ctt gtg gca cga cgc atc	1219
Leu Glu Arg Gly Asp Ala Ala Val Arg Asp Leu Val Ala Arg Arg Ile	
360 365 370	
ccg atg ttt gag ttc gtc atc caa tcg atc atc agc gaa tac acc ctc	1267
Pro Met Phe Glu Phe Val Ile Gln Ser Ile Ile Ser Glu Tyr Thr Leu	
375 380 385	
gac acc gtg gaa ggc cgt ctg gct gcg ctt cgt cgg gca gtc ccc atc	1315
Asp Thr Val Glu Gly Arg Leu Ala Ala Leu Arg Arg Ala Val Pro Ile	
390 395 400 405	
gtg gcg gat att cgc gat aag acg ctg cag tct gaa tac gcc cgc ctg	1363
Val Ala Asp Ile Arg Asp Lys Thr Leu Gln Ser Glu Tyr Ala Arg Leu	
410 415 420	
ctg tct ggt tgg gtc ggc tgg tct gat cct tca gag gtg ctg cgt cag	1411
Leu Ser Gly Trp Val Gly Trp Ser Asp Pro Ser Glu Val Leu Arg Gln	
425 430 435	
gtt cac gag gaa gca cgt cgc ccc aag cgc gat aag aag cct gtg cgt	1459
Val His Glu Glu Ala Arg Arg Pro Lys Arg Asp Lys Lys Pro Val Arg	
440 445 450	
gca aag cgt ttc gat caa ccg ctc gag gat caa agc ctg cga ccc acc	1507
Ala Lys Arg Phe Asp Gln Pro Leu Glu Asp Gln Ser Leu Arg Pro Thr	
455 460 465	
atg gcg ctg cct aat ccg cgg aac cct gtg ctg tgg cag gaa cgg gaa	1555

Met Ala Leu Pro Asn Pro Arg Asn Pro Val Leu Trp Gln Glu Arg Glu
 470 475 480 485

tca ctc aag atc gcc ctg caa tat ccg gag ctc gcg gga tcg tac ttt 1603
 Ser Leu Lys Ile Ala Leu Gln Tyr Pro Glu Leu Ala Gly Ser Tyr Phe
 490 495 500

gat gga ctg cca acc gat agc ttc acc aac cct gcc tac cgc atg gta 1651
 Asp Gly Leu Pro Thr Asp Ser Phe Thr Asn Pro Ala Tyr Arg Met Val
 505 510 515

cgc gat gcc att tcg gct gct ggg gga tgt gaa cgt gcc ctc gat ggc 1699
 Arg Asp Ala Ile Ser Ala Ala Gly Gly Cys Glu Arg Ala Leu Asp Gly
 520 525 530

act gat tgg ttg cct gcc gta tcg gaa aat atg act gat att ttg ggc 1747
 Thr Asp Trp Leu Pro Ala Val Ser Glu Asn Met Thr Asp Ile Leu Gly
 535 540 545

acg tcg ttg gtg tca gag ctg gcg atg gaa ccc atc gag gtg gaa gcg 1795
 Thr Ser Leu Val Ser Glu Leu Ala Met Glu Pro Ile Glu Val Glu Ala
 550 555 560 565

caa gac ctg gaa tca tat acc gat ggt gtg ttg tcc agg ctg cag gaa 1843
 Gln Asp Leu Glu Ser Tyr Thr Asp Gly Val Leu Ser Arg Leu Gln Glu
 570 575 580

aca cga gtg ggc aac cag atc gcc atc ttg aaa gga cag ctg caa aga 1891
 Thr Arg Val Gly Asn Gln Ile Ala Ile Leu Lys Gly Gln Leu Gln Arg
 585 590 595

atg cgt ccg tct gaa gat gag caa gcc tac aac tcg ctg ttt tcc gat 1939
 Met Arg Pro Ser Glu Asp Glu Gln Ala Tyr Asn Ser Leu Phe Ser Asp
 600 605 610

ctg gtt gcc ctg gaa cag gcg cgc cgg gag ctg ttg gcc cgg gcg ttt 1987
 Leu Val Ala Leu Glu Gln Ala Arg Arg Glu Leu Leu Ala Arg Ala Phe
 615 620 625

aga ggg taatttagtc ctggtcttgc tcg 2016
 Arg Gly
 630

<210> 156

<211> 631

<212> PRT

<213> Corynebacterium glutamicum

<400> 156

Met Ala Lys Gly Arg Ile Pro Glu Ser Asp Ile Gln Ala Ile Arg Glu
 1 5 10 15

Arg Thr Pro Ile Glu Glu Ile Val Gly Asp Tyr Val Gln Leu Lys Ser
 20 25 30

Ala Gly Ala Asp Ser Leu Lys Gly Leu Ser Pro Phe Lys Asp Glu Lys
 35 40 45

Thr Pro Ser Phe His Val Arg Pro Asn Arg Gly Tyr Tyr His Cys Phe
 50 55 60

Ser Thr Gly Lys Gly Gly Asp Val Phe Ser Phe Leu Met Glu Met Glu
 65 70 75 80
 His Ile Ser Phe Pro Glu Ala Val Glu Val Cys Ala Glu Lys Ile Gly
 85 90 95
 Tyr Gln Ile Asn Tyr Gln Gly Gly Gly Pro Gly Arg Arg Glu Glu Pro
 100 105 110
 Gly Thr Arg Gln Arg Leu Ile Leu Ala Asn Lys Ala Ala His Gln Phe
 115 120 125
 Tyr Arg Glu Gln Leu Glu Thr Pro Glu Ala Gln Pro Gly Arg Glu Phe
 130 135 140
 Leu Leu Gln Arg Gly Phe Gly Gln Gln His Ile Tyr His Phe Glu Cys
 145 150 155 160
 Gly Tyr Ala Pro Ala Gly Trp Asp Thr Leu Thr Lys His Leu Leu Lys
 165 170 175
 Lys Gly Phe Glu Phe Lys Glu Leu Glu Ala Ala Gly Leu Ser Lys Met
 180 185 190
 Gly Lys Arg Gly Pro Ile Asp Gln Phe Gln Arg Arg Leu Leu Trp Pro
 195 200 205
 Ile Lys Asn Leu Ser Gly Asp Val Ile Gly Phe Gly Ala Arg Lys Leu
 210 215 220
 Phe Asp Asp Asp Lys Met Gly Lys Tyr Met Asn Thr Pro Glu Thr Leu
 225 230 235 240
 Leu Tyr Lys Lys Ser Lys Val Leu Phe Gly Leu Asp Ser Ala Lys Lys
 245 250 255
 Ala Ile Ala Ala Gly His Gln Ala Val Val Val Glu Gly Tyr Thr Asp
 260 265 270
 Val Met Ala Met His Ala Ala Gly Ile Asp Thr Ala Val Ala Ser Cys
 275 280 285
 Gly Thr Ala Phe Gly Glu Glu His Leu Gln Met Leu Arg Arg Leu Met
 290 295 300
 Leu Asp Asp Asn Tyr Phe Arg Gly Glu Leu Ile Tyr Thr Phe Asp Gly
 305 310 315 320
 Asp Glu Ala Gly Gln Lys Ala Ala Met Arg Ala Phe Glu Gly Asp Gln
 325 330 335
 Lys Phe Thr Gly Gln Ser Phe Val Ser Val Ala Pro Asn Gly Met Asp
 340 345 350
 Pro Cys Asp Leu Arg Leu Glu Arg Gly Asp Ala Ala Val Arg Asp Leu
 355 360 365
 Val Ala Arg Arg Ile Pro Met Phe Glu Phe Val Ile Gln Ser Ile Ile
 370 375 380

Ser Glu Tyr Thr Leu Asp Thr Val Glu Gly Arg Leu Ala Ala Leu Arg
 385 390 395 400
 Arg Ala Val Pro Ile Val Ala Asp Ile Arg Asp Lys Thr Leu Gln Ser
 405 410 415
 Glu Tyr Ala Arg Leu Leu Ser Gly Trp Val Gly Trp Ser Asp Pro Ser
 420 425 430
 Glu Val Leu Arg Gln Val His Glu Glu Ala Arg Arg Pro Lys Arg Asp
 435 440 445
 Lys Lys Pro Val Arg Ala Lys Arg Phe Asp Gln Pro Leu Glu Asp Gln
 450 455 460
 Ser Leu Arg Pro Thr Met Ala Leu Pro Asn Pro Arg Asn Pro Val Leu
 465 470 475 480
 Trp Gln Glu Arg Glu Ser Leu Lys Ile Ala Leu Gln Tyr Pro Glu Leu
 485 490 495
 Ala Gly Ser Tyr Phe Asp Gly Leu Pro Thr Asp Ser Phe Thr Asn Pro
 500 505 510
 Ala Tyr Arg Met Val Arg Asp Ala Ile Ser Ala Ala Gly Gly Cys Glu
 515 520 525
 Arg Ala Leu Asp Gly Thr Asp Trp Leu Pro Ala Val Ser Glu Asn Met
 530 535 540
 Thr Asp Ile Leu Gly Thr Ser Leu Val Ser Glu Leu Ala Met Glu Pro
 545 550 555 560
 Ile Glu Val Glu Ala Gln Asp Leu Glu Ser Tyr Thr Asp Gly Val Leu
 565 570 575
 Ser Arg Leu Gln Glu Thr Arg Val Gly Asn Gln Ile Ala Ile Leu Lys
 580 585 590
 Gly Gln Leu Gln Arg Met Arg Pro Ser Glu Asp Glu Gln Ala Tyr Asn
 595 600 605
 Ser Leu Phe Ser Asp Leu Val Ala Leu Glu Gln Ala Arg Arg Glu Leu
 610 615 620
 Leu Ala Arg Ala Phe Arg Gly
 625 630

<210> 157
 <211> 1597
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1597)
 <223> RXN03163

<400> 157
 gcactgattt ggaccttcct tgggaggcta tcgaccgcgt tgatgaactt cgcgcagccc 60

tcaagttggc ctaaaaatct gatgtagtat cttcggattc	atg gca aaa acc cgc	115
	Met Ala Lys Thr Arg	
	1 5	
gtc ccc gct cct gaa aag tcg gtg gcg cgg gtt tta cct ctt ttg ggg	163	
Val Pro Ala Pro Glu Lys Ser Val Ala Arg Val Leu Pro Leu Leu Gly		
	10 15 20	
tta cct cac ctg gat cga ctg ttt gat tac cgc atc agc gaa gac caa	211	
Leu Pro His Leu Asp Arg Leu Phe Asp Tyr Arg Ile Ser Glu Asp Gln		
	25 30 35	
cac gat gat gtg caa cct ggc gtg cgg gtg cgc gtg cgt ttt ggt gga	259	
His Asp Asp Val Gln Pro Gly Val Arg Val Arg Val Arg Phe Gly Gly		
	40 45 50	
cgt tta gtt gat gcc atc gtg atg tca cgc acc gcg caa acc tcg cac	307	
Arg Leu Val Asp Ala Ile Val Met Ser Arg Thr Ala Gln Thr Ser His		
	55 60 65	
gag gga aag ctg atg tgg ctg gat cgg gtg att tcg ccg atc gtg gtg	355	
Glu Gly Lys Leu Met Trp Leu Asp Arg Val Ile Ser Pro Ile Val Val		
	70 75 80 85	
tat cca cct caa aca gca aag cta att gag caa ctc agt gat cgc tat	403	
Tyr Pro Pro Gln Thr Ala Lys Leu Ile Glu Gln Leu Ser Asp Arg Tyr		
	90 95 100	
ggc ggg gta cgt tcg gat ctc atc cgt tcg gcg cta ccg gcg cgg cat	451	
Gly Gly Val Arg Ser Asp Leu Ile Arg Ser Ala Leu Pro Ala Arg His		
	105 110 115	
gct ggg gca gaa gag gca gat acc tcc acg tcg tgg gag tca ttg ggt	499	
Ala Gly Ala Glu Glu Ala Asp Thr Ser Thr Ser Trp Glu Ser Leu Gly		
	120 125 130	
gag gtt aaa gaa ccc gat tta tcg tcg tgg tct gcg tat cag cat ggt	547	
Glu Val Lys Glu Pro Asp Leu Ser Ser Trp Ser Ala Tyr Gln His Gly		
	135 140 145	
caa tca ttt gtt gac gcc gtc ttg gcg gga aca act gcg cgg gcg tca	595	
Gln Ser Phe Val Asp Ala Val Leu Ala Gly Thr Thr Ala Arg Ala Ser		
	150 155 160 165	
tgg cag att gct ccc gga gat gat tgg gcg ctg gct ttg gct tct ttg	643	
Trp Gln Ile Ala Pro Gly Asp Asp Trp Ala Leu Ala Leu Ala Ser Leu		
	170 175 180	
gcg gtc aag gtt gtc aaa gac ggc ggc gga gcg ctt ctc gta gtg cct	691	
Ala Val Lys Val Val Lys Asp Gly Gly Gly Ala Leu Leu Val Val Pro		
	185 190 195	
gat cag cgc gat ctc gac cgc ttg gaa gct gcg ctt cga ggt ttg gtt	739	
Asp Gln Arg Asp Leu Asp Arg Leu Glu Ala Ala Leu Arg Gly Leu Val		
	200 205 210	
gcg gcg aaa caa atc act gtg ctt aat tca ggt ctt ggt ccg cag gca	787	
Ala Ala Lys Gln Ile Thr Val Leu Asn Ser Gly Leu Gly Pro Gln Ala		
	215 220 225	

cga tat cgg cgt ttc cta tcg gta ctc agt ggg cag gga cga ctg att	835
Arg Tyr Arg Arg Phe Leu Ser Val Leu Ser Gly Gln Gly Arg Leu Ile	
230 235 240 245	
att gga acc aga agt gcc gct ttt gca ccc gtg aag gat ctg aaa ctg	883
Ile Gly Thr Arg Ser Ala Ala Phe Ala Pro Val Lys Asp Leu Lys Leu	
250 255 260	
gcc gtc att tta aat gat ggc gac gac aac ctc gtt gat cct aga gcg	931
Ala Val Ile Leu Asn Asp Gly Asp Asp Asn Leu Val Asp Pro Arg Ala	
265 270 275	
ccc tat gcc cac gcc agg gaa gtg ctg acc acg cgt tcc agt ttg gaa	979
Pro Tyr Ala His Ala Arg Glu Val Leu Thr Thr Arg Ser Ser Leu Glu	
280 285 290	
gca agc tcc ttg att att gcg gga cat gcg cgg acc gcg gaa acc caa	1027
Ala Ser Ser Leu Ile Ile Ala Gly His Ala Arg Thr Ala Glu Thr Gln	
295 300 305	
ttg ctg gtg gaa tcg gga tgg atg cac aat ctc atc gca ccg agg gat	1075
Leu Leu Val Glu Ser Gly Trp Met His Asn Leu Ile Ala Pro Arg Asp	
310 315 320 325	
acc att cgc act agg atg ccg cgt att cag gca gtg ggc gat tcc gat	1123
Thr Ile Arg Thr Arg Met Pro Arg Ile Gln Ala Val Gly Asp Ser Asp	
330 335 340	
ttc cag atg gaa cgc gat cca atg gcc cga tca gcg cgg ctg cct ggc	1171
Phe Gln Met Glu Arg Asp Pro Met Ala Arg Ser Ala Arg Leu Pro Gly	
345 350 355	
att gcg ttt cat gcg gtg cgc agc gcc tta gaa cgt gat caa cca gcg	1219
Ile Ala Phe His Ala Val Arg Ser Ala Leu Glu Arg Asp Gln Pro Ala	
360 365 370	
ctt atc cag gta cca agg aaa ggc tac gtg cca acc ttg gcg tgt gga	1267
Leu Ile Gln Val Pro Arg Lys Gly Tyr Val Pro Thr Leu Ala Cys Gly	
375 380 385	
aac tgc cgc acc cca gcg cgg tgc cgg cac tgt aat ggg cct gtg gga	1315
Asn Cys Arg Thr Pro Ala Arg Cys Arg His Cys Asn Gly Pro Val Gly	
390 395 400 405	
ctt ccc cag gga agc tct gat cta gcg gga gtg ccc act tgc cga tgg	1363
Leu Pro Gln Gly Ser Ser Asp Leu Ala Gly Val Pro Thr Cys Arg Trp	
410 415 420	
tgc gga cgc cct gat tcg cgg ttt aag tgc caa aac tgc ggc tct cca	1411
Cys Gly Arg Pro Asp Ser Arg Phe Lys Cys Gln Asn Cys Gly Ser Pro	
425 430 435	
aaa ctg cgt gct gtg gtg ctg gga acg gaa cgc aca gca gaa gaa ctg	1459
Lys Leu Arg Ala Val Val Leu Gly Thr Glu Arg Thr Ala Glu Glu Leu	
440 445 450	
ggc cgc gcg ttc ccg tct gtg cgg gta att acc tct ggt ggc aac aag	1507
Gly Arg Ala Phe Pro Ser Val Arg Val Ile Thr Ser Gly Gly Asn Lys	
455 460 465	
gtg gtg gat tcg gtg gaa aac cga gcc agc att gtg gtg tcc acg cca	1555

Val Val Asp Ser Val Glu Asn Arg Ala Ser Ile Val Val Ser Thr Pro
470 475 480 485

ggt gca gaa cct ttt gtg gcc aac tcg ccg gag aga cca gag
Gly Ala Glu Pro Phe Val Ala Asn Ser Pro Glu Arg Pro Glu
490 495

1597

<210> 158

<211> 499

<212> PRT

<213> Corynebacterium glutamicum

<400> 158

Met Ala Lys Thr Arg Val Pro Ala Pro Glu Lys Ser Val Ala Arg Val
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Leu Pro Leu Leu Gly Leu Pro His Leu Asp Arg Leu Phe Asp Tyr Arg
20 25 30

Ile Ser Glu Asp Gln His Asp Asp Val Gln Pro Gly Val Arg Val Arg
35 40 45

Val Arg Phe Gly Gly Arg Leu Val Asp Ala Ile Val Met Ser Arg Thr
50 55 60

Ala Gln Thr Ser His Glu Gly Lys Leu Met Trp Leu Asp Arg Val Ile
65 70 75 80

Ser Pro Ile Val Val Tyr Pro Pro Gln Thr Ala Lys Leu Ile Glu Gln
85 90 95

Leu Ser Asp Arg Tyr Gly Gly Val Arg Ser Asp Leu Ile Arg Ser Ala
100 105 110

Leu Pro Ala Arg His Ala Gly Ala Glu Glu Ala Asp Thr Ser Thr Ser
115 120 125

Trp Glu Ser Leu Gly Glu Val Lys Glu Pro Asp Leu Ser Ser Trp Ser
130 135 140

Ala Tyr Gln His Gly Gln Ser Phe Val Asp Ala Val Leu Ala Gly Thr
145 150 155 160

Thr Ala Arg Ala Ser Trp Gln Ile Ala Pro Gly Asp Asp Trp Ala Leu
165 170 175

Ala Leu Ala Ser Leu Ala Val Lys Val Val Lys Asp Gly Gly Gly Ala
180 185 190

Leu Leu Val Val Pro Asp Gln Arg Asp Leu Asp Arg Leu Glu Ala Ala
195 200 205

Leu Arg Gly Leu Val Ala Ala Lys Gln Ile Thr Val Leu Asn Ser Gly
210 215 220

Leu Gly Pro Gln Ala Arg Tyr Arg Arg Phe Leu Ser Val Leu Ser Gly
225 230 235 240

Gln Gly Arg Leu Ile Ile Gly Thr Arg Ser Ala Ala Phe Ala Pro Val
245 250 255

Lys Asp Leu Lys Leu Ala Val Ile Leu Asn Asp Gly Asp Asp Asn Leu
 260 265 270
 Val Asp Pro Arg Ala Pro Tyr Ala His Ala Arg Glu Val Leu Thr Thr
 275 280 285
 Arg Ser Ser Leu Glu Ala Ser Ser Leu Ile Ile Ala Gly His Ala Arg
 290 295 300
 Thr Ala Glu Thr Gln Leu Leu Val Glu Ser Gly Trp Met His Asn Leu
 305 310 315 320
 Ile Ala Pro Arg Asp Thr Ile Arg Thr Arg Met Pro Arg Ile Gln Ala
 325 330 335
 Val Gly Asp Ser Asp Phe Gln Met Glu Arg Asp Pro Met Ala Arg Ser
 340 345 350
 Ala Arg Leu Pro Gly Ile Ala Phe His Ala Val Arg Ser Ala Leu Glu
 355 360 365
 Arg Asp Gln Pro Ala Leu Ile Gln Val Pro Arg Lys Gly Tyr Val Pro
 370 375 380
 Thr Leu Ala Cys Gly Asn Cys Arg Thr Pro Ala Arg Cys Arg His Cys
 385 390 395 400
 Asn Gly Pro Val Gly Leu Pro Gln Gly Ser Ser Asp Leu Ala Gly Val
 405 410 415
 Pro Thr Cys Arg Trp Cys Gly Arg Pro Asp Ser Arg Phe Lys Cys Gln
 420 425 430
 Asn Cys Gly Ser Pro Lys Leu Arg Ala Val Val Leu Gly Thr Glu Arg
 435 440 445
 Thr Ala Glu Glu Leu Gly Arg Ala Phe Pro Ser Val Arg Val Ile Thr
 450 455 460
 Ser Gly Gly Asn Lys Val Val Asp Ser Val Glu Asn Arg Ala Ser Ile
 465 470 475 480
 Val Val Ser Thr Pro Gly Ala Glu Pro Phe Val Ala Asn Ser Pro Glu
 485 490 495
 Arg Pro Glu

<210> 159
 <211> 2151
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(2128)
 <223> FRXA02241

 <400> 159

gcgttgatga acttcgcgca gccctcaagt tggcctaaaa atctgatgta gtatcttcgg 60

attcatggca aaaacccgcg tccccgctcc tgaaaagtgcg gtg gcg cgg gtt tta 115
Val Ala Arg Val Leu
1 5

cct ctt ttg ggg tta cct cac ctg gat cga ctg ttt gat tac cgc atc 163
Pro Leu Leu Gly Leu Pro His Leu Asp Arg Leu Phe Asp Tyr Arg Ile
10 15 20

agc gaa gac caa cac gat gat gtg caa cct ggc gtg cgg gtg cgc gtg 211
Ser Glu Asp Gln His Asp Asp Val Gln Pro Gly Val Arg Val Arg Val
25 30 35

cgt ttt ggt gga cgt tta gtt gat gcc atc gtg atg tca cgc acc gcg 259
Arg Phe Gly Gly Arg Leu Val Asp Ala Ile Val Met Ser Arg Thr Ala
40 45 50

caa acc tcg cac gag gga aag ctg atg tgg ctg gat cgg gtg att tcg 307
Gln Thr Ser His Glu Gly Lys Leu Met Trp Leu Asp Arg Val Ile Ser
55 60 65

ccg atc gtg gtg tat cca cct caa aca gca aag cta att gag caa ctc 355
Pro Ile Val Val Tyr Pro Pro Gln Thr Ala Lys Leu Ile Glu Gln Leu
70 75 80 85

agt gat cgc tat ggc ggg gta cgt tcg gat ctc atc cgt tcg gcg cta 403
Ser Asp Arg Tyr Gly Gly Val Arg Ser Asp Leu Ile Arg Ser Ala Leu
90 95 100

ccg gcg cgg cat gct ggg gca gaa gag gca gat acc tcc acg tcg tgg 451
Pro Ala Arg His Ala Gly Ala Glu Glu Ala Asp Thr Ser Thr Ser Trp
105 110 115

gag tca ttg ggt gag gtt aaa gaa ccc gat tta tcg tcg tgg tct gcg 499
Glu Ser Leu Gly Glu Val Lys Glu Pro Asp Leu Ser Ser Trp Ser Ala
120 125 130

tat cag cat ggt caa tca ttt gtt gac gcc gtc ttg gcg gga aca act 547
Tyr Gln His Gly Gln Ser Phe Val Asp Ala Val Leu Ala Gly Thr Thr
135 140 145

gcg cgg gcg tca tgg cag att gct ccc gga gat gat tgg gcg ctg gct 595
Ala Arg Ala Ser Trp Gln Ile Ala Pro Gly Asp Asp Trp Ala Leu Ala
150 155 160 165

ttg gct tct ttg gcg gtc aag gtt gtc aaa gac ggc ggc gga gcg ctt 643
Leu Ala Ser Leu Ala Val Lys Val Val Lys Asp Gly Gly Gly Ala Leu
170 175 180

ctc gta gtg cct gat cag cgc gat ctc gac cgc ttg gaa gct gcg ctt 691
Leu Val Val Pro Asp Gln Arg Asp Leu Asp Arg Leu Glu Ala Ala Leu
185 190 195

cga ggt ttg gtt gcg gcg aaa caa atc act gtg ctt aat tca ggt ctt 739
Arg Gly Leu Val Ala Ala Lys Gln Ile Thr Val Leu Asn Ser Gly Leu
200 205 210

ggt ccg cag gca cga tat cgg cgt ttc cta tcg gta ctc agt ggg cag 787
Gly Pro Gln Ala Arg Tyr Arg Arg Phe Leu Ser Val Leu Ser Gly Gln
215 220 225

gga cga ctg att att gga acc aga agt gcc gct ttt gca ccc gtg aag	835
Gly Arg Leu Ile Ile Gly Thr Arg Ser Ala Ala Phe Ala Pro Val Lys	
230 235 240 245	
gat ctg aaa ctg gcc gtc att tta aat gat ggc gac gac aac ctc gtt	883
Asp Leu Lys Leu Ala Val Ile Leu Asn Asp Gly Asp Asp Asn Leu Val	
250 255 260	
gat cct aga gcg ccc tat gcc cac gcc agg gaa gtg ctg acc acg cgt	931
Asp Pro Arg Ala Pro Tyr Ala His Ala Arg Glu Val Leu Thr Thr Arg	
265 270 275	
tcc agt ttg gaa gca agc tcc ttg att att gcg gga cat gcg cgg acc	979
Ser Ser Leu Glu Ala Ser Ser Leu Ile Ile Ala Gly His Ala Arg Thr	
280 285 290	
gcg gaa acc caa ttg ctg gtg gaa tcg gga tgg atg cac aat ctc atc	1027
Ala Glu Thr Gln Leu Leu Val Glu Ser Gly Trp Met His Asn Leu Ile	
295 300 305	
gca ccg agg gat acc att cgc act agg atg ccg cgt att cag gca gtg	1075
Ala Pro Arg Asp Thr Ile Arg Thr Arg Met Pro Arg Ile Gln Ala Val	
310 315 320 325	
ggc gat tcc gat ttc cag atg gaa cgc gat cca atg gcc cga tca gcg	1123
Gly Asp Ser Asp Phe Gln Met Glu Arg Asp Pro Met Ala Arg Ser Ala	
330 335 340	
cgg ctg cct ggc att gcg ttt cat gcg gtg cgc agc gcc tta gaa cgt	1171
Arg Leu Pro Gly Ile Ala Phe His Ala Val Arg Ser Ala Leu Glu Arg	
345 350 355	
gat caa cca gcg ctt atc cag gta cca agg aaa ggc tac gtg cca acc	1219
Asp Gln Pro Ala Leu Ile Gln Val Pro Arg Lys Gly Tyr Val Pro Thr	
360 365 370	
ttg gcg tgt gga aac tgc cgc acc cca gcg cgg tgc cgg cac tgt aat	1267
Leu Ala Cys Gly Asn Cys Arg Thr Pro Ala Arg Cys Arg His Cys Asn	
375 380 385	
ggg cct gtg gga ctt ccc cag gga agc tct gat cta gcg gga gtg ccc	1315
Gly Pro Val Gly Leu Pro Gln Gly Ser Ser Asp Leu Ala Gly Val Pro	
390 395 400 405	
act tgc cga tgg tgc gga cgc cct gat tcg cgg ttt aag tgc caa aac	1363
Thr Cys Arg Trp Cys Gly Arg Pro Asp Ser Arg Phe Lys Cys Gln Asn	
410 415 420	
tgc ggc tct cca aaa ctg cgt gct gtg gtg ctg gga acg gaa cgc aca	1411
Cys Gly Ser Pro Lys Leu Arg Ala Val Val Leu Gly Thr Glu Arg Thr	
425 430 435	
gca gaa gaa ctg ggc cgc gcg ttc ccg tct gtg cgg gta att acc tct	1459
Ala Glu Glu Leu Gly Arg Ala Phe Pro Ser Val Arg Val Ile Thr Ser	
440 445 450	
ggg ggc aac aag gtg gtg gat tcg gtg gaa aac cga gcc agc att gtg	1507
Gly Gly Asn Lys Val Val Asp Ser Val Glu Asn Arg Ala Ser Ile Val	
455 460 465	

gtg tcc acg cca ggt gca gaa cct ttt gtg gcc aac tcg ccg gag aga	1555
Val Ser Thr Pro Gly Ala Glu Pro Phe Val Ala Asn Ser Pro Glu Arg	
470 475 480 485	
cca gag aaa tcg gag aaa cca gag cac aag ggc gct tac ggt gcc ttg	1603
Pro Glu Lys Ser Glu Lys Pro Glu His Lys Gly Ala Tyr Gly Ala Leu	
490 495 500	
tta ttg ctg gat acc tgg gcg ttg atg ggt cgg caa gat ctg cgc gcc	1651
Leu Leu Leu Asp Thr Trp Ala Leu Met Gly Arg Gln Asp Leu Arg Ala	
505 510 515	
atg gag gac gcg ctg cac aag tgg gca gcg gcg gcc acg ctg gtg cat	1699
Met Glu Asp Ala Leu His Lys Trp Ala Ala Ala Ala Thr Leu Val His	
520 525 530	
tct cat ctg cac cag ggt caa gtc atc gtg gtt gca gat cca tcg ttt	1747
Ser His Leu His Gln Gly Gln Val Ile Val Val Ala Asp Pro Ser Phe	
535 540 545	
cct gct gtg caa tcg ttg att cgg tgg gat atg gca ggt gct gca gcg	1795
Pro Ala Val Gln Ser Leu Ile Arg Trp Asp Met Ala Gly Ala Ala Ala	
550 555 560 565	
caa gag ttg gct agc cga cgc gag gtt atg ttc ccg cct tct gta cac	1843
Gln Glu Leu Ala Ser Arg Arg Glu Val Met Phe Pro Pro Ser Val His	
570 575 580	
atg gca gca atc gat ggg gct acc gct gca ttg gaa agt ttc ttg gat	1891
Met Ala Ala Ile Asp Gly Ala Thr Ala Ala Leu Glu Ser Phe Leu Asp	
585 590 595	
ttg gcg gag ctt ccc gat cat gct gaa gtc ctc ggc cct gtt gat ctg	1939
Leu Ala Glu Leu Pro Asp His Ala Glu Val Leu Gly Pro Val Asp Leu	
600 605 610	
cca ccg ggt gtg agt ttg cct ggt gaa tat gat gag cag cgc ttt ggt	1987
Pro Pro Gly Val Ser Leu Pro Gly Glu Tyr Asp Glu Gln Arg Phe Gly	
615 620 625	
ccg ccg cag cgc ctt ctc atc aga act cca ttg gga ccg ccg tct gag	2035
Pro Pro Gln Arg Leu Leu Ile Arg Thr Pro Leu Gly Pro Arg Ser Glu	
630 635 640 645	
ttg ggt aga gcg ctg cgc tca gcc cag gtg gcg cgt gcg gtg agg aag	2083
Leu Gly Arg Ala Leu Arg Ser Ala Gln Val Ala Arg Ala Val Arg Lys	
650 655 660	
aat gat ttg ccg ttg cgt att cag atg gat ccg att cac atc gga	2128
Asn Asp Leu Pro Leu Arg Ile Gln Met Asp Pro Ile His Ile Gly	
665 670 675	
taaaactgct ggtgaaaggc cta	2151

<210> 160

<211> 676

<212> PRT

<213> Corynebacterium glutamicum

<400> 160

Val Ala Arg Val Leu Pro Leu Leu Gly Leu Pro His Leu Asp Arg Leu
 1 5 10 15
 Phe Asp Tyr Arg Ile Ser Glu Asp Gln His Asp Asp Val Gln Pro Gly
 20 25 30
 Val Arg Val Arg Val Arg Phe Gly Gly Arg Leu Val Asp Ala Ile Val
 35 40 45
 Met Ser Arg Thr Ala Gln Thr Ser His Glu Gly Lys Leu Met Trp Leu
 50 55 60
 Asp Arg Val Ile Ser Pro Ile Val Val Tyr Pro Pro Gln Thr Ala Lys
 65 70 75 80
 Leu Ile Glu Gln Leu Ser Asp Arg Tyr Gly Gly Val Arg Ser Asp Leu
 85 90 95
 Ile Arg Ser Ala Leu Pro Ala Arg His Ala Gly Ala Glu Glu Ala Asp
 100 105 110
 Thr Ser Thr Ser Trp Glu Ser Leu Gly Glu Val Lys Glu Pro Asp Leu
 115 120 125
 Ser Ser Trp Ser Ala Tyr Gln His Gly Gln Ser Phe Val Asp Ala Val
 130 135 140
 Leu Ala Gly Thr Thr Ala Arg Ala Ser Trp Gln Ile Ala Pro Gly Asp
 145 150 155 160
 Asp Trp Ala Leu Ala Leu Ala Ser Leu Ala Val Lys Val Val Lys Asp
 165 170 175
 Gly Gly Gly Ala Leu Leu Val Val Pro Asp Gln Arg Asp Leu Asp Arg
 180 185 190
 Leu Glu Ala Ala Leu Arg Gly Leu Val Ala Ala Lys Gln Ile Thr Val
 195 200 205
 Leu Asn Ser Gly Leu Gly Pro Gln Ala Arg Tyr Arg Arg Phe Leu Ser
 210 215 220
 Val Leu Ser Gly Gln Gly Arg Leu Ile Ile Gly Thr Arg Ser Ala Ala
 225 230 235 240
 Phe Ala Pro Val Lys Asp Leu Lys Leu Ala Val Ile Leu Asn Asp Gly
 245 250 255
 Asp Asp Asn Leu Val Asp Pro Arg Ala Pro Tyr Ala His Ala Arg Glu
 260 265 270
 Val Leu Thr Thr Arg Ser Ser Leu Glu Ala Ser Ser Leu Ile Ile Ala
 275 280 285
 Gly His Ala Arg Thr Ala Glu Thr Gln Leu Leu Val Glu Ser Gly Trp
 290 295 300
 Met His Asn Leu Ile Ala Pro Arg Asp Thr Ile Arg Thr Arg Met Pro
 305 310 315 320
 Arg Ile Gln Ala Val Gly Asp Ser Asp Phe Gln Met Glu Arg Asp Pro

335

Gly Pro Arg Ser Glu Leu Gly Arg Ala Leu Arg Ser Ala Gln Val Ala
645 650 655

Arg Ala Val Arg Lys Asn Asp Leu Pro Leu Arg Ile Gln Met Asp Pro
 660 665 670

Ile His Ile Gly
 675

<210> 161
 <211> 2790
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2767)
 <223> RXN00061

<400> 161
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 atgtgtcgtc aattttttcca ctgcctaca ctcgaggagc gtg act gag aag act 115
 Val Thr Glu Lys Thr
 1 5
 gac cag acc tta atg ctt atc gac ggc cac tcg atg gct ttc cgc gca 163
 Asp Gln Thr Leu Met Leu Ile Asp Gly His Ser Met Ala Phe Arg Ala
 10 15 20
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 Phe Phe Ala Leu Pro Ala Glu Asn Phe Ser Thr Ser Gly Gly Gln Ala
 25 30 35
 acc aat gct gtc tat ggc ttt ctc tcg atg ctg tcc acg ttg ttg aag 259
 Thr Asn Ala Val Tyr Gly Phe Leu Ser Met Leu Ser Thr Leu Leu Lys
 40 45 50
 gat gag cag cct act cat gtg gcg gtg gct ttc gat gtg ggg cgt aag 307
 Asp Glu Gln Pro Thr His Val Ala Val Ala Phe Asp Val Gly Arg Lys
 55 60 65
 acg ttc cgt acc gat atg ttc ccg gcg tat aag gcg cag cgt gaa gca 355
 Thr Phe Arg Thr Asp Met Phe Pro Ala Tyr Lys Ala Gln Arg Glu Ala
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 acg cca cct gag ttt aag ggc cag gtg gaa atc ctc aag gag gtg ttg 403
 Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile Leu Lys Glu Val Leu
 90 95 100
 tcc act ttg gga att acg act att gag aaa atc gat ttt gag gct gat 451
 Ser Thr Leu Gly Ile Thr Thr Ile Glu Lys Ile Asp Phe Glu Ala Asp
 105 110 115
 gat gtg atc gcc acg ttg tct gtg gcg gcg aaa cct tta ggc ttt aag 499
 Asp Val Ile Ala Thr Leu Ser Val Ala Ala Lys Pro Leu Gly Phe Lys
 120 125 130
 acg ctg att gtt acg ggt gac cgt gat tcc ttc cag ttg gtc aat gac 547
 Thr Leu Ile Val Thr Gly Asp Arg Asp Ser Phe Gln Leu Val Asn Asp
 135 140 145

acc acc acg gtg ttg tat ccg atg aag ggc gtg tct gtg ctg cac cgt	595
Thr Thr Thr Val Leu Tyr Pro Met Lys Gly Val Ser Val Leu His Arg	
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Phe Thr Pro Glu Ala Val Glu Glu Lys Tyr Gly Leu Thr Pro Arg Gln	
170 175 180	
tat ccg gag ttt gca gcg ctg cgt ggt gat cct tcc gat aac ttg cct	691
Tyr Pro Glu Phe Ala Ala Leu Arg Gly Asp Pro Ser Asp Asn Leu Pro	
185 190 195	
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Asn Ile Pro Gly Val Gly Glu Lys Thr Ala Thr Lys Trp Ile Ala Gln	
200 205 210	
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Tyr Glu Thr Leu Asp Asn Leu Leu Asp His Ala Asp Glu Ile Lys Gly	
215 220 225	
aag gtt ggc gcc agc ctg cgt gag cgc att gag cag gtc cgg atg aac	835
Lys Val Gly Ala Ser Leu Arg Glu Arg Ile Glu Gln Val Arg Met Asn	
230 235 240 245	
cgc aag ctc acg gag atg gtg aag gat ctg gag ctg ccg ctt ggt ccg	883
Arg Lys Leu Thr Glu Met Val Lys Asp Leu Glu Leu Pro Leu Gly Pro	
250 255 260	
gac gat ttt gag atg aag cct gtg cag gtt gcg gag gtt gcg gcg aag	931
Asp Asp Phe Glu Met Lys Pro Val Gln Val Ala Glu Val Ala Ala Lys	
265 270 275	
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Phe Asp Asp Leu Glu Phe Gly Thr Asn Leu Arg Glu Arg Val Leu Ala	
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Val Val Lys Ala Glu Gly Ser Ala Ala Pro Val Glu Glu Val Glu Ala	
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Glu Gln Val Val Val Asp Thr Gln Ser Leu Ala Gln Trp Leu Pro Ala	
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Arg Ala Gly Gln Ala Leu Ala Leu Ala Leu Ala Gly Val Ala Lys Pro	
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Ala Ala Gly Asp Thr Tyr Ala Leu Ala Ile Ala Asp Thr Lys Arg His	
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Ala Val Leu Val Asp Val Ala Asp Ile Ser Ala Glu Asp Glu Lys Ala	
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Leu Ala Thr Trp Leu Ala Ser Glu Asp Pro Lys Met Leu His Gly Ala	
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Lys	Ala	Ala	Tyr	His	Met	Leu	Ala	Gly	Arg	Gly	Phe	Glu	Leu	His	Gly			
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Val	Val	His	Asp	Thr	Ala	Ile	Ala	Ala	Tyr	Leu	Leu	Arg	Pro	Gly	Gln			
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cgc	acc	tat	gag	ctt	gcc	gac	gtc	tac	cag	cgg	cat	ctt	caa	cga	cag		1411	
Arg	Thr	Tyr	Glu	Leu	Ala	Asp	Val	Tyr	Gln	Arg	His	Leu	Gln	Arg	Gln			
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Leu	Ser	Thr	Asn	Asp	Asn	Gly	Gly	Gln	Leu	Thr	Leu	Leu	Asp	Ala	Ala			
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gat	gac	caa	tcg	ctt	gtt	gat	gat	gtc	att	gca	atc	ctt	gag	ctg	tct		1507	
Asp	Asp	Gln	Ser	Leu	Val	Asp	Asp	Val	Ile	Ala	Ile	Leu	Glu	Leu	Ser			
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gaa	gaa	ttg	acc	aaa	cag	ctt	cag	gag	att	caa	gct	ttt	gag	ctt	tac		1555	
Glu	Glu	Leu	Thr	Lys	Gln	Leu	Gln	Glu	Ile	Gln	Ala	Phe	Glu	Leu	Tyr			
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cat	gac	ctg	gaa	att	ccg	ctg	tcg	gga	att	ctg	gcg	cgc	atg	gag	gcc		1603	
His	Asp	Leu	Glu	Ile	Pro	Leu	Ser	Gly	Ile	Leu	Ala	Arg	Met	Glu	Ala			
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atc	ggt	atc	gct	gtt	gat	gtt	gcc	act	ttg	gaa	gag	cag	ttg	aag	act		1651	
Ile	Gly	Ile	Ala	Val	Asp	Val	Ala	Thr	Leu	Glu	Glu	Gln	Leu	Lys	Thr			
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ttc	att	ggt	cag	gtt	gct	cag	gaa	gag	gaa	gca	gct	cgc	gag	ctc	gct		1699	
Phe	Ile	Gly	Gln	Val	Ala	Gln	Glu	Glu	Glu	Ala	Ala	Arg	Glu	Leu	Ala			
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gag	gat	cca	acc	ctg	aat	ctc	tcg	agc	ccg	aag	cag	ctg	caa	gtg	gtg		1747	
Glu	Asp	Pro	Thr	Leu	Asn	Leu	Ser	Ser	Pro	Lys	Gln	Leu	Gln	Val	Val			
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ctt	ttt	gag	acg	ttc	gga	atg	ccg	aaa	acc	aag	aaa	acc	aag	acc	ggc		1795	
Leu	Phe	Glu	Thr	Phe	Gly	Met	Pro	Lys	Thr	Lys	Lys	Thr	Lys	Thr	Gly			
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tac	tct	acg	gct	gcc	gcg	gaa	att	gaa	gcc	cta	gcg	atc	aag	aat	ccg		1843	
Tyr	Ser	Thr	Ala	Ala	Ala	Glu	Ile	Glu	Ala	Leu	Ala	Ile	Lys	Asn	Pro			
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cac	cca	ttc	cta	gat	cac	ctg	ttg	gca	cac	cgt	cag	tac	caa	aag	atg		1891	
His	Pro	Phe	Leu	Asp	His	Leu	Leu	Ala	His	Arg	Gln	Tyr	Gln	Lys	Met			
				585				590						595				
aag	acc	act	ctg	gaa	ggt	ctc	atc	cgt	gag	gtg	gct	cct	gat	ggc	cgt		1939	
Lys	Thr	Thr	Leu	Glu	Gly	Leu	Ile	Arg	Glu	Val	Ala	Pro	Asp	Gly	Arg			
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att	cac	acc	acc	ttc	aac	cag	acg	gtg	gcg	tct	acg	gga	cgt	ttg	tca		1987	
Ile	His	Thr	Thr	Phe	Asn	Gln	Thr	Val	Ala	Ser	Thr	Gly	Arg	Leu	Ser			
			615			620					625							
tcc	act	gat	ccc	aac	ctg	caa	aac	att	cct	gtg	cgc	act	gag	gct	ggc		2035	
Ser	Thr	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Glu	Ala	Gly			

630	635	640	645	
cga aag att cgt tcg gga ttc gtc gta ggc gag ggg tat gaa acc ttg				2083
Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu Gly Tyr Glu Thr Leu	650	655	660	
ctg act gcc gac tat tcg cag att gaa atg cgc gtg atg gct cac ctt				2131
Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg Val Met Ala His Leu	665	670	675	
tcc cag gac cca ggc ttg att gag gcg tac cgc gaa ggc gaa gac ctg				2179
Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg Glu Gly Glu Asp Leu	680	685	690	
cac aat tac gtg ggt tcc aag gtg ttt aat gtg ccc atc gat ggc gtg				2227
His Asn Tyr Val Gly Ser Lys Val Phe Asn Val Pro Ile Asp Gly Val	695	700	705	
acc cct gag ctg cgt cgc cag gtc aag gcc atg tct tac ggt ctg gtg				2275
Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met Ser Tyr Gly Leu Val	710	715	720	725
tac ggc ttg tcc gcg ttt ggt ttg tct cag cag ctg agc att cct gct				2323
Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln Leu Ser Ile Pro Ala	730	735	740	
ggc gaa gcg aag cag atc atg gag tcc tac ttc gag cgc ttc ggc gga				2371
Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe Glu Arg Phe Gly Gly	745	750	755	
gta cag cgc tac ctc cgg gag atc gtg gag gag gct cga aaa gct ggc				2419
Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu Ala Arg Lys Ala Gly	760	765	770	
tac acg gaa acg ctc ttt ggg cgt cgt cgc tac ctg ccg gaa ctg acc				2467
Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr Leu Pro Glu Leu Thr	775	780	785	
tcg gat aac cgt gtc gct cgt gaa aac gct gaa cgt gcc gca ctg aac				2515
Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu Arg Ala Ala Leu Asn	790	795	800	805
gcc ccg att cag gga act gcc gca gac atc atc aag gtg gcc atg atc				2563
Ala Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Val Ala Met Ile	810	815	820	
cgg gtg gac cgt tca ctc aag gaa gct gcc gtg aaa tct cgc gtg ctg				2611
Arg Val Asp Arg Ser Leu Lys Glu Ala Ala Val Lys Ser Arg Val Leu	825	830	835	
ctt cag gtg cat gat gaa ttg gtc gtg gaa gta gcg gcc ggt gag ttg				2659
Leu Gln Val His Asp Glu Leu Val Val Glu Val Ala Ala Gly Glu Leu	840	845	850	
gaa caa gtc cgt gag att ctg gaa cgc gaa atg gat aac gcc atc aag				2707
Glu Gln Val Arg Glu Ile Leu Glu Arg Glu Met Asp Asn Ala Ile Lys	855	860	865	
ctg tcc gtt cct ttg gaa gtt tca gct ggt gat ggc gtt aac tgg gat				2755
Leu Ser Val Pro Leu Glu Val Ser Ala Gly Asp Gly Val Asn Trp Asp	870	875	880	885

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2790

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<212> PRT

<213> Corynebacterium glutamicum

<400> 162

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Ser Thr Leu Leu Lys Asp Glu Gln Pro Thr His Val Ala Val Ala Phe
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Asp Val Gly Arg Lys Thr Phe Arg Thr Asp Met Phe Pro Ala Tyr Lys
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Ala Gln Arg Glu Ala Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile
85 90 95

Leu Lys Glu Val Leu Ser Thr Leu Gly Ile Thr Thr Ile Glu Lys Ile
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Asp Phe Glu Ala Asp Asp Val Ile Ala Thr Leu Ser Val Ala Ala Lys
115 120 125

Pro Leu Gly Phe Lys Thr Leu Ile Val Thr Gly Asp Arg Asp Ser Phe
130 135 140

Gln Leu Val Asn Asp Thr Thr Thr Val Leu Tyr Pro Met Lys Gly Val
145 150 155 160

Ser Val Leu His Arg Phe Thr Pro Glu Ala Val Glu Glu Lys Tyr Gly
165 170 175

Leu Thr Pro Arg Gln Tyr Pro Glu Phe Ala Ala Leu Arg Gly Asp Pro
180 185 190

Ser Asp Asn Leu Pro Asn Ile Pro Gly Val Gly Glu Lys Thr Ala Thr
195 200 205

Lys Trp Ile Ala Gln Tyr Glu Thr Leu Asp Asn Leu Leu Asp His Ala
210 215 220

Asp Glu Ile Lys Gly Lys Val Gly Ala Ser Leu Arg Glu Arg Ile Glu
225 230 235 240

Gln Val Arg Met Asn Arg Lys Leu Thr Glu Met Val Lys Asp Leu Glu
245 250 255

Leu Pro Leu Gly Pro Asp Asp Phe Glu Met Lys Pro Val Gln Val Ala

270

Glu	Val	Ala	Ala	Lys	Phe	Asp	Asp	Leu	Glu	Phe	Gly	Thr	Asn	Leu	Arg
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Glu	Arg	Val	Leu	Ala	Val	Val	Lys	Ala	Glu	Gly	Ser	Ala	Ala	Pro	Val
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Glu	Glu	Val	Glu	Ala	Glu	Gln	Val	Val	Val	Asp	Thr	Gln	Ser	Leu	Ala
305					310					315					320
Gln	Trp	Leu	Pro	Ala	Arg	Ala	Gly	Gln	Ala	Leu	Ala	Leu	Ala	Leu	Ala
				325					330					335	
Gly	Val	Ala	Lys	Pro	Ala	Ala	Gly	Asp	Thr	Tyr	Ala	Leu	Ala	Ile	Ala
			340					345					350		
Asp	Thr	Lys	Arg	His	Ala	Val	Leu	Val	Asp	Val	Ala	Asp	Ile	Ser	Ala
		355					360					365			
Glu	Asp	Glu	Lys	Ala	Leu	Ala	Thr	Trp	Leu	Ala	Ser	Glu	Asp	Pro	Lys
	370					375					380				
Met	Leu	His	Gly	Ala	Lys	Ala	Ala	Tyr	His	Met	Leu	Ala	Gly	Arg	Gly
385					390					395					400
Phe	Glu	Leu	His	Gly	Val	Val	His	Asp	Thr	Ala	Ile	Ala	Ala	Tyr	Leu
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Leu	Arg	Pro	Gly	Gln	Arg	Thr	Tyr	Glu	Leu	Ala	Asp	Val	Tyr	Gln	Arg
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His	Leu	Gln	Arg	Gln	Leu	Ser	Thr	Asn	Asp	Asn	Gly	Gly	Gln	Leu	Thr
		435					440					445			
Leu	Leu	Asp	Ala	Ala	Asp	Asp	Gln	Ser	Leu	Val	Asp	Asp	Val	Ile	Ala
	450					455					460				
Ile	Leu	Glu	Leu	Ser	Glu	Glu	Leu	Thr	Lys	Gln	Leu	Gln	Glu	Ile	Gln
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Ala	Phe	Glu	Leu	Tyr	His	Asp	Leu	Glu	Ile	Pro	Leu	Ser	Gly	Ile	Leu
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Glu	Gln	Leu	Lys	Thr	Phe	Ile	Gly	Gln	Val	Ala	Gln	Glu	Glu	Glu	Ala
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Ala	Arg	Glu	Leu	Ala	Glu	Asp	Pro	Thr	Leu	Asn	Leu	Ser	Ser	Pro	Lys
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Gln	Leu	Gln	Val	Val	Leu	Phe	Glu	Thr	Phe	Gly	Met	Pro	Lys	Thr	Lys
545					550					555					560
Lys	Thr	Lys	Thr	Gly	Tyr	Ser	Thr	Ala	Ala	Ala	Glu	Ile	Glu	Ala	Leu
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Ala	Ile	Lys	Asn	Pro	His	Pro	Phe	Leu	Asp	His	Leu	Leu	Ala	His	Arg
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Gln Tyr Gln Lys Met Lys Thr Thr Leu Glu Gly Leu Ile Arg Glu Val
 595 600 605
 Ala Pro Asp Gly Arg Ile His Thr Thr Phe Asn Gln Thr Val Ala Ser
 610 615 620
 Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Val
 625 630 635 640
 Arg Thr Glu Ala Gly Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu
 645 650 655
 Gly Tyr Glu Thr Leu Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg
 660 665 670
 Val Met Ala His Leu Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg
 675 680 685
 Glu Gly Glu Asp Leu His Asn Tyr Val Gly Ser Lys Val Phe Asn Val
 690 695 700
 Pro Ile Asp Gly Val Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met
 705 710 715 720
 Ser Tyr Gly Leu Val Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln
 725 730 735
 Leu Ser Ile Pro Ala Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe
 740 745 750
 Glu Arg Phe Gly Gly Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu
 755 760 765
 Ala Arg Lys Ala Gly Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr
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 Lys Val Ala Met Ile Arg Val Asp Arg Ser Leu Lys Glu Ala Ala Val
 820 825 830
 Lys Ser Arg Val Leu Leu Gln Val His Asp Glu Leu Val Val Glu Val
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<220>

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<222> (101)..(2557)

<223> FRXA00060

<400> 163

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Asp Gln Thr Leu Met Leu Ile Asp Gly His Ser Met Ala Phe Arg Ala
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Phe Phe Ala Leu Pro Ala Glu Asn Phe Ser Thr Ser Gly Gly Gln Ala
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acc aat gct gtc tat ggc ttt ctc tcg atg ctg tcc acg ttg ttg aag 259
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Asp Glu Gln Pro Thr His Val Ala Val Ala Phe Asp Val Gly Arg Lys
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acg ttc cgt acc gat atg ttc ccg gcg tat aag gcg cag cgt gaa gca 355
Thr Phe Arg Thr Asp Met Phe Pro Ala Tyr Lys Ala Gln Arg Glu Ala
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Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile Leu Lys Glu Val Leu
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tcc act ttg gga att acg act att gag aaa atc gat ttt gag gct gat 451
Ser Thr Leu Gly Ile Thr Thr Ile Glu Lys Ile Asp Phe Glu Ala Asp
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Asp Val Ile Ala Thr Leu Ser Val Ala Ala Lys Pro Leu Gly Phe Lys
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Thr Leu Ile Val Thr Gly Asp Arg Asp Ser Phe Gln Leu Val Asn Asp
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acc acc acg gtg ttg tat ccg atg aag ggc gtg tct gtg ctg cac cgt 595
Thr Thr Thr Val Leu Tyr Pro Met Lys Gly Val Ser Val Leu His Arg
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ttc acg ccg gaa gca gtg gag gag aag tat gga ctg aca ccg agg cag 643
Phe Thr Pro Glu Ala Val Glu Glu Lys Tyr Gly Leu Thr Pro Arg Gln
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tat ccg gag ttt gca gcg ctg cgt ggt gat cct tcc gat aac ttg cct 691
Tyr Pro Glu Phe Ala Ala Leu Arg Gly Asp Pro Ser Asp Asn Leu Pro

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Lys	Val	Gly	Ala	Ser	Leu	Arg	Glu	Arg	Ile	Glu	Gln	Val	Arg	Met	Asn			
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Phe	Asp	Asp	Leu	Glu	Phe	Gly	Thr	Asn	Leu	Arg	Glu	Arg	Val	Leu	Ala			
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Val	Val	Lys	Ala	Glu	Gly	Ser	Ala	Ala	Pro	Val	Glu	Glu	Val	Glu	Ala			
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Arg	Ala	Gly	Gln	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Gly	Val	Ala	Lys	Pro			
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Ala	Val	Leu	Val	Asp	Val	Ala	Asp	Ile	Ser	Ala	Glu	Asp	Glu	Lys	Ala			
360						365						370						
ctg	gcc	acg	tgg	ttg	gcg	tcg	gaa	gat	cca	aag	atg	ctg	cac	ggc	gct	1267		
Leu	Ala	Thr	Trp	Leu	Ala	Ser	Glu	Asp	Pro	Lys	Met	Leu	His	Gly	Ala			
375						380						385						
aag	gcc	gcc	tat	cat	atg	ctc	gct	ggg	cgc	ggt	ttt	gag	ctg	cac	ggc	1315		
Lys	Ala	Ala	Tyr	His	Met	Leu	Ala	Gly	Arg	Gly	Phe	Glu	Leu	His	Gly			
390						395						405						
gtg	gtg	cat	gac	acg	gcg	atc	gcg	gca	tac	ttg	ctg	cgt	ccg	ggc	caa	1363		
Val	Val	His	Asp	Thr	Ala	Ile	Ala	Ala	Tyr	Leu	Leu	Arg	Pro	Gly	Gln			
410						415						420						
cgc	acc	tat	gag	ctt	gcc	gac	gtc	tac	cag	cgg	cat	ctt	caa	cga	cag	1411		
Arg	Thr	Tyr	Glu	Leu	Ala	Asp	Val	Tyr	Gln	Arg	His	Leu	Gln	Arg	Gln			
425						430						435						

ttg tct aca aac gac aat ggc ggc cag ctc acg ctg ctc gac gca gct	1459
Leu Ser Thr Asn Asp Asn Gly Gly Gln Leu Thr Leu Leu Asp Ala Ala	
440 445 450	
gat gac caa tcg ctt gtt gat gat gtc att gca atc ctt gag ctg tct	1507
Asp Asp Gln Ser Leu Val Asp Asp Val Ile Ala Ile Leu Glu Leu Ser	
455 460 465	
gaa gaa ttg acc aaa cag ctt cag gag att caa gct ttt gag ctt tac	1555
Glu Glu Leu Thr Lys Gln Leu Gln Glu Ile Gln Ala Phe Glu Leu Tyr	
470 475 480 485	
cat gac ctg gaa att ccg ctg tcg gga att ctg gcg cgc atg gag gcc	1603
His Asp Leu Glu Ile Pro Leu Ser Gly Ile Leu Ala Arg Met Glu Ala	
490 495 500	
atc ggt atc gct gtt gat gtt gcc act ttg gaa gag cag ttg aag act	1651
Ile Gly Ile Ala Val Asp Val Ala Thr Leu Glu Glu Gln Leu Lys Thr	
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ttc att ggt cag gtt gct cag gaa gag gaa gca gct cgc gag ctc gct	1699
Phe Ile Gly Gln Val Ala Gln Glu Glu Glu Ala Ala Arg Glu Leu Ala	
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gag gat cca acc ctg aat ctc tcg agc ccg aag cag ctg caa gtg gtg	1747
Glu Asp Pro Thr Leu Asn Leu Ser Ser Pro Lys Gln Leu Gln Val Val	
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ctt ttt gag acg ttc gga atg ccg aaa acc aag aaa acc aag acc ggc	1795
Leu Phe Glu Thr Phe Gly Met Pro Lys Thr Lys Lys Thr Lys Thr Gly	
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tac tct acg gct gcc gcg gaa att gaa gcc cta gcg atc aag aat ccg	1843
Tyr Ser Thr Ala Ala Ala Glu Ile Glu Ala Leu Ala Ile Lys Asn Pro	
570 575 580	
cac cca ttc cta gat cac ctg ttg gca cac cgt cag tac caa aag atg	1891
His Pro Phe Leu Asp His Leu Leu Ala His Arg Gln Tyr Gln Lys Met	
585 590 595	
aag acc act ctg gaa ggt ctc atc cgt gag gtg gct cct gat ggc cgt	1939
Lys Thr Thr Leu Glu Gly Leu Ile Arg Glu Val Ala Pro Asp Gly Arg	
600 605 610	
att cac acc acc ttc aac cag acg gtg gcg tct acg gga cgt ttg tca	1987
Ile His Thr Thr Phe Asn Gln Thr Val Ala Ser Thr Gly Arg Leu Ser	
615 620 625	
tcc act gat ccc aac ctg caa aac att cct gtg cgc act gag gct ggc	2035
Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Glu Ala Gly	
630 635 640 645	
cga aag att cgt tcg gga ttc gtc gta ggc gag ggg tat gaa acc ttg	2083
Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu Gly Tyr Glu Thr Leu	
650 655 660	
ctg act gcc gac tat tcg cag att gaa atg cgc gtg atg gct cac ctt	2131
Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg Val Met Ala His Leu	
665 670 675	

tcc cag gac cca ggc ttg att gag gcg tac cgc gaa ggc gaa gac ctg 2179
 Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg Glu Gly Glu Asp Leu
 680 685 690

cac aat tac gtg ggt tcc aag gtg ttt aat gtg ccc atc gat ggc gtg 2227
 His Asn Tyr Val Gly Ser Lys Val Phe Asn Val Pro Ile Asp Gly Val
 695 700 705

acc cct gag ctg cgt cgc cag gtc aag gcc atg tct tac ggt ctg gtg 2275
 Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met Ser Tyr Gly Leu Val
 710 715 720 725

tac ggc ttg tcc gcg ttt ggt ttg tct cag cag ctg agc att cct gct 2323
 Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln Leu Ser Ile Pro Ala
 730 735 740

ggc gaa gcg aag cag atc atg gag tcc tac ttc gag cgc ttc ggc gga 2371
 Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe Glu Arg Phe Gly Gly
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gta cag gcg tac ctc cgg gag atc gtg gag gag gct cga aaa gct ggc 2419
 Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu Ala Arg Lys Ala Gly
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 Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr Leu Pro Glu Leu Thr
 775 780 785

tcg gat aac cgt gtc gct cgt gaa aac gct gaa cgt gcc gca ctg aac 2515
 Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu Arg Ala Ala Leu Asn
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gcc ccg att agg gaa ctg ccg cag aca tca tca agg tgg cca 2557
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<211> 819

<212> PRT

<213> Corynebacterium glutamicum

<400> 164

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Ser Gly Gly Gln Ala Thr Asn Ala Val Tyr Gly Phe Leu Ser Met Leu
 35 40 45

Ser Thr Leu Leu Lys Asp Glu Gln Pro Thr His Val Ala Val Ala Phe
 50 55 60

Asp Val Gly Arg Lys Thr Phe Arg Thr Asp Met Phe Pro Ala Tyr Lys
 65 70 75 80

Ala Gln Arg Glu Ala Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile

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Leu	Lys	Glu	Val	Leu	Ser	Thr	Leu	Gly	Ile	Thr	Thr	Ile	Glu	Lys	Ile			
			100					105					110					
Asp	Phe	Glu	Ala	Asp	Asp	Val	Ile	Ala	Thr	Leu	Ser	Val	Ala	Ala	Lys			
		115					120					125						
Pro	Leu	Gly	Phe	Lys	Thr	Leu	Ile	Val	Thr	Gly	Asp	Arg	Asp	Ser	Phe			
	130					135					140							
Gln	Leu	Val	Asn	Asp	Thr	Thr	Thr	Val	Leu	Tyr	Pro	Met	Lys	Gly	Val			
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Ser	Val	Leu	His	Arg	Phe	Thr	Pro	Glu	Ala	Val	Glu	Glu	Lys	Tyr	Gly			
				165					170					175				
Leu	Thr	Pro	Arg	Gln	Tyr	Pro	Glu	Phe	Ala	Ala	Leu	Arg	Gly	Asp	Pro			
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Ser	Asp	Asn	Leu	Pro	Asn	Ile	Pro	Gly	Val	Gly	Glu	Lys	Thr	Ala	Thr			
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Lys	Trp	Ile	Ala	Gln	Tyr	Glu	Thr	Leu	Asp	Asn	Leu	Leu	Asp	His	Ala			
	210					215					220							
Asp	Glu	Ile	Lys	Gly	Lys	Val	Gly	Ala	Ser	Leu	Arg	Glu	Arg	Ile	Glu			
225					230					235					240			
Gln	Val	Arg	Met	Asn	Arg	Lys	Leu	Thr	Glu	Met	Val	Lys	Asp	Leu	Glu			
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Leu	Pro	Leu	Gly	Pro	Asp	Asp	Phe	Glu	Met	Lys	Pro	Val	Gln	Val	Ala			
			260					265					270					
Glu	Val	Ala	Ala	Lys	Phe	Asp	Asp	Leu	Glu	Phe	Gly	Thr	Asn	Leu	Arg			
		275					280					285						
Glu	Arg	Val	Leu	Ala	Val	Val	Lys	Ala	Glu	Gly	Ser	Ala	Ala	Pro	Val			
	290					295					300							
Glu	Glu	Val	Glu	Ala	Glu	Gln	Val	Val	Val	Asp	Thr	Gln	Ser	Leu	Ala			
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Gln	Trp	Leu	Pro	Ala	Arg	Ala	Gly	Gln	Ala	Leu	Ala	Leu	Ala	Leu	Ala			
				325				330						335				
Gly	Val	Ala	Lys	Pro	Ala	Ala	Gly	Asp	Thr	Tyr	Ala	Leu	Ala	Ile	Ala			
			340					345				350						
Asp	Thr	Lys	Arg	His	Ala	Val	Leu	Val	Asp	Val	Ala	Asp	Ile	Ser	Ala			
		355					360					365						
Glu	Asp	Glu	Lys	Ala	Leu	Ala	Thr	Trp	Leu	Ala	Ser	Glu	Asp	Pro	Lys			
	370					375					380							
Met	Leu	His	Gly	Ala	Lys	Ala	Ala	Tyr	His	Met	Leu	Ala	Gly	Arg	Gly			
385					390					395					400			
Phe	Glu	Leu	His	Gly	Val	Val	His	Asp	Thr	Ala	Ile	Ala	Ala	Tyr	Leu			
				405					410					415				

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100

Leu Arg Pro Gly Gln Arg Thr Tyr Glu Leu Ala Asp Val Tyr Gln Arg
 420 425 430
 His Leu Gln Arg Gln Leu Ser Thr Asn Asp Asn Gly Gly Gln Leu Thr
 435 440 445
 Leu Leu Asp Ala Ala Asp Asp Gln Ser Leu Val Asp Asp Val Ile Ala
 450 455 460
 Ile Leu Glu Leu Ser Glu Glu Leu Thr Lys Gln Leu Gln Glu Ile Gln
 465 470 475 480
 Ala Phe Glu Leu Tyr His Asp Leu Glu Ile Pro Leu Ser Gly Ile Leu
 485 490 495
 Ala Arg Met Glu Ala Ile Gly Ile Ala Val Asp Val Ala Thr Leu Glu
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 Glu Gln Leu Lys Thr Phe Ile Gly Gln Val Ala Gln Glu Glu Glu Ala
 515 520 525
 Ala Arg Glu Leu Ala Glu Asp Pro Thr Leu Asn Leu Ser Ser Pro Lys
 530 535 540
 Gln Leu Gln Val Val Leu Phe Glu Thr Phe Gly Met Pro Lys Thr Lys
 545 550 555 560
 Lys Thr Lys Thr Gly Tyr Ser Thr Ala Ala Ala Glu Ile Glu Ala Leu
 565 570 575
 Ala Ile Lys Asn Pro His Pro Phe Leu Asp His Leu Leu Ala His Arg
 580 585 590
 Gln Tyr Gln Lys Met Lys Thr Thr Leu Glu Gly Leu Ile Arg Glu Val
 595 600 605
 Ala Pro Asp Gly Arg Ile His Thr Thr Phe Asn Gln Thr Val Ala Ser
 610 615 620
 Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Val
 625 630 635 640
 Arg Thr Glu Ala Gly Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu
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 Gly Tyr Glu Thr Leu Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg
 660 665 670
 Val Met Ala His Leu Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg
 675 680 685
 Glu Gly Glu Asp Leu His Asn Tyr Val Gly Ser Lys Val Phe Asn Val
 690 695 700
 Pro Ile Asp Gly Val Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met
 705 710 715 720
 Ser Tyr Gly Leu Val Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln
 725 730 735

Leu Ser Ile Pro Ala Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe
740 745 750

Glu Arg Phe Gly Gly Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu
755 760 765

Ala Arg Lys Ala Gly Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr
770 775 780

Leu Pro Glu Leu Thr Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu
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Arg Trp Pro

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<211> 333

<212> DNA

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<223> FRXA00061

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Met Ile Arg Val Asp
1 5

cgt tca ctc aag gaa gct gcc gtg aaa tct cgc gtg ctg ctt cag gtg 163
Arg Ser Leu Lys Glu Ala Ala Val Lys Ser Arg Val Leu Leu Gln Val
10 15 20

cat gat gaa ttg gtc gtg gaa gta gcg gcc ggt gag ttg gaa caa gtc 211
His Asp Glu Leu Val Val Glu Val Ala Ala Gly Glu Leu Glu Gln Val
25 30 35

cgt gag att ctg gaa cgc gaa atg gat aac gcc atc aag ctg tcc gtt 259
Arg Glu Ile Leu Glu Arg Glu Met Asp Asn Ala Ile Lys Leu Ser Val
40 45 50

cct ttg gaa gtt tca gct ggt gat ggc gtt aac tgg gat gct gca gcg 307
Pro Leu Glu Val Ser Ala Gly Asp Gly Val Asn Trp Asp Ala Ala Ala
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cac taagaggtaa ctgccttttc gtc 333
His
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<210> 166

<211> 70

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<400> 166

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 20 25 30

Glu Leu Glu Gln Val Arg Glu Ile Leu Glu Arg Glu Met Asp Asn Ala
 35 40 45

Ile Lys Leu Ser Val Pro Leu Glu Val Ser Ala Gly Asp Gly Val Asn
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Trp Asp Ala Ala Ala His
 65 70

<210> 167

<211> 3705

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(3682)

<223> RXA02657

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 Met Ala Arg Leu Ser
 1 5

cac atg gcc aag caa tcc tca ttt gta cat ctt cac aac cac acc gag 163
 His Met Ala Lys Gln Ser Ser Phe Val His Leu His Asn His Thr Glu
 10 15 20

ttt tcc atg ctt gat gga atg gcc aag atc gat atg ttg gcc gat gag 211
 Phe Ser Met Leu Asp Gly Met Ala Lys Ile Asp Met Leu Ala Asp Glu
 25 30 35

gtt aaa gcc cag gga atg cct gcg gtc gga atc acc gac cac ggc aat 259
 Val Lys Ala Gln Gly Met Pro Ala Val Gly Ile Thr Asp His Gly Asn
 40 45 50

atg tat ggc tcc aac ccc ttt tat cgc aag atg aca gag atg ggc att 307
 Met Tyr Gly Ser Asn Pro Phe Tyr Arg Lys Met Thr Glu Met Gly Ile
 55 60 65

aag ccc atc att ggc att gaa acg tat atg gca cct gag tct cgt ttt 355
 Lys Pro Ile Ile Gly Ile Glu Thr Tyr Met Ala Pro Glu Ser Arg Phe
 70 75 80 85

aag aaa gag cgt gtg cgt tgg ggc gaa cca cac caa aaa tca gat gat 403
 Lys Lys Glu Arg Val Arg Trp Gly Glu Pro His Gln Lys Ser Asp Asp
 90 95 100

gtt tct ggt tcc ggt gcg tat ttg cac cag acg atg ctt gca gaa aac 451
 Val Ser Gly Ser Gly Ala Tyr Leu His Gln Thr Met Leu Ala Glu Asn

105					110					115						
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Thr	Thr	Gly	Leu	Arg	Asn	Leu	Phe	Tyr	Leu	Ser	Ser	Met	Ala	Ser	Tyr	
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gaa	ggc	cag	cta	ggc	aag	tgg	ccc	cgc	atg	gac	gcc	gat	atc	atc	gct	547
Glu	Gly	Gln	Leu	Gly	Lys	Trp	Pro	Arg	Met	Asp	Ala	Asp	Ile	Ile	Ala	
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gag	cac	gcc	gaa	ggc	atc	atc	gcc	acc	acg	ggt	tgc	cct	tcc	ggc	gat	595
Glu	His	Ala	Glu	Gly	Ile	Ile	Ala	Thr	Thr	Gly	Cys	Pro	Ser	Gly	Asp	
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Val	Gln	Thr	Arg	Leu	Arg	Leu	Gly	Gln	Phe	Asp	Glu	Ala	Leu	Glu	Ala	
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gcc	gcc	atg	tgg	cag	gac	atc	tat	ggt	cgc	gac	aac	tac	ttc	ctc	gag	691
Ala	Ala	Met	Trp	Gln	Asp	Ile	Tyr	Gly	Arg	Asp	Asn	Tyr	Phe	Leu	Glu	
		185						190					195			
ttg	atg	gac	cac	ggg	ctc	gac	att	gaa	acc	cgt	gtg	cgc	agt	gag	ctg	739
Leu	Met	Asp	His	Gly	Leu	Asp	Ile	Glu	Thr	Arg	Val	Arg	Ser	Glu	Leu	
		200					205					210				
ctc	gaa	atc	gga	cgc	aag	ctc	aat	ttg	cca	ccc	ctg	gtc	acc	aac	gac	787
Leu	Glu	Ile	Gly	Arg	Lys	Leu	Asn	Leu	Pro	Pro	Leu	Val	Thr	Asn	Asp	
		215				220					225					
tgc	cac	tat	gtg	ctg	gaa	tct	cag	gcg	caa	gcc	cac	gag	gca	atg	ctc	835
Cys	His	Tyr	Val	Leu	Glu	Ser	Gln	Ala	Gln	Ala	His	Glu	Ala	Met	Leu	
		230			235				240						245	
tgc	gtg	caa	aca	ggc	aag	acg	ctt	cat	gat	gaa	gac	cga	ttc	aaa	ttc	883
Cys	Val	Gln	Thr	Gly	Lys	Thr	Leu	His	Asp	Glu	Asp	Arg	Phe	Lys	Phe	
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ggc	gga	acc	ggc	tat	tac	gtt	aaa	tct	gca	gaa	caa	atg	cgt	gca	ctc	931
Gly	Gly	Thr	Gly	Tyr	Tyr	Val	Lys	Ser	Ala	Glu	Gln	Met	Arg	Ala	Leu	
			265				270						275			
tgg	gac	gac	atg	gtt	cca	gat	ggc	tgc	gac	aac	acc	ctg	tgg	atc	gct	979
Trp	Asp	Asp	Met	Val	Pro	Asp	Gly	Cys	Asp	Asn	Thr	Leu	Trp	Ile	Ala	
		280					285					290				
gaa	cgt	gtg	cag	tcc	tat	gac	gaa	atc	tgg	gaa	gaa	cac	tca	cac	gac	1027
Glu	Arg	Val	Gln	Ser	Tyr	Asp	Glu	Ile	Trp	Glu	Glu	His	Ser	His	Asp	
		295				300					305					
cgc	atg	cct	atc	gct	gat	gtt	cca	gaa	ggc	tac	acc	cca	acc	act	tgg	1075
Arg	Met	Pro	Ile	Ala	Asp	Val	Pro	Glu	Gly	Tyr	Thr	Pro	Thr	Thr	Trp	
		310			315					320					325	
ttg	cac	cat	gaa	gtg	atg	gct	ggc	ttg	gag	gat	cgt	ttc	tct	gga	cag	1123
Leu	His	His	Glu	Val	Met	Ala	Gly	Leu	Glu	Asp	Arg	Phe	Ser	Gly	Gln	
			330						335					340		
caa	gtt	cct	gag	gat	tat	att	gag	cgc	gcg	gag	tat	gag	atc	tcc	gtt	1171
Gln	Val	Pro	Glu	Asp	Tyr	Ile	Glu	Arg	Ala	Glu	Tyr	Glu	Ile	Ser	Val	
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Ile Asp Met Lys Gly Tyr Pro Ser Tyr Phe Leu Ile Val Ala Glu Ile	
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Ile Lys His Ala Arg Ser Ile Gly Ile Arg Val Gly Pro Gly Arg Gly	
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Ser Ala Ala Gly Ala Leu Val Ala Tyr Ala Leu Thr Ile Thr Asn Ile	
390 395 400 405	
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Asp Pro Met Glu His Gly Leu Leu Phe Glu Arg Phe Leu Asn Pro Glu	
410 415 420	
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Arg Pro Ser Ala Pro Asp Ile Asp Ile Asp Phe Asp Asp Arg Arg Arg	
425 430 435	
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Gly Glu Met Ile Arg Tyr Ala Ala Asp Arg Trp Gly Glu Asp Lys Ile	
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Ala Gln Val Ile Thr Phe Gly Thr Val Lys Thr Lys Gln Ala Leu Lys	
455 460 465	
gac tcc gcc cgt gtg caa atg ggg cag cca ggc tat caa atc gct gac	1555
Asp Ser Ala Arg Val Gln Met Gly Gln Pro Gly Tyr Gln Ile Ala Asp	
470 475 480 485	
cgc gtg atc aag gag ctt cca cct gcc att atg gcg aag gat att ccg	1603
Arg Val Ile Lys Glu Leu Pro Pro Ala Ile Met Ala Lys Asp Ile Pro	
490 495 500	
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Leu Ser Gly Ile Thr Asp Pro Asp His Pro Arg Phe Asn Glu Ala Gly	
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Ala Val Arg Gln Leu Ile Glu Thr Asp Pro Asp Val Lys Arg Ile Tyr	
520 525 530	
gac acc gct cgt ggt ttg gaa ggc gtg gtg cgc caa tct ggc gtg cac	1747
Asp Thr Ala Arg Gly Leu Glu Gly Val Val Arg Gln Ser Gly Val His	
535 540 545	
gcg tgt gcc gtg att atg tct tct gta ccg ctg ctg gac tgc att ccg	1795
Ala Cys Ala Val Ile Met Ser Ser Val Pro Leu Leu Asp Cys Ile Pro	
550 555 560 565	
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Met Trp Lys Arg Pro Ala Asp Gly Ala Leu Ile Thr Gly Trp Asp Tyr	
570 575 580	
cca gca tgt gag gcc att ggc ctg ttg aag atg gac ttc ctg gga ctt	1891
Pro Ala Cys Glu Ala Ile Gly Leu Leu Lys Met Asp Phe Leu Gly Leu	
585 590 595	

cga Arg	aac Asn	ctt Leu 600	acc Thr	gtt Val	att Ile	ggc Gly	gat Asp 605	gcg Ala	att Ile	gaa Glu	aac Asn	att Ile 610	aag Lys	gcc Ala	aac Asn	1939
cgc Arg	gat Asp 615	ggg Gly	gaa Glu	gtg Val	ctt Leu	gat Asp 620	cta Leu	gaa Glu	aac Asn	cta Leu	gcg Ala 625	atc Ile	gag Glu	gat Asp	gaa Glu	1987
gaa Glu 630	acc Thr	tac Tyr	aag Lys	ctg Leu	cta Leu 635	ggc Gly	cgt Arg	gga Gly	gaa Glu	acc Thr 640	ctt Leu	ggt Gly	gtg Val	ttc Phe	cag Gln 645	2035
ctt Leu	gat Asp	ggt Gly	ggt Gly	ggc Gly 650	atg Met	cag Gln	gag Glu	ctg Leu	ctg Leu 655	aag Lys	cgt Arg	atg Met	cag Gln	cca Pro 660	acc Thr	2083
ggc Gly	ttc Phe	aat Asn	gac Asp 665	atc Ile	gtc Val	gca Ala	gcg Ala	ctt Leu 670	gcg Ala	ctg Leu	tat Tyr	cgc Arg	cca Pro 675	ggc Gly	ccc Pro	2131
atg Met	ggt Gly 680	gtg Val	aac Asn	gcg Ala	cac His	tgg Trp	gat Asp 685	tac Tyr	gcc Ala	gac Asp	cgt Arg	aaa Lys 690	aac Asn	gga Gly	cgc Arg	2179
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atc Ile 710	ctt Leu	ggt Gly	gaa Glu	acc Thr	tat Tyr 715	ggc Gly	ctg Leu	att Ile	gtg Val	tac Tyr 720	cag Gln	gag Glu	cag Gln	atc Ile	atg Met 725	2275
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gcg Ala	att Ile 775	aag Lys	act Thr	ttg Leu	tgg Trp	gat Asp 780	acc Thr	att Ile	ctg Leu	ccg Pro	ttc Phe 785	gcc Ala	ggc Gly	tac Tyr	gcg Ala	2467
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Cys	Arg	His	Leu	Gly	Ile	Arg	Val	Leu	Ser	Pro	Asp	Ile	Asn	Glu	Ser	
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Ser	Leu	Asn	Phe	Leu	Pro	Val	Gly	Thr	Asp	Ile	Arg	Tyr	Gly	Leu	Gly	
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gcc	att	aga	aac	gtg	ggg	gct	gaa	gtt	gtg	gat	tcc	att	ttg	gat	acc	2755
Ala	Ile	Arg	Asn	Val	Gly	Ala	Glu	Val	Val	Asp	Ser	Ile	Leu	Asp	Thr	
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Ile	Asp	Thr	Leu	Pro	Cys	Asn	Lys	Arg	Ile	Thr	Glu	Ser	Leu	Ile	Lys	
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Gly	Gly	Ala	Phe	Asp	Ser	Leu	Gly	His	Ala	Arg	Lys	Gly	Leu	Met	Leu	
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Val	Phe	Glu	Asp	Ala	Val	Asp	Ser	Val	Ile	Ala	Thr	Lys	Lys	Ala	Ala	
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Asp	Lys	Gly	Gln	Phe	Asp	Leu	Phe	Ala	Ala	Phe	Asp	Ser	Asp	Asn	Asn	
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Asp	Asp	Val	Ala	Ser	Phe	Phe	Gln	Ile	Thr	Val	Pro	Asp	Asp	Glu	Trp	
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Asp	Arg	Lys	His	Glu	Leu	Ala	Leu	Glu	Arg	Glu	Met	Leu	Gly	Leu	Tyr	
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Ala	Glu	Val	Thr	Val	Gly	Gly	Ile	Ile	Ser	Gly	Val	Asp	Arg	Arg	Phe	
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tcc	aag	aag	gac	ggg	tcc	cct	tgg	gcg	att	gtc	acc	att	gaa	gat	cac	3283
Ser	Lys	Lys	Asp	Gly	Ser	Pro</										

1080	1085	1090	
atc tcc att cga gat gat cgt atg agc ctt ttc tgt gat gat ctc cgc			3427
Ile Ser Ile Arg Asp Asp Arg Met Ser Leu Phe Cys Asp Asp Leu Arg			
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gtt cca gag ctt ggg cca gga aac ggg caa gga ctt ccg ctt cgt ttg			3475
Val Pro Glu Leu Gly Pro Gly Asn Gly Gln Gly Leu Pro Leu Arg Leu			
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tcc atg cgt act gat cag tgc acc atg tcc aac att gcc aag ctc aag			3523
Ser Met Arg Thr Asp Gln Cys Thr Met Ser Asn Ile Ala Lys Leu Lys			
1130	1135	1140	
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Gln Val Leu Val Asp Asn Lys Gly Glu Ser Asp Val Tyr Leu Asn Leu			
1145	1150	1155	
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Ile Asp Gly Asp Asn Ser Thr Val Met Ile Leu Gly Asp His Leu Arg			
1160	1165	1170	
gtc aac cga tcc gca agt ttg atg ggc gac ctc aag gca acg atg ggg			3667
Val Asn Arg Ser Ala Ser Leu Met Gly Asp Leu Lys Ala Thr Met Gly			
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Met Leu Ala Asp Glu Val Lys Ala Gln Gly Met Pro Ala Val Gly Ile			
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Thr Asp His Gly Asn Met Tyr Gly Ser Asn Pro Phe Tyr Arg Lys Met			
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Thr Glu Met Gly Ile Lys Pro Ile Ile Gly Ile Glu Thr Tyr Met Ala			
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Pro Glu Ser Arg Phe Lys Lys Glu Arg Val Arg Trp Gly Glu Pro His			
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Gln Lys Ser Asp Asp Val Ser Gly Ser Gly Ala Tyr Leu His Gln Thr			
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Met Leu Ala Glu Asn Thr Thr Gly Leu Arg Asn Leu Phe Tyr Leu Ser			
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Ser Met Ala Ser Tyr Glu Gly Gln Leu Gly Lys Trp Pro Arg Met Asp
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 Cys Pro Ser Gly Asp Val Gln Thr Arg Leu Arg Leu Gly Gln Phe Asp
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 Glu Ala Leu Glu Ala Ala Ala Met Trp Gln Asp Ile Tyr Gly Arg Asp
 180 185 190
 Asn Tyr Phe Leu Glu Leu Met Asp His Gly Leu Asp Ile Glu Thr Arg
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 225 230 235 240
 His Glu Ala Met Leu Cys Val Gln Thr Gly Lys Thr Leu His Asp Glu
 245 250 255
 Asp Arg Phe Lys Phe Gly Gly Thr Gly Tyr Tyr Val Lys Ser Ala Glu
 260 265 270
 Gln Met Arg Ala Leu Trp Asp Asp Met Val Pro Asp Gly Cys Asp Asn
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 Thr Leu Trp Ile Ala Glu Arg Val Gln Ser Tyr Asp Glu Ile Trp Glu
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 Glu His Ser His Asp Arg Met Pro Ile Ala Asp Val Pro Glu Gly Tyr
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 Thr Pro Thr Thr Trp Leu His His Glu Val Met Ala Gly Leu Glu Asp
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 Tyr Glu Ile Ser Val Ile Asp Met Lys Gly Tyr Pro Ser Tyr Phe Leu
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 Gly Pro Gly Arg Gly Ser Ala Ala Gly Ala Leu Val Ala Tyr Ala Leu
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 Phe Leu Asn Pro Glu Arg Pro Ser Ala Pro Asp Ile Asp Ile Asp Phe
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 Asp Asp Arg Arg Arg Gly Glu Met Ile Arg Tyr Ala Ala Asp Arg Trp
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 Gly Glu Asp Lys Ile Ala Gln Val Ile Thr Phe Gly Thr Val Lys Thr

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Tyr	Gln	Ile	Ala	Asp	Arg	Val	Ile	Lys	Glu	Leu	Pro	Pro	Ala	Ile	Met
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Ala	Lys	Asp	Ile	Pro	Leu	Ser	Gly	Ile	Thr	Asp	Pro	Asp	His	Pro	Arg
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Leu	Asp	Cys	Ile	Pro	Met	Trp	Lys	Arg	Pro	Ala	Asp	Gly	Ala	Leu	Ile
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Thr	Gly	Trp	Asp	Tyr	Pro	Ala	Cys	Glu	Ala	Ile	Gly	Leu	Leu	Lys	Met
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Asp	Phe	Leu	Gly	Leu	Arg	Asn	Leu	Thr	Val	Ile	Gly	Asp	Ala	Ile	Glu
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Asn	Ile	Lys	Ala	Asn	Arg	Asp	Gly	Glu	Val	Leu	Asp	Leu	Glu	Asn	Leu
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Gln	Glu	Gln	Ile	Met	Arg	Ile	Ser	Gln	Lys	Val	Ala	Asn	Tyr	Thr	Ala
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Gly	Tyr	Ser	Asp	Ala	Ala	Ile	Lys	Thr	Leu	Trp	Asp	Thr	Ile	Leu	Pro
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Phe Ala Gly Tyr Ala Phe Asn Lys Ser His Ala Ala Gly Tyr Gly Leu
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 Val Ser Phe Trp Thr Ala Tyr Leu Lys Ala His Tyr Ala Pro Glu Tyr
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 Met Ala Ala Leu Leu Thr Ser Val Gly Asp Asn Lys Asp Lys Ser Ala
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 Ile Tyr Leu Ser Asp Cys Arg His Leu Gly Ile Arg Val Leu Ser Pro
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 Asp Ile Asn Glu Ser Ser Leu Asn Phe Leu Pro Val Gly Thr Asp Ile
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 Arg Tyr Gly Leu Gly Ala Ile Arg Asn Val Gly Ala Glu Val Val Asp
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 Ser Ile Leu Asp Thr Arg Lys Glu Lys Gly Leu Phe Lys Asp Phe Ser
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 Lys Gly Leu Met Leu Val Phe Glu Asp Ala Val Asp Ser Val Ile Ala
 930 935 940
 Thr Lys Lys Ala Ala Asp Lys Gly Gln Phe Asp Leu Phe Ala Ala Phe
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 Asp Ser Asp Asn Asn Asp Asp Val Ala Ser Phe Phe Gln Ile Thr Val
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 Pro Asp Asp Glu Trp Asp Arg Lys His Glu Leu Ala Leu Glu Arg Glu
 980 985 990
 Met Leu Gly Leu Tyr Val Ser Gly His Pro Leu Asp Gly Tyr Glu Asp
 995 1000 1005
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 Glu Leu Lys His Gly Ala Glu Val Thr Val Gly Gly Ile Ile Ser Gly
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 Lys Val Tyr Ser Ile Val Gly Ser Met Ile Val Glu Asp Asn Ile Ile
 1075 1080 1085
 Leu Ala Lys Ala His Ile Ser Ile Arg Asp Asp Arg Met Ser Leu Phe
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Cys Asp Asp Leu Arg Val Pro Glu Leu Gly Pro Gly Asn Gly Gln Gly
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Leu Pro Leu Arg Leu Ser Met Arg Thr Asp Gln Cys Thr Met Ser Asn
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Ile Ala Lys Leu Lys Gln Val Leu Val Asp Asn Lys Gly Glu Ser Asp
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Val Tyr Leu Asn Leu Ile Asp Gly Asp Asn Ser Thr Val Met Ile Leu
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 Val Ile Ala Ala Tyr
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 Gly Ala Ser Ile Ser Leu Asp Asp Ser Thr Leu Thr Ile Ser Tyr Ser
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 Pro Leu Leu Ala Ala Leu Ser Lys Ser Ser Ala Gln Ser Glu Ser Val
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Asp Ala Asp Pro Ser Ser Ile	Leu Tyr Gly Gln Asn Val	Thr Leu Thr	
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Leu Val Ala Gly Pro Trp Ala	Thr Ile Thr Ser Lys Gln	Lys Arg Ala	
425	430	435	
gag gag ttg aaa gaa aaa gga	cag gac atc cag atc tgg	gat gaa aag	1459
Glu Glu Leu Lys Glu Lys Gly	Gln Asp Ile Gln Ile Trp	Asp Glu Lys	
440	445	450	
cag ctg ttt acg gct ctg ggg	tta gat gaa cag ccc ccg	ttt	1501
Gln Leu Phe Thr Ala Leu Gly	Leu Asp Glu Gln Pro Pro	Phe	
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Thr Ile Ser Tyr Ser Pro Leu	Leu Ala Ala Leu Ser Lys	Ser Ser Ala	
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Gln Ser Glu Ser Val Asp Leu	Thr Gln Val Ser Gly Val	Ser Val Gln	
35	40	45	
Asp Pro Thr Ala Phe Thr His	Gly Phe Leu Asn Leu Glu	Gly Val Asp	
50	55	60	
Lys Ser Ile Ala Phe Ala Pro	Asn Ser Ser Ala Asp Leu	Ala Ala Leu	
65	70	75 80	
Ala Ala Asp Ile Asp Ala Val	Leu Lys Gly Glu Lys Pro	Gln His Leu	
85	90	95	
Gly Gly Gly Ala Pro Val Val	Pro Ser Ala Pro Ser Thr	Val Ala Gly	
100	105	110	
Leu Asn Phe Val Gly Phe Asp Val Glu Thr Ala Asn Asp Asp Trp Gly			

115					120					125					
Ser	Ile	Cys	Gln	Ile	Gly	Leu	Val	Lys	Tyr	Val	Asp	Gly	Val	Glu	Glu
130						135					140				
Ser	Ser	Glu	Ser	Trp	Leu	Cys	Thr	Pro	Pro	Glu	Ser	Leu	Asn	Phe	Phe
145					150					155					160
Asn	Glu	Ile	Asn	Ile	Gly	Ile	His	Gly	Ile	Thr	Pro	Glu	Met	Val	Ala
				165					170					175	
Asp	Gln	Pro	Arg	Phe	Ala	Asp	Leu	Val	Pro	Lys	Met	Val	Glu	Phe	Val
			180					185					190		
Gly	Asp	Leu	Pro	Leu	Val	Ala	His	Asn	Ala	Gln	Phe	Asp	Phe	Thr	Ala
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Ile	Ala	Leu	Ala	Lys	Arg	His	Ser	Phe	Glu	Gly	Ser	Phe	Val	Asp	Phe
		275					280					285			
Val	His	Ser	Arg	Gly	Phe	Thr	Met	Gly	Thr	Val	Asp	Asn	Ala	Arg	Val
	290					295					300				
Tyr	Pro	Val	Leu	Lys	Asp	Arg	Ser	Gly	Ala	Asn	Val	Ala	Leu	Gln	Arg
305					310					315					320
Arg	Asn	Phe	Gly	Leu	Asp	Ala	Gly	Lys	Thr	Glu	Val	Pro	Val	Gln	Pro
				325					330					335	
Ala	Val	Asp	Pro	Ala	Trp	Glu	Thr	Pro	Lys	Ala	Glu	Pro	Lys	Lys	Gln
			340					345					350		
Ser	Gly	Arg	Arg	Ala	Pro	Trp	Asp	Lys	Val	Ala	Thr	Pro	Glu	Val	Ile
	355						360					365			
Pro	Asp	Pro	Asn	Pro	Asp	Ala	Asp	Pro	Ser	Ser	Ile	Leu	Tyr	Gly	Gln
	370					375					380				
Asn	Val	Thr	Leu	Thr	Gly	Asp	Phe	Glu	Pro	Tyr	Glu	Lys	Gly	Ala	Leu
385					390					395					400
Trp	Gln	Arg	Ile	Ala	Asp	Gln	Gly	Ala	Leu	Ile	Gly	Lys	Asn	Val	Thr
				405					410					415	
Lys	Lys	Thr	Thr	Ile	Leu	Val	Ala	Gly	Pro	Trp	Ala	Thr	Ile	Thr	Ser
			420					425					430		
Lys	Gln	Lys	Arg	Ala	Glu	Glu	Leu	Lys	Glu	Lys	Gly	Gln	Asp	Ile	Gln
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Pro Pro Phe
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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2764)

<223> RXN00407

<400> 171

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 Met Val Ala Glu His
 1 5

gct gca ggg gat tgg gtg gtc ctt gca ggt ttt cag tgg ttg gac aaa 163
 Ala Ala Gly Asp Trp Val Val Leu Ala Gly Phe Gln Trp Leu Asp Lys
 10 15 20

atc gac tat gtg atc gat tgc ttt aaa ccg gaa aat att gtg ctg gaa 211
 Ile Asp Tyr Val Ile Asp Cys Phe Lys Pro Glu Asn Ile Val Leu Glu
 25 30 35

ttc ggt tca acc atg aca ccg gaa gac gcc gac cgc aat gaa tac ctc 259
 Phe Gly Ser Thr Met Thr Pro Glu Asp Ala Asp Arg Asn Glu Tyr Leu
 40 45 50

aga aga acg caa gcc aaa ttc cag ctt cga ggc atc cta agc acc aac 307
 Arg Arg Thr Gln Ala Lys Phe Gln Leu Arg Gly Ile Leu Ser Thr Asn
 55 60 65

cca gaa tcc gct gcc cgg ggg agc gtg cgg ctt gcc ggc gcc aag cag 355
 Pro Glu Ser Ala Ala Arg Gly Ser Val Arg Leu Ala Gly Ala Lys Gln
 70 75 80 85

gca cta gcc cgc aag atg ccg ctt gcc gac gcc gaa agc gag cta cat 403
 Ala Leu Ala Arg Lys Met Pro Leu Ala Asp Ala Glu Ser Glu Leu His
 90 95 100

ccc atg ggc act acc tgg atg cgc agc ggg gat aca ttg tta aaa gca 451
 Pro Met Gly Thr Thr Trp Met Arg Ser Gly Asp Thr Leu Leu Lys Ala
 105 110 115

cac cct gat tac gcg gat ctc att gca acc acg gtg gaa tta gct gct 499
 His Pro Asp Tyr Ala Asp Leu Ile Ala Thr Thr Val Glu Leu Ala Ala
 120 125 130

gaa tgt gct ttc acc cta gat ttg gtg gcc ccg aat ctg ccc aag tgg 547
 Glu Cys Ala Phe Thr Leu Asp Leu Val Ala Pro Asn Leu Pro Lys Trp
 135 140 145

gat acc cct ggt gaa cac acg gaa atg tcc tgg ctt gcg cac ctg gtt	595
Asp Thr Pro Gly Glu His Thr Glu Met Ser Trp Leu Ala His Leu Val	
150 155 160 165	
tcc act cgg att gat acc cgc tat gtg ggg cgc tcc gca gac atc aaa	643
Ser Thr Arg Ile Asp Thr Arg Tyr Val Gly Arg Ser Ala Asp Ile Lys	
170 175 180	
gca cga gct gcc aca caa att gac tat gaa tta ggc gtt att gaa aag	691
Ala Arg Ala Ala Thr Gln Ile Asp Tyr Glu Leu Gly Val Ile Glu Lys	
185 190 195	
ctg ggt ttt cca ggc tat ttc ctc gtc gtt aat gat ctg gtg gag ttt	739
Leu Gly Phe Pro Gly Tyr Phe Leu Val Val Asn Asp Leu Val Glu Phe	
200 205 210	
tgt cgc gat tcc aat att ttg tgc caa ggc aga ggt tcc gcg gcg aac	787
Cys Arg Asp Ser Asn Ile Leu Cys Gln Gly Arg Gly Ser Ala Ala Asn	
215 220 225	
tcg gcg gtg tgc ttt gtc cta ggc atc acc aac gcg gag ccg atc tct	835
Ser Ala Val Cys Phe Val Leu Gly Ile Thr Asn Ala Glu Pro Ile Ser	
230 235 240 245	
gct gga ttg ttg ttt gaa cgg ttt tta tct cct gac cgg gat ggt cca	883
Ala Gly Leu Leu Phe Glu Arg Phe Leu Ser Pro Asp Arg Asp Gly Pro	
250 255 260	
cca gat att gac att gat att gaa tcc ggc agg cgc gaa gaa gta atc	931
Pro Asp Ile Asp Ile Asp Ile Glu Ser Gly Arg Arg Glu Glu Val Ile	
265 270 275	
caa tac gtg tat gaa aaa tac gga agg gat aac gca gct caa gta gcc	979
Gln Tyr Val Tyr Glu Lys Tyr Gly Arg Asp Asn Ala Ala Gln Val Ala	
280 285 290	
aat gtc att acc tac cga aca aaa ggc gcg atg cgt gat gct gcc cgt	1027
Asn Val Ile Thr Tyr Arg Thr Lys Gly Ala Met Arg Asp Ala Ala Arg	
295 300 305	
gca ctg ggt tac ccg caa ggt gct gcc gat gcc tgg gct aaa gga acc	1075
Ala Leu Gly Tyr Pro Gln Gly Ala Ala Asp Ala Trp Ala Lys Gly Thr	
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Ser Glu Pro Pro Asp Asp Val Leu Glu Ala Ala Gln Phe Lys Gly	
330 335 340	
caa cca cgg cat ttg ggt att cac tcc ggt ggc atg gtc att tgc gat	1171
Gln Pro Arg His Leu Gly Ile His Ser Gly Gly Met Val Ile Cys Asp	
345 350 355	
cgc ccc atc gcc gat gtg gtg cca gtg gaa tgg gct cgg atg gat aac	1219
Arg Pro Ile Ala Asp Val Val Pro Val Glu Trp Ala Arg Met Asp Asn	
360 365 370	
cgc tcg gtt gtg caa tgg gat aaa gat gac tgt gcc acg gca ggc ttg	1267
Arg Ser Val Val Gln Trp Asp Lys Asp Asp Cys Ala Thr Ala Gly Leu	
375 380 385	
gtc aaa ttc gac ctt ttg gga ttg ggc atg ttg gaa gcc atc cat cac	1315

Val 390	Lys	Phe	Asp	Leu	Leu 395	Gly	Leu	Gly	Met	Leu 400	Glu	Ala	Ile	His	His 405	
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Met	Leu	Asp	Leu	Val	Ala	Glu	His	Arg	Gly	Lys	Lys	Ile	Asn	Leu	Trp	
				410					415					420		
gaa	cta	gat	ctg	gcg	gaa	ccg	gag	gtc	tat	gac	atg	ttg	tgc	aag	gca	1411
Glu	Leu	Asp	Leu	Ala	Glu	Pro	Glu	Val	Tyr	Asp	Met	Leu	Cys	Lys	Ala	
			425					430					435			
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Asp	Ala	Val	Gly	Val	Phe	Gln	Val	Glu	Ser	Arg	Ala	Gln	Leu	Ser	Thr	
		440					445					450				
ctg	cct	cga	ctc	aag	ccc	cg	acc	ttc	ttt	gac	ctg	gtc	gtg	gag	gta	1507
Leu	Pro	Arg	Leu	Lys	Pro	Arg	Thr	Phe	Phe	Asp	Leu	Val	Val	Glu	Val	
	455					460					465					
gct	ctg	att	cgt	cca	ggg	ccc	atc	caa	ggc	gga	tcg	gtg	cac	ccg	tat	1555
Ala	Leu	Ile	Arg	Pro	Gly	Pro	Ile	Gln	Gly	Gly	Ser	Val	His	Pro	Tyr	
470					475					480					485	
ttg	cg	cg	cgt	gct	ggg	gaa	gag	gcc	atc	act	tat	gac	cac	ccc	gtg	1603
Leu	Arg	Arg	Arg	Ala	Gly	Glu	Glu	Ala	Ile	Thr	Tyr	Asp	His	Pro	Val	
				490					495					500		
ttg	gaa	aag	tct	ttg	ggg	aaa	acc	tta	gga	atc	cca	ctg	ttt	cag	gaa	1651
Leu	Glu	Lys	Ser	Leu	Gly	Lys	Thr	Leu	Gly	Ile	Pro	Leu	Phe	Gln	Glu	
			505					510					515			
cag	ctc	atg	cag	gta	gct	gtt	gat	gct	gca	ggg	ttt	agt	ggg	ggg	gaa	1699
Gln	Leu	Met	Gln	Val	Ala	Val	Asp	Ala	Ala	Gly	Phe	Ser	Gly	Gly	Glu	
		520					525					530				
gcg	gat	tcc	ttg	cg	aga	gcg	atg	ggg	tcg	aaa	cg	tca	cct	gaa	cg	1747
Ala	Asp	Ser	Leu	Arg	Arg	Ala	Met	Gly	Ser	Lys	Arg	Ser	Pro	Glu	Arg	
	535					540					545					
atg	gct	gcg	ttg	cg	tcg	cg	ttt	ttc	caa	ggg	ctg	aaa	gat	acc	aat	1795
Met	Ala	Ala	Leu	Arg	Ser	Arg	Phe	Phe	Gln	Gly	Leu	Lys	Asp	Thr	Asn	
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ggg	att	gtg	ggg	gag	acc	gcc	gag	aaa	ctg	tgg	aac	aaa	att	gtg	gcc	1843
Gly	Ile	Val	Gly	Glu	Thr	Ala	Glu	Lys	Leu	Trp	Asn	Lys	Ile	Val	Ala	
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ttt	gct	gcc	tac	ggg	ttt	ccg	gaa	tcg	cat	tcg	cag	tcg	ttt	gcg	tcc	1891
Phe	Ala	Ala	Tyr	Gly	Phe	Pro	Glu	Ser	His	Ser	Gln	Ser	Phe	Ala	Ser	
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ttg	gtg	tat	ttc	tcc	gcg	tgg	ttt	aaa	tac	cac	tac	ccg	gct	gaa	ttc	1939
Leu	Val	Tyr	Phe	Ser	Ala	Trp	Phe	Lys	Tyr	His	Tyr	Pro	Ala	Glu	Phe	
		600					605					610				
tgc	gtg	gga	tta	ttg	cg	gca	caa	ccc	atg	ggg	ttc	tat	tca	cca	cag	1987
Cys	Val	Gly	Leu	Leu	Arg	Ala	Gln	Pro	Met	Gly	Phe	Tyr	Ser	Pro	Gln	
	615					620					625					
tct	ttg	atc	agt	gat	gcc	aga	cg	cac	ggc	gtg	agt	atc	ctg	ccg	atc	2035
Ser	Leu	Ile	Ser	Asp	Ala	Arg	Arg	His	Gly	Val	Ser	Ile	Leu	Pro	Ile	

630	635	640	645	
acg gtc aat gat tcc ggt gtg gag gcc gat gct ccg aat ggt gcg att	Thr Val Asn Asp Ser Gly Val Glu Ala Asp Ala Pro Asn Gly Ala Ile	2083		
	650	655	660	
cga ttg ggg ctc aac ctg gtg aaa ggc ctt ggc cac gat gcc gcg caa	Arg Leu Gly Leu Asn Leu Val Lys Gly Leu Gly His Asp Ala Ala Gln	2131		
	665	670	675	
aga ata gag gac aac gcc ccg ttt gat tcc att ccg gat tta tcg cgc	Arg Ile Glu Asp Asn Ala Pro Phe Asp Ser Ile Pro Asp Leu Ser Arg	2179		
	680	685	690	
cgg gct gat ctt aat gtt gct caa gtt gag gca ttg gcg cga gcg gga	Arg Ala Asp Leu Asn Val Ala Gln Val Glu Ala Leu Ala Arg Ala Gly	2227		
	695	700	705	
gcg gtg gac tgc ttg ggg gtc gga cgt cga caa gca tta tgg caa gcg	Ala Val Asp Cys Leu Gly Val Gly Arg Arg Gln Ala Leu Trp Gln Ala	2275		
	710	715	720	725
ggc gtc gca gcg acc gaa aaa cct gga atg ctg cct ggc ctt tcg gtg	Gly Val Ala Ala Thr Glu Lys Pro Gly Met Leu Pro Gly Leu Ser Val	2323		
	730	735	740	
att gaa gct ccg gcg ttg ccg ggg atg agc gcc ttt gag ctg atg gcg	Ile Glu Ala Pro Ala Leu Pro Gly Met Ser Ala Phe Glu Leu Met Ala	2371		
	745	750	755	
acc aat att tcc gcc acg gga gtc acc gcg gat tat cag ccg atg gcg	Thr Asn Ile Ser Ala Thr Gly Val Thr Ala Asp Tyr Gln Pro Met Ala	2419		
	760	765	770	
ttg att cgg gag cgg atg gag gag ctg ggg atc gtg ccg gcg gat cgg	Leu Ile Arg Glu Arg Met Glu Glu Leu Gly Ile Val Pro Ala Asp Arg	2467		
	775	780	785	
cta ttg gag gtg gaa gat ggc acg cgg ctg cgg atc gct ggc att gtc	Leu Leu Glu Val Glu Asp Gly Thr Arg Leu Arg Ile Ala Gly Ile Val	2515		
	790	795	800	805
acg cac cgg cag cgc ccg caa act gcg tcg ggg ctg aca ttt tta ggg	Thr His Arg Gln Arg Pro Gln Thr Ala Ser Gly Leu Thr Phe Leu Gly	2563		
	810	815	820	
atg gag gat gag acc ggg ctg atg aat gtg atg gtg tcc gtt ggg ttg	Met Glu Asp Glu Thr Gly Leu Met Asn Val Met Val Ser Val Gly Leu	2611		
	825	830	835	
tgg cag cgg cag cgc gtg ctg gcc aga aat gcc aag gcg ttg att att	Trp Gln Arg Gln Arg Val Leu Ala Arg Asn Ala Lys Ala Leu Ile Ile	2659		
	840	845	850	
cga ggg att gtg cag aat gcg caa ggg gtg gcg aca gtt gtc gct gac	Arg Gly Ile Val Gln Asn Ala Gln Gly Val Ala Thr Val Val Ala Asp	2707		
	855	860	865	
cgg ttg gaa ccg ttg gac atg ggg gag ttt ctc agc cgt ggc tca cga	Arg Leu Glu Pro Leu Asp Met Gly Glu Phe Leu Ser Arg Gly Ser Arg	2755		
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gat ttt cga taatttggca aagtgacat tat
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2787

<210> 172

<211> 888

<212> PRT

<213> Corynebacterium glutamicum

<400> 172

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 20 25 30

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 35 40 45

Arg Asn Glu Tyr Leu Arg Arg Thr Gln Ala Lys Phe Gln Leu Arg Gly
 50 55 60

Ile Leu Ser Thr Asn Pro Glu Ser Ala Ala Arg Gly Ser Val Arg Leu
 65 70 75 80

Ala Gly Ala Lys Gln Ala Leu Ala Arg Lys Met Pro Leu Ala Asp Ala
 85 90 95

Glu Ser Glu Leu His Pro Met Gly Thr Thr Trp Met Arg Ser Gly Asp
 100 105 110

Thr Leu Leu Lys Ala His Pro Asp Tyr Ala Asp Leu Ile Ala Thr Thr
 115 120 125

Val Glu Leu Ala Ala Glu Cys Ala Phe Thr Leu Asp Leu Val Ala Pro
 130 135 140

Asn Leu Pro Lys Trp Asp Thr Pro Gly Glu His Thr Glu Met Ser Trp
 145 150 155 160

Leu Ala His Leu Val Ser Thr Arg Ile Asp Thr Arg Tyr Val Gly Arg
 165 170 175

Ser Ala Asp Ile Lys Ala Arg Ala Ala Thr Gln Ile Asp Tyr Glu Leu
 180 185 190

Gly Val Ile Glu Lys Leu Gly Phe Pro Gly Tyr Phe Leu Val Val Asn
 195 200 205

Asp Leu Val Glu Phe Cys Arg Asp Ser Asn Ile Leu Cys Gln Gly Arg
 210 215 220

Gly Ser Ala Ala Asn Ser Ala Val Cys Phe Val Leu Gly Ile Thr Asn
 225 230 235 240

Ala Glu Pro Ile Ser Ala Gly Leu Leu Phe Glu Arg Phe Leu Ser Pro
 245 250 255

Asp Arg Asp Gly Pro Pro Asp Ile Asp Ile Asp Ile Glu Ser Gly Arg

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Arg	Asp	Ala	Ala	Arg	Ala	Leu	Gly	Tyr	Pro	Gln	Gly	Ala	Ala	Asp	Ala		
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Trp	Ala	Lys	Gly	Thr	Ser	Glu	Pro	Pro	Asp	Asp	Val	Leu	Glu	Leu	Ala		
325						330						335					
Ala	Gln	Phe	Lys	Gly	Gln	Pro	Arg	His	Leu	Gly	Ile	His	Ser	Gly	Gly		
340						345						350					
Met	Val	Ile	Cys	Asp	Arg	Pro	Ile	Ala	Asp	Val	Val	Pro	Val	Glu	Trp		
355						360						365					
Ala	Arg	Met	Asp	Asn	Arg	Ser	Val	Val	Gln	Trp	Asp	Lys	Asp	Asp	Cys		
370						375						380					
Ala	Thr	Ala	Gly	Leu	Val	Lys	Phe	Asp	Leu	Leu	Gly	Leu	Gly	Met	Leu		
385						390						395					
Glu	Ala	Ile	His	His	Met	Leu	Asp	Leu	Val	Ala	Glu	His	Arg	Gly	Lys		
405						410						415					
Lys	Ile	Asn	Leu	Trp	Glu	Leu	Asp	Leu	Ala	Glu	Pro	Glu	Val	Tyr	Asp		
420						425						430					
Met	Leu	Cys	Lys	Ala	Asp	Ala	Val	Gly	Val	Phe	Gln	Val	Glu	Ser	Arg		
435						440						445					
Ala	Gln	Leu	Ser	Thr	Leu	Pro	Arg	Leu	Lys	Pro	Arg	Thr	Phe	Phe	Asp		
450						455						460					
Leu	Val	Val	Glu	Val	Ala	Leu	Ile	Arg	Pro	Gly	Pro	Ile	Gln	Gly	Gly		
465						470						475					
Ser	Val	His	Pro	Tyr	Leu	Arg	Arg	Arg	Ala	Gly	Glu	Glu	Ala	Ile	Thr		
485						490						495					
Tyr	Asp	His	Pro	Val	Leu	Glu	Lys	Ser	Leu	Gly	Lys	Thr	Leu	Gly	Ile		
500						505						510					
Pro	Leu	Phe	Gln	Glu	Gln	Leu	Met	Gln	Val	Ala	Val	Asp	Ala	Ala	Gly		
515						520						525					
Phe	Ser	Gly	Gly	Glu	Ala	Asp	Ser	Leu	Arg	Arg	Ala	Met	Gly	Ser	Lys		
530						535						540					
Arg	Ser	Pro	Glu	Arg	Met	Ala	Ala	Leu	Arg	Ser	Arg	Phe	Phe	Gln	Gly		
545						550						555					
Leu	Lys	Asp	Thr	Asn	Gly	Ile	Val	Gly	Glu	Thr	Ala	Glu	Lys	Leu	Trp		
565						570						575					
Asn	Lys	Ile	Val	Ala	Phe	Ala	Ala	Tyr	Gly	Phe	Pro	Glu	Ser	His	Ser		
580						585						590					

Gln Ser Phe Ala Ser Leu Val Tyr Phe Ser Ala Trp Phe Lys Tyr His
 595 600 605
 Tyr Pro Ala Glu Phe Cys Val Gly Leu Leu Arg Ala Gln Pro Met Gly
 610 615 620
 Phe Tyr Ser Pro Gln Ser Leu Ile Ser Asp Ala Arg Arg His Gly Val
 625 630 635 640
 Ser Ile Leu Pro Ile Thr Val Asn Asp Ser Gly Val Glu Ala Asp Ala
 645 650 655
 Pro Asn Gly Ala Ile Arg Leu Gly Leu Asn Leu Val Lys Gly Leu Gly
 660 665 670
 His Asp Ala Ala Gln Arg Ile Glu Asp Asn Ala Pro Phe Asp Ser Ile
 675 680 685
 Pro Asp Leu Ser Arg Arg Ala Asp Leu Asn Val Ala Gln Val Glu Ala
 690 695 700
 Leu Ala Arg Ala Gly Ala Val Asp Cys Leu Gly Val Gly Arg Arg Gln
 705 710 715 720
 Ala Leu Trp Gln Ala Gly Val Ala Ala Thr Glu Lys Pro Gly Met Leu
 725 730 735
 Pro Gly Leu Ser Val Ile Glu Ala Pro Ala Leu Pro Gly Met Ser Ala
 740 745 750
 Phe Glu Leu Met Ala Thr Asn Ile Ser Ala Thr Gly Val Thr Ala Asp
 755 760 765
 Tyr Gln Pro Met Ala Leu Ile Arg Glu Arg Met Glu Glu Leu Gly Ile
 770 775 780
 Val Pro Ala Asp Arg Leu Leu Glu Val Glu Asp Gly Thr Arg Leu Arg
 785 790 795 800
 Ile Ala Gly Ile Val Thr His Arg Gln Arg Pro Gln Thr Ala Ser Gly
 805 810 815
 Leu Thr Phe Leu Gly Met Glu Asp Glu Thr Gly Leu Met Asn Val Met
 820 825 830
 Val Ser Val Gly Leu Trp Gln Arg Gln Arg Val Leu Ala Arg Asn Ala
 835 840 845
 Lys Ala Leu Ile Ile Arg Gly Ile Val Gln Asn Ala Gln Gly Val Ala
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 Ser Arg Gly Ser Arg Asp Phe Arg
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<211> 599

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(576)

<223> FRXA00407

<400> 173

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Cys Leu Gly Val Gly Arg Arg Gln Ala Leu Trp Gln Ala Gly Val Ala	
20 25 30	
gcg acc gaa aaa cct gga atg ctg cct ggc ctt tcg gtg att gaa gct	144
Ala Thr Glu Lys Pro Gly Met Leu Pro Gly Leu Ser Val Ile Glu Ala	
35 40 45	
ccg gcg ttg ccg ggg atg agc gcc ttt gag ctg atg gcg acc aat att	192
Pro Ala Leu Pro Gly Met Ser Ala Phe Glu Leu Met Ala Thr Asn Ile	
50 55 60	
tcc gcc acg gga gtc acc gcg gat tat cag ccg atg gcg ttg att cgg	240
Ser Ala Thr Gly Val Thr Ala Asp Tyr Gln Pro Met Ala Leu Ile Arg	
65 70 75 80	
gag cgg atg gag gag ctg ggg atc gtg ccg gcg gat cgg cta ttg gag	288
Glu Arg Met Glu Glu Leu Gly Ile Val Pro Ala Asp Arg Leu Leu Glu	
85 90 95	
gtg gaa gat ggc acg cgg ctg cgg atc gct ggc att gtc acg cac cgg	336
Val Glu Asp Gly Thr Arg Leu Arg Ile Ala Gly Ile Val Thr His Arg	
100 105 110	
cag cgc ccg caa act gcg tcg ggg ctg aca ttt tta ggg atg gag gat	384
Gln Arg Pro Gln Thr Ala Ser Gly Leu Thr Phe Leu Gly Met Glu Asp	
115 120 125	
gag acc ggg ctg atg aat gtg atg gtg tcc gtt ggg ttg tgg cag cgg	432
Glu Thr Gly Leu Met Asn Val Met Val Ser Val Gly Leu Trp Gln Arg	
130 135 140	
cag cgc gtg ctg gcc aga aat gcc aag gcg ttg att att cga ggg att	480
Gln Arg Val Leu Ala Arg Asn Ala Lys Ala Leu Ile Ile Arg Gly Ile	
145 150 155 160	
gtg cag aat gcg caa ggg gtg gcg aca gtt gtc gct gac cgg ttg gaa	528
Val Gln Asn Ala Gln Gly Val Ala Thr Val Val Ala Asp Arg Leu Glu	
165 170 175	
ccg ttg gac atg ggg gag ttt ctc agc cgt ggc tca cga gat ttt cga	576
Pro Leu Asp Met Gly Glu Phe Leu Ser Arg Gly Ser Arg Asp Phe Arg	
180 185 190	
taattttggca aagtggacat tat	599

<210> 174

<400> 174

Pro Leu Asp Met Gly Glu Phe Leu Ser Arg Gly Ser Arg Asp Phe Arg
180 185 190

<400> 175

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Met Val Ala Glu His
1 5

gct gca ggg gat tgg gtg gtc ctt gca ggt ttt cag tgg ttg gac aaa 163
 Ala Ala Gly Asp Trp Val Val Leu Ala Gly Phe Gln Trp Leu Asp Lys
 10 15 20

atc gac tat gtg atc gat tgc ttt aaa ccg gaa aat att gtg ctg gaa 211
 Ile Asp Tyr Val Ile Asp Cys Phe Lys Pro Glu Asn Ile Val Leu Glu
 25 30 35

ttc ggt tca acc atg aca ccg gaa gac gcc gac cgc aat gaa tac ctc 259
 Phe Gly Ser Thr Met Thr Pro Glu Asp Ala Asp Arg Asn Glu Tyr Leu
 40 45 50

aga aga acg caa gcc aaa ttc cag ctt cga ggc atc cta agc acc aac 307
 Arg Arg Thr Gln Ala Lys Phe Gln Leu Arg Gly Ile Leu Ser Thr Asn
 55 60 65

cca gaa tcc gct gcc cgg ggg agc gtg cgg ctt gcc ggc gcc aag cag 355
 Pro Glu Ser Ala Ala Arg Gly Ser Val Arg Leu Ala Gly Ala Lys Gln
 70 75 80 85

gca cta gcc cgc aag atg ccg ctt gcc gac gcc gaa agc gag cta cat 403
 Ala Leu Ala Arg Lys Met Pro Leu Ala Asp Ala Glu Ser Glu Leu His
 90 95 100

ccc atg ggc act acc tgg atg cgc agc ggg gat aca ttg tta aaa gca 451
 Pro Met Gly Thr Thr Trp Met Arg Ser Gly Asp Thr Leu Leu Lys Ala
 105 110 115

cac cct gat tac gcg gat ctc att gca acc acg gtg gaa tta gct gct 499
 His Pro Asp Tyr Ala Asp Leu Ile Ala Thr Thr Val Glu Leu Ala Ala
 120 125 130

gaa tgt gct ttc acc cta gat ttg gtg gcc ccg aat ctg ccc aag tgg 547
 Glu Cys Ala Phe Thr Leu Asp Leu Val Ala Pro Asn Leu Pro Lys Trp
 135 140 145

gat acc cct ggt gaa cac acg gaa atg tcc tgg ctt gcg cac ctg gtt 595
 Asp Thr Pro Gly Glu His Thr Glu Met Ser Trp Leu Ala His Leu Val
 150 155 160 165

tcc act cgg att gat acc cgc tat gtg ggg cgc tcc gca gac atc aaa 643
 Ser Thr Arg Ile Asp Thr Arg Tyr Val Gly Arg Ser Ala Asp Ile Lys
 170 175 180

gca cga gct gcc aca caa att gac tat gaa tta ggc gtt att gaa aag 691
 Ala Arg Ala Ala Thr Gln Ile Asp Tyr Glu Leu Gly Val Ile Glu Lys
 185 190 195

ctg ggt ttt cca ggc tat ttc ctc gtc gtt aat gat ctg gtg gag ttt 739
 Leu Gly Phe Pro Gly Tyr Phe Leu Val Val Asn Asp Leu Val Glu Phe
 200 205 210

tgt cgc gat tcc aat att ttg tgc caa ggc aga ggt tcc gcg gcg aac 787
 Cys Arg Asp Ser Asn Ile Leu Cys Gln Gly Arg Gly Ser Ala Ala Asn
 215 220 225

tgc gcg gtg tgc ttt gtc cta ggc atc acc aac gcg gag ccg atc tct 835
 Ser Ala Val Cys Phe Val Leu Gly Ile Thr Asn Ala Glu Pro Ile Ser
 230 235 240 245

gct gga ttg ttg ttt gaa cgg ttt tta tct cct gac cgg gat ggt cca	883
Ala Gly Leu Leu Phe Glu Arg Phe Leu Ser Pro Asp Arg Asp Gly Pro	
250 255 260	
cca gat att gac att gat att gaa tcc ggc agg cgc gaa gaa gta atc	931
Pro Asp Ile Asp Ile Asp Ile Glu Ser Gly Arg Arg Glu Glu Val Ile	
265 270 275	
caa tac gtg tat gaa aaa tac gga agg gat aac gca gct caa gta gcc	979
Gln Tyr Val Tyr Glu Lys Tyr Gly Arg Asp Asn Ala Ala Gln Val Ala	
280 285 290	
aat gtc att acc tac cga aca aaa ggc gcg atg cgt gat gct gcc cgt	1027
Asn Val Ile Thr Tyr Arg Thr Lys Gly Ala Met Arg Asp Ala Ala Arg	
295 300 305	
gca ctg ggt tac ccg caa ggt gct gcc gat gcc tgg gct aaa gga acc	1075
Ala Leu Gly Tyr Pro Gln Gly Ala Ala Asp Ala Trp Ala Lys Gly Thr	
310 315 320 325	
tcg gaa cca ccc gat gat gtg ctg gaa tta gct gcg caa ttt aaa ggg	1123
Ser Glu Pro Pro Asp Asp Val Leu Glu Leu Ala Ala Gln Phe Lys Gly	
330 335 340	
caa cca cgg cat ttg ggt att cac tcc ggt ggc atg gtc att tgc gat	1171
Gln Pro Arg His Leu Gly Ile His Ser Gly Gly Met Val Ile Cys Asp	
345 350 355	
cgc ccc atc gcc gat gtg gtg cca gtg gaa tgg gct cgg atg gat aac	1219
Arg Pro Ile Ala Asp Val Val Pro Val Glu Trp Ala Arg Met Asp Asn	
360 365 370	
cgc tcg gtt gtg caa tgg gat aaa gat gac tgt gcc acg gca ggc ttg	1267
Arg Ser Val Val Gln Trp Asp Lys Asp Asp Cys Ala Thr Ala Gly Leu	
375 380 385	
gtc aaa ttc gac ctt ttg gga ttg ggc atg ttg gaa gcc atc cat cac	1315
Val Lys Phe Asp Leu Leu Gly Leu Gly Met Leu Glu Ala Ile His His	
390 395 400 405	
atg ctg gat ctg gtg gca gaa cac cga ggt aaa aag atc aat ttg tgg	1363
Met Leu Asp Leu Val Ala Glu His Arg Gly Lys Lys Ile Asn Leu Trp	
410 415 420	
gaa cta gat ctg gcg gaa ccg gag gtc tat gac atg ttg tgc aag gca	1411
Glu Leu Asp Leu Ala Glu Pro Glu Val Tyr Asp Met Leu Cys Lys Ala	
425 430 435	
gat gcc gtg ggt gtg ttc cag gtg gaa tca cgt gcg cag tta tcc acg	1459
Asp Ala Val Gly Val Phe Gln Val Glu Ser Arg Ala Gln Leu Ser Thr	
440 445 450	
ctg cct cga ctc aag ccc cgc acc ttc ttt gac ctg gtc gtg gag gta	1507
Leu Pro Arg Leu Lys Pro Arg Thr Phe Phe Asp Leu Val Val Glu Val	
455 460 465	
gct ctg att cgt cca ggt ccc atc caa ggc gga tcg gtg cac ccg tat	1555
Ala Leu Ile Arg Pro Gly Pro Ile Gln Gly Gly Ser Val His Pro Tyr	
470 475 480 485	
ttg cgg cgc cgt gct ggt gaa gag gcc atc act tat gac cac ccc gtg	1603

Leu	Arg	Arg	Arg	Ala	Gly	Glu	Glu	Ala	Ile	Thr	Tyr	Asp	His	Pro	Val	
				490					495					500		
ttg	gaa	aag	tct	ttg	ggt	aaa	acc	tta	gga	atc	cca	ctg	ttt	cag	gaa	1651
Leu	Glu	Lys	Ser	Leu	Gly	Lys	Thr	Leu	Gly	Ile	Pro	Leu	Phe	Gln	Glu	
			505					510					515			
cag	ctc	atg	cag	gta	gct	gtt	gat	gct	gca	ggt	ttt	agt	ggt	ggg	gaa	1699
Gln	Leu	Met	Gln	Val	Ala	Val	Asp	Ala	Ala	Gly	Phe	Ser	Gly	Gly	Glu	
		520					525					530				
gcg	gat	tcc	ttg	cgc	aga	gcg	atg	ggg	tcg	aaa	cgc	tca	cct	gaa	cgc	1747
Ala	Asp	Ser	Leu	Arg	Arg	Ala	Met	Gly	Ser	Lys	Arg	Ser	Pro	Glu	Arg	
	535					540					545					
atg	gct	gcg	ttg	cgc	tcg	cgg	ttt	ttc	caa	ggg	ctg	aaa	gat	acc	aat	1795
Met	Ala	Ala	Leu	Arg	Ser	Arg	Phe	Phe	Gln	Gly	Leu	Lys	Asp	Thr	Asn	
550				555						560					565	
ggg	att	gtg	ggg	gag	acc	gcc	gag	aaa	ctg	tgg	aac	aaa	att	gtg	gcc	1843
Gly	Ile	Val	Gly	Glu	Thr	Ala	Glu	Lys	Leu	Trp	Asn	Lys	Ile	Val	Ala	
			570					575						580		
ttt	gct	gcc	tac	ggt	ttt	ccg	gaa	tcg	cat	tcg	cag	tcg	ttt	gcg	tcc	1891
Phe	Ala	Ala	Tyr	Gly	Phe	Pro	Glu	Ser	His	Ser	Gln	Ser	Phe	Ala	Ser	
			585					590					595			
ttg	gtg	tat	ttc	tcc	gcg	tgg	ttt	aaa	tac	cac	tac	ccg	gct	gaa	ttc	1939
Leu	Val	Tyr	Phe	Ser	Ala	Trp	Phe	Lys	Tyr	His	Tyr	Pro	Ala	Glu	Phe	
	600					605						610				
tgc	gtg	gga	tta	ttg	cgg	gca	caa	ccc	atg	ggt	ttc	tat	tca	cca	cag	1987
Cys	Val	Gly	Leu	Leu	Arg	Ala	Gln	Pro	Met	Gly	Phe	Tyr	Ser	Pro	Gln	
	615					620					625					
tct	ttg	atc	agt	gat	gcc	aga	cgc	cac	ggc	gtg	agt	atc	ctg	ccg	atc	2035
Ser	Leu	Ile	Ser	Asp	Ala	Arg	Arg	His	Gly	Val	Ser	Ile	Leu	Pro	Ile	
630				635					640						645	
acg	gtc	aat	gat	tcc	ggt	gtg	gag	gcc								2062
Thr	Val	Asn	Asp	Ser	Gly	Val	Glu	Ala								
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<210> 176

<211> 654

<212> PRT

<213> Corynebacterium glutamicum

<400> 176

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Gln	Trp	Leu	Asp	Lys	Ile	Asp	Tyr	Val	Ile	Asp	Cys	Phe	Lys	Pro	Glu
		20						25					30		

Asn	Ile	Val	Leu	Glu	Phe	Gly	Ser	Thr	Met	Thr	Pro	Glu	Asp	Ala	Asp
		35					40					45			

Arg	Asn	Glu	Tyr	Leu	Arg	Arg	Thr	Gln	Ala	Lys	Phe	Gln	Leu	Arg	Gly
	50					55					60				

Ile	Leu	Ser	Thr	Asn	Pro	Glu	Ser	Ala	Ala	Arg	Gly	Ser	Val	Arg	Leu	65	70	75	80
Ala	Gly	Ala	Lys	Gln	Ala	Leu	Ala	Arg	Lys	Met	Pro	Leu	Ala	Asp	Ala	85	90	95	
Glu	Ser	Glu	Leu	His	Pro	Met	Gly	Thr	Thr	Trp	Met	Arg	Ser	Gly	Asp	100	105	110	
Thr	Leu	Leu	Lys	Ala	His	Pro	Asp	Tyr	Ala	Asp	Leu	Ile	Ala	Thr	Thr	115	120	125	
Val	Glu	Leu	Ala	Ala	Glu	Cys	Ala	Phe	Thr	Leu	Asp	Leu	Val	Ala	Pro	130	135	140	
Asn	Leu	Pro	Lys	Trp	Asp	Thr	Pro	Gly	Glu	His	Thr	Glu	Met	Ser	Trp	145	150	155	160
Leu	Ala	His	Leu	Val	Ser	Thr	Arg	Ile	Asp	Thr	Arg	Tyr	Val	Gly	Arg	165	170	175	
Ser	Ala	Asp	Ile	Lys	Ala	Arg	Ala	Ala	Thr	Gln	Ile	Asp	Tyr	Glu	Leu	180	185	190	
Gly	Val	Ile	Glu	Lys	Leu	Gly	Phe	Pro	Gly	Tyr	Phe	Leu	Val	Val	Asn	195	200	205	
Asp	Leu	Val	Glu	Phe	Cys	Arg	Asp	Ser	Asn	Ile	Leu	Cys	Gln	Gly	Arg	210	215	220	
Gly	Ser	Ala	Ala	Asn	Ser	Ala	Val	Cys	Phe	Val	Leu	Gly	Ile	Thr	Asn	225	230	235	240
Ala	Glu	Pro	Ile	Ser	Ala	Gly	Leu	Leu	Phe	Glu	Arg	Phe	Leu	Ser	Pro	245	250	255	
Asp	Arg	Asp	Gly	Pro	Pro	Asp	Ile	Asp	Ile	Asp	Ile	Glu	Ser	Gly	Arg	260	265	270	
Arg	Glu	Glu	Val	Ile	Gln	Tyr	Val	Tyr	Glu	Lys	Tyr	Gly	Arg	Asp	Asn	275	280	285	
Ala	Ala	Gln	Val	Ala	Asn	Val	Ile	Thr	Tyr	Arg	Thr	Lys	Gly	Ala	Met	290	295	300	
Arg	Asp	Ala	Ala	Arg	Ala	Leu	Gly	Tyr	Pro	Gln	Gly	Ala	Ala	Asp	Ala	305	310	315	320
Trp	Ala	Lys	Gly	Thr	Ser	Glu	Pro	Pro	Asp	Asp	Val	Leu	Glu	Leu	Ala	325	330	335	
Ala	Gln	Phe	Lys	Gly	Gln	Pro	Arg	His	Leu	Gly	Ile	His	Ser	Gly	Gly	340	345	350	
Met	Val	Ile	Cys	Asp	Arg	Pro	Ile	Ala	Asp	Val	Val	Pro	Val	Glu	Trp	355	360	365	
Ala	Arg	Met	Asp	Asn	Arg	Ser	Val	Val	Gln	Trp	Asp	Lys	Asp	Asp	Cys	370	375	380	

Ala Thr Ala Gly Leu Val Lys Phe Asp Leu Leu Gly Leu Gly Met Leu
 385 390 395 400
 Glu Ala Ile His His Met Leu Asp Leu Val Ala Glu His Arg Gly Lys
 405 410 415
 Lys Ile Asn Leu Trp Glu Leu Asp Leu Ala Glu Pro Glu Val Tyr Asp
 420 425 430
 Met Leu Cys Lys Ala Asp Ala Val Gly Val Phe Gln Val Glu Ser Arg
 435 440 445
 Ala Gln Leu Ser Thr Leu Pro Arg Leu Lys Pro Arg Thr Phe Phe Asp
 450 455 460
 Leu Val Val Glu Val Ala Leu Ile Arg Pro Gly Pro Ile Gln Gly Gly
 465 470 475 480
 Ser Val His Pro Tyr Leu Arg Arg Arg Ala Gly Glu Glu Ala Ile Thr
 485 490 495
 Tyr Asp His Pro Val Leu Glu Lys Ser Leu Gly Lys Thr Leu Gly Ile
 500 505 510
 Pro Leu Phe Gln Glu Gln Leu Met Gln Val Ala Val Asp Ala Ala Gly
 515 520 525
 Phe Ser Gly Gly Glu Ala Asp Ser Leu Arg Arg Ala Met Gly Ser Lys
 530 535 540
 Arg Ser Pro Glu Arg Met Ala Ala Leu Arg Ser Arg Phe Phe Gln Gly
 545 550 555 560
 Leu Lys Asp Thr Asn Gly Ile Val Gly Glu Thr Ala Glu Lys Leu Trp
 565 570 575
 Asn Lys Ile Val Ala Phe Ala Ala Tyr Gly Phe Pro Glu Ser His Ser
 580 585 590
 Gln Ser Phe Ala Ser Leu Val Tyr Phe Ser Ala Trp Phe Lys Tyr His
 595 600 605
 Tyr Pro Ala Glu Phe Cys Val Gly Leu Leu Arg Ala Gln Pro Met Gly
 610 615 620
 Phe Tyr Ser Pro Gln Ser Leu Ile Ser Asp Ala Arg Arg His Gly Val
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 Ser Ile Leu Pro Ile Thr Val Asn Asp Ser Gly Val Glu Ala
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<210> 177

<211> 477

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(454)

<223> RXN00414

<400> 177

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ggtgctgcat gagccggatg cgcaggcgcc ttcattctgcc atg cag ggg gaa gcg 115
Met Gln Gly Glu Ala
1 5

tcg gtt cct ttt gcc gag ctg cat gcc acc agc agt tat aac ttt ctc 163
Ser Val Pro Phe Ala Glu Leu His Ala Thr Ser Ser Tyr Asn Phe Leu
10 15 20

act ggc gca tcg gat ccg tct gat gtg gtt gtg cag gcc aaa aag tta 211
Thr Gly Ala Ser Asp Pro Ser Asp Val Val Val Gln Ala Lys Lys Leu
25 30 35

gga ctt gct gct cta tca gtc atg gat agg gat ggt ttt tat ggt gca 259
Gly Leu Ala Ala Leu Ser Val Met Asp Arg Asp Gly Phe Tyr Gly Ala
40 45 50

gtg aga ttt gcg gaa gct gcc gcg gaa gct gga atg cat acc gtt tat 307
Val Arg Phe Ala Glu Ala Ala Ala Glu Ala Gly Met His Thr Val Tyr
55 60 65

ggt gcg gag ctg agt ctg caa gaa ggc gtg ttg aca gtc ttg tgt aaa 355
Gly Ala Glu Leu Ser Leu Gln Glu Gly Val Leu Thr Val Leu Cys Lys
70 75 80 85

aat ccg gaa ggc tac aaa aag ctc agt cac ctg atc agt gac gcg aaa 403
Asn Pro Glu Gly Tyr Lys Lys Leu Ser His Leu Ile Ser Asp Ala Lys
90 95 100

atg gca cgg gag aaa agg gga agt tcg cta tcc gcc gct gcc aat ggt 451
Met Ala Arg Glu Lys Arg Gly Ser Ser Leu Ser Ala Ala Ala Asn Gly
105 110 115

tgc tgaacatgct gcaggggatt ggg 477
Cys

<210> 178

<211> 118

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 178

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Ser Tyr Asn Phe Leu Thr Gly Ala Ser Asp Pro Ser Asp Val Val Val
20 25 30

Gln Ala Lys Lys Leu Gly Leu Ala Ala Leu Ser Val Met Asp Arg Asp
35 40 45

Gly Phe Tyr Gly Ala Val Arg Phe Ala Glu Ala Ala Ala Glu Ala Gly
50 55 60

Met His Thr Val Tyr Gly Ala Glu Leu Ser Leu Gln Glu Gly Val Leu
65 70 75 80

<400> 179																
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Met Gln Gly Glu Ala 1 5																
tcg gtt cct ttt gcc gag ctg cat gcc acc agc agt tat aac ttt ctc																163
Ser Val Pro Phe Ala Glu Leu His Ala Thr Ser Ser Tyr Asn Phe Leu 10 15 20																
act ggc gca tcg gat ccg tct gat gtg gtt gtg cag gcc aaa aag tta																211
Thr Gly Ala Ser Asp Pro Ser Asp Val Val Val Gln Ala Lys Lys Leu 25 30 35																
gga ctt gct gct cta tca gtc atg gat agg gat ggt ttt tat ggt gca																259
Gly Leu Ala Ala Leu Ser Val Met Asp Arg Asp Gly Phe Tyr Gly Ala 40 45 50																
gtg aga ttt gcg gaa gct gcc gcg gaa gct gga atg cat acc gtt tat																307
Val Arg Phe Ala Glu Ala Ala Ala Glu Ala Gly Met His Thr Val Tyr 55 60 65																
ggt gcg gag ctg agt ctg caa gaa ggc gtg ttg aca gtc ttg tgt aaa																355
Gly Ala Glu Leu Ser Leu Gln Glu Gly Val Leu Thr Val Leu Cys Lys 70 75 80 85																
aat ccg gaa ggc tac aaa aag ctc agt cac ctg atc agt gac gcg aaa																403
Asn Pro Glu Gly Tyr Lys Lys Leu Ser His Leu Ile Ser Asp Ala Lys 90 95 100																
atg gca cgg gga gaa aag ggg aag ttc gct atc cgc cgc tgc caa tgg																451
Met Ala Arg Gly Glu Lys Gly Lys Phe Ala Ile Arg Arg Cys Gln Trp 105 110 115																
ttg ctg aac atg ctg cag ggg att ggg tgg tcc ttg cag gtt ttc agt																499
Leu Leu Asn Met Leu Gln Gly Ile Gly Trp Ser Leu Gln Val Phe Ser 120 125 130																
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Gly Trp Thr Lys Ser Thr Met
135 140

<210> 180

<211> 140

<212> PRT

<213> Corynebacterium glutamicum

<400> 180

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20 25 30

Gln Ala Lys Lys Leu Gly Leu Ala Ala Leu Ser Val Met Asp Arg Asp
35 40 45

Gly Phe Tyr Gly Ala Val Arg Phe Ala Glu Ala Ala Glu Ala Gly
50 55 60

Met His Thr Val Tyr Gly Ala Glu Leu Ser Leu Gln Glu Gly Val Leu
65 70 75 80

Thr Val Leu Cys Lys Asn Pro Glu Gly Tyr Lys Lys Leu Ser His Leu
85 90 95

Ile Ser Asp Ala Lys Met Ala Arg Gly Glu Lys Gly Lys Phe Ala Ile
100 105 110

Arg Arg Cys Gln Trp Leu Leu Asn Met Leu Gln Gly Ile Gly Trp Ser
115 120 125

Leu Gln Val Phe Ser Gly Trp Thr Lys Ser Thr Met
130 135 140

<210> 181

<211> 1365

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1342)

<223> RXN00807

<400> 181

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Val Phe Asp Ser Leu
1 5

gcc ggc tcc aaa aca gtg tcc aag acg ctt ttc gac gcg gcc tcc agc 163
Ala Gly Ser Lys Thr Val Ser Lys Thr Leu Phe Asp Ala Ala Ser Ser
10 15 20

gcg cgt gcc ctt gtc cgc gcc cga acc aca gaa cgt gcc cgc gcc cgg 211
Ala Arg Ala Leu Val Arg Ala Arg Thr Thr Glu Arg Ala Arg Ala Arg

25					30					35						
gca	gaa	cac	caa	aac	cct	gca	atg	atc	cac	gac	tcc	ggc	ttt	gcc	cag	259
Ala	Glu	His	Gln	Asn	Pro	Ala	Met	Ile	His	Asp	Ser	Gly	Phe	Ala	Gln	
	40						45					50				
tca	tgg	ctg	ttt	aca	ggc	cct	ccc	gga	tcg	gga	cgt	tct	gtg	gca	gcc	307
Ser	Trp	Leu	Phe	Thr	Gly	Pro	Pro	Gly	Ser	Gly	Arg	Ser	Val	Ala	Ala	
	55					60					65					
aag	gtt	ttc	gcc	gct	acg	ctc	gta	tgt	tcg	aat	ccg	gat	gtt	gtg	ggc	355
Lys	Val	Phe	Ala	Ala	Thr	Leu	Val	Cys	Ser	Asn	Pro	Asp	Val	Val	Gly	
	70				75				80						85	
tgt	gga	caa	tgc	gag	gat	tgc	cgc	gcc	gcc	atg	gga	ggc	agc	cac	ccc	403
Cys	Gly	Gln	Cys	Glu	Asp	Cys	Arg	Ala	Ala	Met	Gly	Gly	Ser	His	Pro	
				90				95						100		
gat	att	gaa	cac	atc	gtc	ccg	cag	caa	ttg	tct	atc	ggt	gtt	gat	gca	451
Asp	Ile	Glu	His	Ile	Val	Pro	Gln	Gln	Leu	Ser	Ile	Gly	Val	Asp	Ala	
			105				110							115		
gct	aga	gag	gtc	atc	aaa	gcc	gca	gcg	gtc	agt	cct	gtt	gca	gga	aac	499
Ala	Arg	Glu	Val	Ile	Lys	Ala	Ala	Ala	Val	Ser	Pro	Val	Ala	Gly	Asn	
			120				125					130				
tgg	cga	gtc	gtc	atc	ttc	gaa	aac	gcc	gac	cga	ctc	acc	atg	caa	gcc	547
Trp	Arg	Val	Val	Ile	Phe	Glu	Asn	Ala	Asp	Arg	Leu	Thr	Met	Gln	Ala	
	135					140					145					
gcc	aac	gcc	ttg	ctg	aaa	acc	gtg	gag	gaa	cca	acc	gaa	agc	acc	gtg	595
Ala	Asn	Ala	Leu	Leu	Lys	Thr	Val	Glu	Glu	Pro	Thr	Glu	Ser	Thr	Val	
	150				155					160					165	
atg	att	ctg	tgc	gca	ccc	acc	aca	gac	ccc	cgc	gac	att	gcg	atc	acc	643
Met	Ile	Leu	Cys	Ala	Pro	Thr	Thr	Asp	Pro	Arg	Asp	Ile	Ala	Ile	Thr	
				170				175						180		
ctc	cgc	tcc	cgc	tgc	agg	cac	ctc	tac	att	ccc	acc	ccc	tcc	atc	gcg	691
Leu	Arg	Ser	Arg	Cys	Arg	His	Leu	Tyr	Ile	Pro	Thr	Pro	Ser	Ile	Ala	
			185				190						195			
gaa	gtc	gca	cga	atc	ctc	gta	gct	gaa	ggc	aac	gtc	agc	caa	gcg	gat	739
Glu	Val	Ala	Arg	Ile	Leu	Val	Ala	Glu	Gly	Asn	Val	Ser	Gln	Ala	Asp	
	200					205						210				
gca	gaa	tta	gcg	gcg	gct	gcc	tca	ggc	gct	cac	atc	ggc	agg	gct	cga	787
Ala	Glu	Leu	Ala	Ala	Ala	Ala	Ser	Gly	Ala	His	Ile	Gly	Arg	Ala	Arg	
	215					220					225					
tac	tta	gcg	cac	aac	aac	gcc	gcc	caa	cgc	aga	cgc	gcc	agc	atc	ctc	835
Tyr	Leu	Ala	His	Asn	Asn	Ala	Ala	Gln	Arg	Arg	Arg	Ala	Ser	Ile	Leu	
	230				235					240					245	
aac	ctg	gcc	gaa	tta	atc	ttc	cac	ggt	gat	gtc	gcc	ttc	cgc	tcc	gta	883
Asn	Leu	Ala	Glu	Leu	Ile	Phe	His	Gly	Asp	Val	Ala	Phe	Arg	Ser	Val	
				250				255						260		
aac	acc	ttg	gtc	aaa	atg	gtg	gaa	acc	gaa	gcc	aaa	gac	agc	aac	aaa	931
Asn	Thr	Leu	Val	Lys	Met	Val	Glu	Thr	Glu	Ala	Lys	Asp	Ser	Asn	Lys	
			265				270						275			

gaa aaa gaa gaa ggc gat ctc gaa gcc gta aga atc tca ctc ggc atg 979
 Glu Lys Glu Glu Gly Asp Leu Glu Ala Val Arg Ile Ser Leu Gly Met
 280 285 290

ggg gcc aaa ggc aaa ggt gtc cac aaa gca gta cgt gga gga gcg gga 1027
 Gly Ala Lys Gly Lys Gly Val His Lys Ala Val Arg Gly Gly Ala Gly
 295 300 305

gat ttc aaa gca ctc gaa gac caa caa aaa ctc cga cgc acc cga ttc 1075
 Asp Phe Lys Ala Leu Glu Asp Gln Gln Lys Leu Arg Arg Thr Arg Phe
 310 315 320 325

ctc cgc gac agc ctc gac ctc gca ctc gtc gac cta gcc ggc atc tac 1123
 Leu Arg Asp Ser Leu Asp Leu Ala Leu Val Asp Leu Ala Gly Ile Tyr
 330 335 340

cgc gat gcc atc atc att tcc tcc caa gcc caa gtc gga ctc aca cac 1171
 Arg Asp Ala Ile Ile Ile Ser Ser Gln Ala Gln Val Gly Leu Thr His
 345 350 355

ccc gat atg gaa ggc ctc tcc caa gaa ctc gca aca aaa gta agc caa 1219
 Pro Asp Met Glu Gly Leu Ser Gln Glu Leu Ala Thr Lys Val Ser Gln
 360 365 370

gaa gga ctc ctg gca tgc ctc gac gcg atc tcc aaa tgc cgc gaa tcc 1267
 Glu Gly Leu Leu Ala Cys Leu Asp Ala Ile Ser Lys Cys Arg Glu Ser
 375 380 385

ttc ggc ttc aat gta cga ccc atc gtg gcc atg gac gcc ctg gta gga 1315
 Phe Gly Phe Asn Val Arg Pro Ile Val Ala Met Asp Ala Leu Val Gly
 390 395 400 405

cgc ctg cgc aaa gcc tac aaa gtg tcc taaacacccc aaattattga 1362
 Arg Leu Arg Lys Ala Tyr Lys Val Ser
 410

agt 1365

<210> 182

<211> 414

<212> PRT

<213> Corynebacterium glutamicum

<400> 182

Val Phe Asp Ser Leu Ala Gly Ser Lys Thr Val Ser Lys Thr Leu Phe
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Asp Ala Ala Ser Ser Ala Arg Ala Leu Val Arg Ala Arg Thr Thr Glu
 20 25 30

Arg Ala Arg Ala Arg Ala Glu His Gln Asn Pro Ala Met Ile His Asp
 35 40 45

Ser Gly Phe Ala Gln Ser Trp Leu Phe Thr Gly Pro Pro Gly Ser Gly
 50 55 60

Arg Ser Val Ala Ala Lys Val Phe Ala Ala Thr Leu Val Cys Ser Asn
 65 70 75 80

Pro Asp Val Val Gly Pys Gly Gln Cys Glu Asp Cys Arg Ala Ala Met
 85 90 95
 Gly Gly Ser His Pro Asp Ile Glu His Ile Val Pro Gln Gln Leu Ser
 100 105 110
 Ile Gly Val Asp Ala Ala Arg Glu Val Ile Lys Ala Ala Ala Val Ser
 115 120 125
 Pro Val Ala Gly Asn Trp Arg Val Val Ile Phe Glu Asn Ala Asp Arg
 130 135 140
 Leu Thr Met Gln Ala Ala Asn Ala Leu Leu Lys Thr Val Glu Glu Pro
 145 150 155 160
 Thr Glu Ser Thr Val Met Ile Leu Cys Ala Pro Thr Thr Asp Pro Arg
 165 170 175
 Asp Ile Ala Ile Thr Leu Arg Ser Arg Cys Arg His Leu Tyr Ile Pro
 180 185 190
 Thr Pro Ser Ile Ala Glu Val Ala Arg Ile Leu Val Ala Glu Gly Asn
 195 200 205
 Val Ser Gln Ala Asp Ala Glu Leu Ala Ala Ala Ser Gly Ala His
 210 215 220
 Ile Gly Arg Ala Arg Tyr Leu Ala His Asn Asn Ala Ala Gln Arg Arg
 225 230 235 240
 Arg Ala Ser Ile Leu Asn Leu Ala Glu Leu Ile Phe His Gly Asp Val
 245 250 255
 Ala Phe Arg Ser Val Asn Thr Leu Val Lys Met Val Glu Thr Glu Ala
 260 265 270
 Lys Asp Ser Asn Lys Glu Lys Glu Glu Gly Asp Leu Glu Ala Val Arg
 275 280 285
 Ile Ser Leu Gly Met Gly Ala Lys Gly Lys Gly Val His Lys Ala Val
 290 295 300
 Arg Gly Gly Ala Gly Asp Phe Lys Ala Leu Glu Asp Gln Gln Lys Leu
 305 310 315 320
 Arg Arg Thr Arg Phe Leu Arg Asp Ser Leu Asp Leu Ala Leu Val Asp
 325 330 335
 Leu Ala Gly Ile Tyr Arg Asp Ala Ile Ile Ile Ser Ser Gln Ala Gln
 340 345 350
 Val Gly Leu Thr His Pro Asp Met Glu Gly Leu Ser Gln Glu Leu Ala
 355 360 365
 Thr Lys Val Ser Gln Glu Gly Leu Leu Ala Cys Leu Asp Ala Ile Ser
 370 375 380
 Lys Cys Arg Glu Ser Phe Gly Phe Asn Val Arg Pro Ile Val Ala Met
 385 390 395 400
 Asp Ala Leu Val Gly Arg Leu Arg Lys Ala Tyr Lys Val Ser

405

410

<210> 183
 <211> 1242
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1219)
 <223> FRXA00807

<400> 183

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gtagtgagga agtagtntag agatcgtgac taattcgagt gtg ttt gac agt ctc 115
 Val Phe Asp Ser Leu
 1 5

gcc ggc tcc aaa aca gtg tcc aag acg ctt ttc gac gcg gcc tcc agc 163
 Ala Gly Ser Lys Thr Val Ser Lys Thr Leu Phe Asp Ala Ala Ser Ser
 10 15 20

gcg cgt gcc ctt gtc cgc gcc cga acc aca gaa cgt gcc cgc gcc cgg 211
 Ala Arg Ala Leu Val Arg Ala Arg Thr Thr Glu Arg Ala Arg Ala Arg
 25 30 35

gca gaa cac caa aac cct gca atg atc cac gac tcc gcc ttt gcc cag 259
 Ala Glu His Gln Asn Pro Ala Met Ile His Asp Ser Gly Phe Ala Gln
 40 45 50

tca tgg ctg ttt aca ggc cct ccc gga tgc gga cgt tct gtg gca gcc 307
 Ser Trp Leu Phe Thr Gly Pro Pro Gly Ser Gly Arg Ser Val Ala Ala
 55 60 65

aag gtt ttc gcc gct acg ctc gta tgt tgc aat ccg gat gtt gtg ggc 355
 Lys Val Phe Ala Ala Thr Leu Val Cys Ser Asn Pro Asp Val Val Gly
 70 75 80 85

tgt gga caa tgc gag gat tgc cgc gcc gcc atg gga ggc agc cac ccc 403
 Cys Gly Gln Cys Glu Asp Cys Arg Ala Ala Met Gly Gly Ser His Pro
 90 95 100

gat att gaa cac atc gtc ccg cag caa ttg tct atc ggt gtt gat gca 451
 Asp Ile Glu His Ile Val Pro Gln Gln Leu Ser Ile Gly Val Asp Ala
 105 110 115

gct aga gag gtc atc aaa gcc gca gcg gtc agt cct gtt gca gga aac 499
 Ala Arg Glu Val Ile Lys Ala Ala Ala Val Ser Pro Val Ala Gly Asn
 120 125 130

tgg cga gtc gtc atc ttc gaa aac gcc gac cga ctc acc atg caa gcc 547
 Trp Arg Val Val Ile Phe Glu Asn Ala Asp Arg Leu Thr Met Gln Ala
 135 140 145

gcc aac gcc ttg ctg aaa acc gtg gag gaa cca acc gaa agc acc gtg 595
 Ala Asn Ala Leu Leu Lys Thr Val Glu Glu Pro Thr Glu Ser Thr Val
 150 155 160 165

atg att ctg tgc gca ccc acc aca gac ccc cgc gac att gcg atc acc 643

Met	Ile	Leu	Cys	Ala	Pro	Thr	Thr	Asp	Pro	Arg	Asp	Ile	Ala	Ile	Thr		
				170					175					180			
ctc	cgc	tcc	cgc	tgc	agg	cac	ctc	tac	att	ccc	acc	ccc	tcc	atc	gcg	691	
Leu	Arg	Ser	Arg	Cys	Arg	His	Leu	Tyr	Ile	Pro	Thr	Pro	Ser	Ile	Ala		
			185					190					195				
gaa	gtc	gca	cga	atc	ctc	gta	gct	gaa	ggc	aac	gtc	agc	caa	gcg	gat	739	
Glu	Val	Ala	Arg	Ile	Leu	Val	Ala	Glu	Gly	Asn	Val	Ser	Gln	Ala	Asp		
		200					205					210					
gca	gaa	tta	gcg	gcg	gct	gcc	tca	ggc	gct	cac	atc	ggc	agg	gct	cga	787	
Ala	Glu	Leu	Ala	Ala	Ala	Ala	Ser	Gly	Ala	His	Ile	Gly	Arg	Ala	Arg		
	215					220					225						
tac	tta	gcg	cac	aac	aac	gcc	gcc	caa	cgc	aga	cgc	gcc	agc	atc	ctc	835	
Tyr	Leu	Ala	His	Asn	Asn	Ala	Ala	Gln	Arg	Arg	Arg	Ala	Ser	Ile	Leu		
230				235					240						245		
aac	ctg	gcc	gaa	tta	atc	ttc	cac	ggc	gat	gtc	gcc	ttc	cgc	tcc	gta	883	
Asn	Leu	Ala	Glu	Leu	Ile	Phe	His	Gly	Asp	Val	Ala	Phe	Arg	Ser	Val		
			250						255					260			
aac	acc	ttg	gtc	aaa	atg	gtg	gaa	acc	gaa	gcc	aaa	gac	agc	aac	aaa	931	
Asn	Thr	Leu	Val	Lys	Met	Val	Glu	Thr	Glu	Ala	Lys	Asp	Ser	Asn	Lys		
			265				270						275				
gaa	aaa	gaa	gaa	ggc	gat	ctc	gaa	gcc	gta	aga	atc	tca	ctc	ggc	atg	979	
Glu	Lys	Glu	Glu	Gly	Asp	Leu	Glu	Ala	Val	Arg	Ile	Ser	Leu	Gly	Met		
		280					285					290					
gcg	gcc	aaa	ggc	aaa	ggc	gtc	cac	aaa	gca	gta	cgt	gga	gga	gcg	gga	1027	
Ala	Ala	Lys	Gly	Lys	Gly	Val	His	Lys	Ala	Val	Arg	Gly	Gly	Ala	Gly		
		295				300					305						
gat	ttc	aaa	gca	ctc	gaa	gac	caa	caa	aaa	ctc	cga	cgc	acc	cga	ttc	1075	
Asp	Phe	Lys	Ala	Leu	Glu	Asp	Gln	Gln	Lys	Leu	Arg	Arg	Thr	Arg	Phe		
310				315						320					325		
ctc	cgc	gac	agc	ctc	gac	ctc	gca	ctc	gtc	gac	cta	gcc	ggc	atc	tac	1123	
Leu	Arg	Asp	Ser	Leu	Asp	Leu	Ala	Leu	Val	Asp	Leu	Ala	Gly	Ile	Tyr		
				330					335					340			
cgc	gat	gcc	atc	atc	att	tcc	tcc	caa	gcc	caa	gtc	gga	ctc	aca	cac	1171	
Arg	Asp	Ala	Ile	Ile	Ile	Ser	Ser	Gln	Ala	Gln	Val	Gly	Leu	Thr	His		
			345					350					355				
ccc	gat	atg	gaa	ggc	ctc	tcc	caa	gaa	ctc	gca	aca	aaa	gta	agc	caa	1219	
Pro	Asp	Met	Glu	Gly	Leu	Ser	Gln	Glu	Leu	Ala	Thr	Lys	Val	Ser	Gln		
		360					365					370					
taagcactcc	tgatgcct	cca														1242	

<210> 184

<211> 373

<212> PRT

<213> Corynebacterium glutamicum

<400> 184

Val Phe Asp Ser Leu Ala Gly Ser Lys Thr Val Ser Lys Thr Leu Phe

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Asp Ala Ala Ser 20	Ser Ala Arg Ala	Leu Val Arg Ala Arg	Thr Thr Glu 30
Arg Ala Arg Ala Arg Ala Glu His 35	Gln Asn Pro Ala Met	Ile His Asp 45	
Ser Gly Phe Ala Gln Ser Trp Leu Phe Thr Gly Pro Pro Gly Ser Gly 50		60	
Arg Ser Val Ala Ala Lys Val Phe Ala Ala Thr Leu Val Cys Ser Asn 65	70	75	80
Pro Asp Val Val Gly Cys Gly Gln Cys Glu Asp Cys Arg Ala Ala Met 85		90	95
Gly Gly Ser His Pro Asp Ile Glu His Ile Val Pro Gln Gln Leu Ser 100		105	110
Ile Gly Val Asp Ala Ala Arg Glu Val Ile Lys Ala Ala Ala Val Ser 115		120	125
Pro Val Ala Gly Asn Trp Arg Val Val Ile Phe Glu Asn Ala Asp Arg 130		135	140
Leu Thr Met Gln Ala Ala Asn Ala Leu Leu Lys Thr Val Glu Glu Pro 145		150	155
Thr Glu Ser Thr Val Met Ile Leu Cys Ala Pro Thr Thr Asp Pro Arg 165		170	175
Asp Ile Ala Ile Thr Leu Arg Ser Arg Cys Arg His Leu Tyr Ile Pro 180		185	190
Thr Pro Ser Ile Ala Glu Val Ala Arg Ile Leu Val Ala Glu Gly Asn 195		200	205
Val Ser Gln Ala Asp Ala Glu Leu Ala Ala Ala Ser Gly Ala His 210		215	220
Ile Gly Arg Ala Arg Tyr Leu Ala His Asn Asn Ala Ala Gln Arg Arg 225		230	235
Arg Ala Ser Ile Leu Asn Leu Ala Glu Leu Ile Phe His Gly Asp Val 245		250	255
Ala Phe Arg Ser Val Asn Thr Leu Val Lys Met Val Glu Thr Glu Ala 260		265	270
Lys Asp Ser Asn Lys Glu Lys Glu Glu Gly Asp Leu Glu Ala Val Arg 275		280	285
Ile Ser Leu Gly Met Ala Ala Lys Gly Lys Gly Val His Lys Ala Val 290		295	300
Arg Gly Gly Ala Gly Asp Phe Lys Ala Leu Glu Asp Gln Gln Lys Leu 305		310	315
Arg Arg Thr Arg Phe Leu Arg Asp Ser Leu Asp Leu Ala Leu Val Asp 325		330	335

Leu Ala Gly Ile Tyr Arg Asp Ala Ile Ile Ile Ser Ser Gln Ala Gln
 340 345 350

Val Gly Leu Thr His Pro Asp Met Glu Gly Leu Ser Gln Glu Leu Ala
 355 360 365

Thr Lys Val Ser Gln
 370

<210> 185

<211> 834

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(811)

<223> RXA00214

<400> 185

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 gggcaccggtg tgtcccatgc gactattagg gtttaggaacc atg aac tca cca agc 115
 Met Asn Ser Pro Ser
 1 5
 aat cca tct ccc acc gtc cca agc ttg gac acc acc aag atg ctc tcc 163
 Asn Pro Ser Pro Thr Val Pro Ser Leu Asp Thr Thr Lys Met Leu Ser
 10 15 20
 ttc gac ctg gaa aca acg ggc gtc aat ccc ttt gac acc cgc atc gtc 211
 Phe Asp Leu Glu Thr Thr Gly Val Asn Pro Phe Asp Thr Arg Ile Val
 25 30 35
 acc tcc gca atg gtt acg atc acc agc aaa ggc gct gag cct att gag 259
 Thr Ser Ala Met Val Thr Ile Thr Ser Lys Gly Ala Glu Pro Ile Glu
 40 45 50
 cta ttg gct gac ccc ggc atc gaa atc ccc gag gcc gcc act gca gtc 307
 Leu Leu Ala Asp Pro Gly Ile Glu Ile Pro Glu Ala Ala Thr Ala Val
 55 60 65
 cac ggc atc acc acc gaa cat gcc cgc gcc aac ggc cgt ccg cac gat 355
 His Gly Ile Thr Thr Glu His Ala Arg Ala Asn Gly Arg Pro His Asp
 70 75 80 85
 gag gtg tta gcc gaa acc atc tcc agg ctg cgc gcc ggc tgg cag gca 403
 Glu Val Leu Ala Glu Thr Ile Ser Arg Leu Arg Ala Gly Trp Gln Ala
 90 95 100
 gga ctg tcg gtc att gtc ttc aac gca tcc tat gac ctg acc gta tta 451
 Gly Leu Ser Val Ile Val Phe Asn Ala Ser Tyr Asp Leu Thr Val Leu
 105 110 115
 aga aac cat gat cca agc ttc acc atc gac ggc cta gtt tat gac ccc 499
 Arg Asn His Asp Pro Ser Phe Thr Ile Asp Gly Leu Val Tyr Asp Pro
 120 125 130
 ttc gtt atc gac aaa gtc aaa gac cgt tac cgc aaa ggc aag cgc aca 547

Phe Val Ile Asp Lys Val Lys Asp Arg Tyr Arg Lys Gly Lys Arg Thr
 135 140 145
 ctc act gat atg tgt gct cac tac gac gtt caa tta ggc aac gcc cac 595
 Leu Thr Asp Met Cys Ala His Tyr Asp Val Gln Leu Gly Asn Ala His
 150 155 160 165
 gaa gcc acc tca gat gcg ctc gca gcc gca cgc atc gcc tgg aag cag 643
 Glu Ala Thr Ser Asp Ala Leu Ala Ala Arg Ile Ala Trp Lys Gln
 170 175 180
 gtc cgc ctg tgg cca gaa ctc acc aag atg aca ggc gaa gaa ctc atg 691
 Val Arg Leu Trp Pro Glu Leu Thr Lys Met Thr Gly Glu Glu Leu Met
 185 190 195
 gag ttc caa gca gtc aac tat tac gag caa caa aag agc ttc cgt agc 739
 Glu Phe Gln Ala Val Asn Tyr Tyr Glu Gln Gln Lys Ser Phe Arg Ser
 200 205 210
 tat ctc atc ggg caa ggc cgc gat gcc agc gat gtg aac act tca tgg 787
 Tyr Leu Ile Gly Gln Gly Arg Asp Ala Ser Asp Val Asn Thr Ser Trp
 215 220 225
 cca gtg caa act gac ccc gca tcc taaaccgcgc cagatttcta cct 834
 Pro Val Gln Thr Asp Pro Ala Ser
 230 235
 <210> 186
 <211> 237
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 186
 Met Asn Ser Pro Ser Asn Pro Ser Pro Thr Val Pro Ser Leu Asp Thr
 1 5 10 15
 Thr Lys Met Leu Ser Phe Asp Leu Glu Thr Thr Gly Val Asn Pro Phe
 20 25 30
 Asp Thr Arg Ile Val Thr Ser Ala Met Val Thr Ile Thr Ser Lys Gly
 35 40 45
 Ala Glu Pro Ile Glu Leu Leu Ala Asp Pro Gly Ile Glu Ile Pro Glu
 50 55 60
 Ala Ala Thr Ala Val His Gly Ile Thr Thr Glu His Ala Arg Ala Asn
 65 70 75 80
 Gly Arg Pro His Asp Glu Val Leu Ala Glu Thr Ile Ser Arg Leu Arg
 85 90 95
 Ala Gly Trp Gln Ala Gly Leu Ser Val Ile Val Phe Asn Ala Ser Tyr
 100 105 110
 Asp Leu Thr Val Leu Arg Asn His Asp Pro Ser Phe Thr Ile Asp Gly
 115 120 125
 Leu Val Tyr Asp Pro Phe Val Ile Asp Lys Val Lys Asp Arg Tyr Arg
 130 135 140

Lys Gly Lys Arg Thr Leu Thr Asp Met Cys Ala His Tyr Asp Val Gln
 145 150 155 160
 Leu Gly Asn Ala His Glu Ala Thr Ser Asp Ala Leu Ala Ala Ala Arg
 165 170 175
 Ile Ala Trp Lys Gln Val Arg Leu Trp Pro Glu Leu Thr Lys Met Thr
 180 185 190
 Gly Glu Glu Leu Met Glu Phe Gln Ala Val Asn Tyr Tyr Glu Gln Gln
 195 200 205
 Lys Ser Phe Arg Ser Tyr Leu Ile Gly Gln Gly Arg Asp Ala Ser Asp
 210 215 220
 Val Asn Thr Ser Trp Pro Val Gln Thr Asp Pro Ala Ser
 225 230 235

<210> 187
 <211> 1203
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1180)
 <223> RXA01255

<400> 187
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 aaatgctgtg aaacctctct aagcaactag agttgtaaaa atg agc acc act tcg 115
 Met Ser Thr Thr Ser
 1 5
 gaa tca caa gat cac gcc gca aga atc gaa gct gag cgc caa gaa gct 163
 Glu Ser Gln Asp His Ala Ala Arg Ile Glu Ala Glu Arg Gln Glu Ala
 10 15 20
 att gag gcg gct cct ttt gtt tcc gtc agc att caa tca agt gga atc 211
 Ile Glu Ala Ala Pro Phe Val Ser Val Ser Ile Gln Ser Ser Gly Ile
 25 30 35
 cac cca tcg act tca cgc atg gtc acc att gat ttg gta acg ctg tcc 259
 His Pro Ser Thr Ser Arg Met Val Thr Ile Asp Leu Val Thr Leu Ser
 40 45 50
 cct aat ttg gag ccg gtg gaa act ttt cat gcc gtg ttg gat tcc aaa 307
 Pro Asn Leu Glu Pro Val Glu Thr Phe His Ala Val Leu Asp Ser Lys
 55 60 65
 act gat cct ggc ccc ttc cac ctt cat ggc gtg aca gag gaa gaa ttt 355
 Thr Asp Pro Gly Pro Phe His Leu His Gly Val Thr Glu Glu Glu Phe
 70 75 80 85
 gcc agc gct aag cgt ttc ggc cag att ttg aaa agc ttg gac cgc ctc 403
 Ala Ser Ala Lys Arg Phe Gly Gln Ile Leu Lys Ser Leu Asp Arg Leu
 90 95 100
 atc gat ggt cgt acc ctg ttg atc cac aat gct gcg cga agt tgg ggc 451

Ile	Asp	Gly	Arg	Thr	Leu	Leu	Ile	His	Asn	Ala	Ala	Arg	Ser	Trp	Gly		
			105					110					115				
ttt	att	gtt	tcc	gaa	gcc	aag	cgc	gct	atg	aat	gat	gct	gcg	cgc	gcc	499	
Phe	Ile	Val	Ser	Glu	Ala	Lys	Arg	Ala	Met	Asn	Asp	Ala	Ala	Arg	Ala		
		120					125					130					
aat	cgc	aac	agc	aat	cgt	gga	aat	cgc	cgt	ggt	ggt	cgc	gga	cgc	cgc	547	
Asn	Arg	Asn	Ser	Asn	Arg	Gly	Asn	Arg	Arg	Gly	Gly	Arg	Gly	Arg	Arg		
		135				140					145						
agg	cag	cgc	gtg	ggg	cac	atc	cca	aag	ccg	ctg	gtg	atc	gtc	gat	acg	595	
Arg	Gln	Arg	Val	Gly	His	Ile	Pro	Lys	Pro	Leu	Val	Ile	Val	Asp	Thr		
					155					160					165		
ctt	gca	tcg	gcg	cgt	cga	caa	gca	atc	gct	tta	gac	gac	gtg	cgc	atc	643	
Leu	Ala	Ser	Ala	Arg	Arg	Gln	Ala	Ile	Ala	Leu	Asp	Asp	Val	Arg	Ile		
				170					175					180			
cgg	ggt	gtc	gca	cac	acc	ctc	ggc	ctt	gac	gcg	cct	gca	gcg	gag	gcg	691	
Arg	Gly	Val	Ala	His	Thr	Leu	Gly	Leu	Asp	Ala	Pro	Ala	Ala	Glu	Ala		
			185					190					195				
tcg	gtg	gaa	cgc	gcg	cag	gtg	tcg	cac	cgc	cag	ttg	tgc	cgc	gaa	gaa	739	
Ser	Val	Glu	Arg	Ala	Gln	Val	Ser	His	Arg	Gln	Leu	Cys	Arg	Glu	Glu		
		200					205					210					
act	ttg	ctt	gtg	gca	cgg	ctt	tat	ggt	gcg	ttg	aag	cag	tca	gga	ccg	787	
Thr	Leu	Leu	Val	Ala	Arg	Leu	Tyr	Gly	Ala	Leu	Lys	Gln	Ser	Gly	Pro		
		215				220					225						
ctg	gcg	gaa	atc	gat	ccc	cag	tcc	ttg	cgc	gcc	gat	aag	ttt	ggt	ttg	835	
Leu	Ala	Glu	Ile	Asp	Pro	Gln	Ser	Leu	Arg	Ala	Asp	Lys	Phe	Gly	Leu		
		230			235					240					245		
caa	cgc	tcg	atc	atc	cgg	gtg	cag	gcg	cag	gaa	gct	tcg	cca	acg	ctg	883	
Gln	Arg	Ser	Ile	Ile	Arg	Val	Gln	Ala	Gln	Glu	Ala	Ser	Pro	Thr	Leu		
				250					255					260			
gtc	aac	cct	ggt	acg	tat	gag	ccg	gga	aag	acg	ctg	atc	gct	ggg	atg	931	
Val	Asn	Pro	Gly	Thr	Tyr	Glu	Pro	Gly	Lys	Thr	Leu	Ile	Ala	Gly	Met		
			265					270					275				
gaa	gtt	gtg	gtc	gcg	ccg	gaa	att	gag	atg	gat	ccg	gac	atc	att	atc	979	
Glu	Val	Val	Val	Ala	Pro	Glu	Ile	Glu	Met	Asp	Pro	Asp	Ile	Ile	Ile		
		280					285					290					
caa	gcg	tgc	gtc	gat	gca	gat	ttg	tcc	tat	tct	gag	aag	ctc	acc	cgg	1027	
Gln	Ala	Cys	Val	Asp	Ala	Asp	Leu	Ser	Tyr	Ser	Glu	Lys	Leu	Thr	Arg		
		295				300					305						
caa	acc	tca	gtg	gtg	gtg	tgc	aat	caa	acc	cgc	gac	att	gac	ggc	aaa	1075	
Gln	Thr	Ser	Val	Val	Val	Cys	Asn	Gln	Thr	Arg	Asp	Ile	Asp	Gly	Lys		
					315					320					325		
gcg	atg	cat	gcc	cag	cgt	aaa	gga	att	ccg	ctg	ctg	tcc	gat	gtt	gcc	1123	
Ala	Met	His	Ala	Gln	Arg	Lys	Gly	Ile	Pro	Leu	Leu	Ser	Asp	Val	Ala		
				330					335					340			
ttc	tta	gca	gct	gtt	aaa	agg	gta	aaa	gaa	ggg	aag	aaa	gtg	gac	gtc	1171	
Phe	Leu	Ala	Ala	Val	Lys	Arg	Val	Lys	Glu	Gly	Lys	Lys	Val	Asp	Val		

345

350

355

gaa aag cgc tagtgccact tgcttaacta gac
 Glu Lys Arg
 360

1203

<210> 188

<211> 360

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

Met Ser Thr Thr Ser Glu Ser Gln Asp His Ala Ala Arg Ile Glu Ala
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Glu Arg Gln Glu Ala Ile Glu Ala Ala Pro Phe Val Ser Val Ser Ile
 20 25 30

Gln Ser Ser Gly Ile His Pro Ser Thr Ser Arg Met Val Thr Ile Asp
 35 40 45

Leu Val Thr Leu Ser Pro Asn Leu Glu Pro Val Glu Thr Phe His Ala
 50 55 60

Val Leu Asp Ser Lys Thr Asp Pro Gly Pro Phe His Leu His Gly Val
 65 70 75 80

Thr Glu Glu Glu Phe Ala Ser Ala Lys Arg Phe Gly Gln Ile Leu Lys
 85 90 95

Ser Leu Asp Arg Leu Ile Asp Gly Arg Thr Leu Leu Ile His Asn Ala
 100 105 110

Ala Arg Ser Trp Gly Phe Ile Val Ser Glu Ala Lys Arg Ala Met Asn
 115 120 125

Asp Ala Ala Arg Ala Asn Arg Asn Ser Asn Arg Gly Asn Arg Arg Gly
 130 135 140

Gly Arg Gly Arg Arg Arg Gln Arg Val Gly His Ile Pro Lys Pro Leu
 145 150 155 160

Val Ile Val Asp Thr Leu Ala Ser Ala Arg Arg Gln Ala Ile Ala Leu
 165 170 175

Asp Asp Val Arg Ile Arg Gly Val Ala His Thr Leu Gly Leu Asp Ala
 180 185 190

Pro Ala Ala Glu Ala Ser Val Glu Arg Ala Gln Val Ser His Arg Gln
 195 200 205

Leu Cys Arg Glu Glu Thr Leu Leu Val Ala Arg Leu Tyr Gly Ala Leu
 210 215 220

Lys Gln Ser Gly Pro Leu Ala Glu Ile Asp Pro Gln Ser Leu Arg Ala
 225 230 235 240

Asp Lys Phe Gly Leu Gln Arg Ser Ile Ile Arg Val Gln Ala Gln Glu
 245 250 255

Ala Ser Pro Thr Leu Val Asn Pro Gly Thr Tyr Glu Pro Gly Lys Thr
 260 265 270

Leu Ile Ala Gly Met Glu Val Val Val Ala Pro Glu Ile Glu Met Asp
 275 280 285

Pro Asp Ile Ile Ile Gln Ala Cys Val Asp Ala Asp Leu Ser Tyr Ser
 290 295 300

Glu Lys Leu Thr Arg Gln Thr Ser Val Val Val Cys Asn Gln Thr Arg
 305 310 315 320

Asp Ile Asp Gly Lys Ala Met His Ala Gln Arg Lys Gly Ile Pro Leu
 325 330 335

Leu Ser Asp Val Ala Phe Leu Ala Ala Val Lys Arg Val Lys Glu Gly
 340 345 350

Lys Lys Val Asp Val Glu Lys Arg
 355 360

<210> 189
 <211> 913
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(913)
 <223> RXN00066

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tcgaccggca agttttggtg aactagttgg gcagtcgcaa gtg act gac cct ctg 115
 Val Thr Asp Pro Leu
 1 5

tcc gca gct ttg gat agc ggg cgc atc aac cat gcg tac ctt ttt tcg 163
 Ser Ala Ala Leu Asp Ser Gly Arg Ile Asn His Ala Tyr Leu Phe Ser
 10 15 20

ggt ccg cgt ggt tgt ggc aag acg tcg tcg gca cgc atc ctt gcc cgg 211
 Gly Pro Arg Gly Cys Gly Lys Thr Ser Ser Ala Arg Ile Leu Ala Arg
 25 30 35

tcc ctc aac tgc gtg gaa ggc cca act tcc acg ccg tgt ggg gtg tgt 259
 Ser Leu Asn Cys Val Glu Gly Pro Thr Ser Thr Pro Cys Gly Val Cys
 40 45 50

aat tct tgc gta gcg ctg gcc ccg ggt ggc cct gga acc ctt gat gta 307
 Asn Ser Cys Val Ala Leu Ala Pro Gly Gly Pro Gly Thr Leu Asp Val
 55 60 65

aca gag ctc gac gcc gcg agt aac aat ggt gtc gat gac atg cgt gaa 355
 Thr Glu Leu Asp Ala Ala Ser Asn Asn Gly Val Asp Asp Met Arg Glu
 70 75 80 85

ctg cgc gaa cgc gcg aac tac gcc ccg gcg gaa tct cgc tac cgc gtg 403
 Leu Arg Glu Arg Ala Asn Tyr Ala Pro Ala Glu Ser Arg Tyr Arg Val

90										95										100										
ttc atc att gac gaa gcc cac atg atc agt acc caa ggc ttc aac gcc	451																													
Phe Ile Ile Asp Glu Ala His Met Ile Ser Thr Gln Gly Phe Asn Ala																														
105	110	115																												
ttg ctg aaa atc gtt gaa gag cca cca gcg cac ctg att ttc atc ttc	499																													
Leu Leu Lys Ile Val Glu Glu Pro Pro Ala His Leu Ile Phe Ile Phe																														
120	125	130																												
gcc acc acc gag ccg gac aaa atg atc ggt acg atc cgt tcc cgc acg	547																													
Ala Thr Thr Glu Pro Asp Lys Met Ile Gly Thr Ile Arg Ser Arg Thr																														
135	140	145																												
cac aat tac cca ttc cgc ctg ctc acc cca ggg gat atg cgc aaa gtg	595																													
His Asn Tyr Pro Phe Arg Leu Leu Thr Pro Gly Asp Met Arg Lys Val																														
150	155	160	165																											
ctg aaa aat gcg gtc gat ggc gaa ggc gtc cac gtc gac gat tcc gtt	643																													
Leu Lys Asn Ala Val Asp Gly Glu Gly Val His Val Asp Asp Ser Val																														
170	175	180																												
tac cca ctg gtc atc cgc gcc ggc ggc ggc agc ccc cgc gac agc ctc	691																													
Tyr Pro Leu Val Ile Arg Ala Gly Gly Gly Ser Pro Arg Asp Ser Leu																														
185	190	195																												
tcc atc ctc gac cag ctc atc gcc ggc tcg ggc ccg gag ggc ttg aca	739																													
Ser Ile Leu Asp Gln Leu Ile Ala Gly Ser Gly Pro Glu Gly Leu Thr																														
200	205	210																												
tat gag cgc gcc ttg ccg ctg ctc ggt gtc aca agc ttc acg ctt atc	787																													
Tyr Glu Arg Ala Leu Pro Leu Leu Gly Val Thr Ser Phe Thr Leu Ile																														
215	220	225																												
gac gat tcg atc cat gcc ctt gca tct aaa gac aac gca agc atg ttc	835																													
Asp Asp Ser Ile His Ala Leu Ala Ser Lys Asp Asn Ala Ser Met Phe																														
230	235	240	245																											
acc acg atc gat aac gtc atc gaa gaa ggc ctc gaa ccg cga cgc ttc	883																													
Thr Thr Ile Asp Asn Val Ile Glu Glu Gly Leu Glu Pro Arg Arg Phe																														
250	255	260																												
acg atc gac ttt ctt tcg acc cgc tcc ggg	913																													
Thr Ile Asp Phe Leu Ser Thr Arg Ser Gly																														
265	270																													

<210> 190

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 190

Val Thr Asp Pro Leu Ser Ala Ala Leu Asp Ser Gly Arg Ile Asn His
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Ala Tyr Leu Phe Ser Gly Pro Arg Gly Cys Gly Lys Thr Ser Ser Ala
20 25 30

Arg Ile Leu Ala Arg Ser Leu Asn Cys Val Glu Gly Pro Thr Ser Thr
35 40 45

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Pro Cys Gly Val Cys Asn Ser Cys Val Ala Leu Ala Pro Gly Gly Pro
  50                      55                      60

Gly Thr Leu Asp Val Thr Glu Leu Asp Ala Ala Ser Asn Asn Gly Val
  65                      70                      75                      80

Asp Asp Met Arg Glu Leu Arg Glu Arg Ala Asn Tyr Ala Pro Ala Glu
                      85                      90                      95

Ser Arg Tyr Arg Val Phe Ile Ile Asp Glu Ala His Met Ile Ser Thr
          100                      105                      110

Gln Gly Phe Asn Ala Leu Leu Lys Ile Val Glu Glu Pro Pro Ala His
          115                      120                      125

Leu Ile Phe Ile Phe Ala Thr Thr Glu Pro Asp Lys Met Ile Gly Thr
          130                      135                      140

Ile Arg Ser Arg Thr His Asn Tyr Pro Phe Arg Leu Leu Thr Pro Gly
          145                      150                      155                      160

Asp Met Arg Lys Val Leu Lys Asn Ala Val Asp Gly Glu Gly Val His
          165                      170                      175

Val Asp Asp Ser Val Tyr Pro Leu Val Ile Arg Ala Gly Gly Gly Ser
          180                      185                      190

Pro Arg Asp Ser Leu Ser Ile Leu Asp Gln Leu Ile Ala Gly Ser Gly
          195                      200                      205

Pro Glu Gly Leu Thr Tyr Glu Arg Ala Leu Pro Leu Leu Gly Val Thr
          210                      215                      220

Ser Phe Thr Leu Ile Asp Asp Ser Ile His Ala Leu Ala Ser Lys Asp
          225                      230                      235                      240

Asn Ala Ser Met Phe Thr Thr Ile Asp Asn Val Ile Glu Glu Gly Leu
          245                      250                      255

Glu Pro Arg Arg Phe Thr Ile Asp Phe Leu Ser Thr Arg Ser Gly
          260                      265                      270

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<210> 191
<211> 913
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(913)
<223> FRXA00066

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Val Thr Asp Pro Leu
          1                      5

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tcc gca gct ttg gat agc ggg cgc atc aac cat gcg tac ctt ttt tcg	163
Ser Ala Ala Leu Asp Ser Gly Arg Ile Asn His Ala Tyr Leu Phe Ser	
10 15 20	
ggg ccg cgt ggt tgt ggc aag acg tcg tcg gca cgc atc ctt gcc cgg	211
Gly Pro Arg Gly Cys Gly Lys Thr Ser Ser Ala Arg Ile Leu Ala Arg	
25 30 35	
tcc ctc aac tgc gtg gaa ggc cca act tcc acg ccg tgt ggg gtg tgt	259
Ser Leu Asn Cys Val Glu Gly Pro Thr Ser Thr Pro Cys Gly Val Cys	
40 45 50	
aat tct tgc gta gcg ctg gcc ccg ggt ggc cct gga acc ctt gat gta	307
Asn Ser Cys Val Ala Leu Ala Pro Gly Gly Pro Gly Thr Leu Asp Val	
55 60 65	
aca gag ctc gac gcc gcg agt aac aat ggt gtc gat gac atg cgt gaa	355
Thr Glu Leu Asp Ala Ala Ser Asn Asn Gly Val Asp Asp Met Arg Glu	
70 75 80 85	
ctg cgc gaa cgc gcg aac tac gcc ccg gcg gaa tct cgc tac cgc gtg	403
Leu Arg Glu Arg Ala Asn Tyr Ala Pro Ala Glu Ser Arg Tyr Arg Val	
90 95 100	
ttc atc att gac gaa gcc cac atg atc agt acc caa ggc ttc aac gcc	451
Phe Ile Ile Asp Glu Ala His Met Ile Ser Thr Gln Gly Phe Asn Ala	
105 110 115	
ttg ctg aaa atc gtt gaa gag cca cca gcg cac ctg att ttc atc ttc	499
Leu Leu Lys Ile Val Glu Glu Pro Pro Ala His Leu Ile Phe Ile Phe	
120 125 130	
gcc acc acc gag ccg gac aaa atg atc ggt acg atc cgt tcc cgc acg	547
Ala Thr Thr Glu Pro Asp Lys Met Ile Gly Thr Ile Arg Ser Arg Thr	
135 140 145	
cac aat tac cca ttc cgc ctg ctc acc cca ggg gat atg cgc aaa gtg	595
His Asn Tyr Pro Phe Arg Leu Leu Thr Pro Gly Asp Met Arg Lys Val	
150 155 160 165	
ctg aaa aat gcg gtc gat ggc gaa ggc gtc cac gtc gac gat tcc gtt	643
Leu Lys Asn Ala Val Asp Gly Glu Gly Val His Val Asp Asp Ser Val	
170 175 180	
tac cca ctg gtc atc cgc gcc ggc ggc ggc agc ccc cgc gac agc ctc	691
Tyr Pro Leu Val Ile Arg Ala Gly Gly Gly Ser Pro Arg Asp Ser Leu	
185 190 195	
tcc atc ctc gac cag ctc atc gcc ggc tcg ggc ccg gag ggc ttg aca	739
Ser Ile Leu Asp Gln Leu Ile Ala Gly Ser Gly Pro Glu Gly Leu Thr	
200 205 210	
tat gag cgc gcc ttg ccg ctg ctc ggt gtc aca agc ttc acg ctt atc	787
Tyr Glu Arg Ala Leu Pro Leu Leu Gly Val Thr Ser Phe Thr Leu Ile	
215 220 225	
gac gat tcg atc cat gcc ctt gca tct aaa gac aac gca agc atg ttc	835
Asp Asp Ser Ile His Ala Leu Ala Ser Lys Asp Asn Ala Ser Met Phe	
230 235 240 245	
acc acg atc gat aac gtc atc gaa gaa ggc ctc gaa ccg cga cgc ttc	883

Thr Thr Ile Asp Asn Val Ile Glu Glu Gly Leu Glu Pro Arg Arg Phe
 250 255 260

acg atc gac ctt cct tcg gac ccg ctc cgg
 Thr Ile Asp Leu Pro Ser Asp Pro Leu Arg
 265 270

913

<210> 192

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 192

Val Thr Asp Pro Leu Ser Ala Ala Leu Asp Ser Gly Arg Ile Asn His
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Ala Tyr Leu Phe Ser Gly Pro Arg Gly Cys Gly Lys Thr Ser Ser Ala
 20 25 30

Arg Ile Leu Ala Arg Ser Leu Asn Cys Val Glu Gly Pro Thr Ser Thr
 35 40 45

Pro Cys Gly Val Cys Asn Ser Cys Val Ala Leu Ala Pro Gly Gly Pro
 50 55 60

Gly Thr Leu Asp Val Thr Glu Leu Asp Ala Ala Ser Asn Asn Gly Val
 65 70 75 80

Asp Asp Met Arg Glu Leu Arg Glu Arg Ala Asn Tyr Ala Pro Ala Glu
 85 90 95

Ser Arg Tyr Arg Val Phe Ile Ile Asp Glu Ala His Met Ile Ser Thr
 100 105 110

Gln Gly Phe Asn Ala Leu Leu Lys Ile Val Glu Glu Pro Pro Ala His
 115 120 125

Leu Ile Phe Ile Phe Ala Thr Thr Glu Pro Asp Lys Met Ile Gly Thr
 130 135 140

Ile Arg Ser Arg Thr His Asn Tyr Pro Phe Arg Leu Leu Thr Pro Gly
 145 150 155 160

Asp Met Arg Lys Val Leu Lys Asn Ala Val Asp Gly Glu Gly Val His
 165 170 175

Val Asp Asp Ser Val Tyr Pro Leu Val Ile Arg Ala Gly Gly Gly Ser
 180 185 190

Pro Arg Asp Ser Leu Ser Ile Leu Asp Gln Leu Ile Ala Gly Ser Gly
 195 200 205

Pro Glu Gly Leu Thr Tyr Glu Arg Ala Leu Pro Leu Leu Gly Val Thr
 210 215 220

Ser Phe Thr Leu Ile Asp Asp Ser Ile His Ala Leu Ala Ser Lys Asp
 225 230 235 240

Asn Ala Ser Met Phe Thr Thr Ile Asp Asn Val Ile Glu Glu Gly Leu
 245 250 255

Glu Pro Arg Arg Phe Thr Ile Asp Leu Pro Ser Asp Pro Leu Arg
 260 265 270

<210> 193

<211> 751

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (89)..(751)

<223> RXN01637

<400> 193

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gcaaacgagc tcgccaaacc tagcctccatg gtg aac tcc gga ctc gac gac atg 115
 Met Val Asn Ser Gly Leu Asp Asp Met
 1 5

cgt ggt gcc acc tca ccg cgc ctc ctt ctg gaa atc ctc tgc gcc cga 163
 Arg Gly Ala Thr Ser Pro Arg Leu Leu Leu Glu Ile Leu Cys Ala Arg
 10 15 20 25

ctg ctc ctg gca agc aat acc gtg gca ggt cca gcg gtc agt agt tcg 211
 Leu Leu Leu Ala Ser Asn Thr Val Ala Gly Pro Ala Val Ser Ser Ser
 30 35 40

act gac gct gcg cct gca gct act ccg ggt ggt ctc act ggt att gct 259
 Thr Asp Ala Ala Pro Ala Ala Thr Pro Gly Gly Leu Thr Gly Ile Ala
 45 50 55

gct gcc cgc gcg aaa gca cgg gag tat gga cag aag aag gca gct cca 307
 Ala Ala Arg Ala Lys Ala Arg Glu Tyr Gly Gln Lys Lys Ala Ala Pro
 60 65 70

gct cct gca cca act cct gcg ccc gag cca gtg cgc gaa cag tct ctt 355
 Ala Pro Ala Pro Thr Pro Ala Pro Glu Pro Val Arg Glu Gln Ser Leu
 75 80 85

gca cca acg cct gaa cca acg cca gcg gct gaa cct aca tct cag ccc 403
 Ala Pro Thr Pro Glu Pro Thr Pro Ala Ala Glu Pro Thr Ser Gln Pro
 90 95 100 105

gcg ccg gaa ccg gaa ccc gcc agg gaa cca gtg gtg gaa gtg cgg gag 451
 Ala Pro Glu Pro Glu Pro Ala Arg Glu Pro Val Val Glu Val Arg Glu
 110 115 120

gcg agc gtc gaa aag cag cct gca agc agt gat ccc ctc gaa acc att 499
 Ala Ser Val Glu Lys Gln Pro Ala Ser Ser Asp Pro Leu Glu Thr Ile
 125 130 135

cga agc cgc tgg tca gag ctg cgc aac atc gtg gaa aaa caa agt gtg 547
 Arg Ser Arg Trp Ser Glu Leu Arg Asn Ile Val Glu Lys Gln Ser Val
 140 145 150

cgc acc tca atc atg ctg acc gaa gcg cga gtt ttg gga ctg cga ggc 595
 Arg Thr Ser Ile Met Leu Thr Glu Ala Arg Val Leu Gly Leu Arg Gly
 155 160 165

gaa gct gga ttt 751
Glu Ala Gly Phe
220

<213> Corynebacterium glutamicum

Ile Leu Val Lys Val Leu Ala Glu Glu Thr Gly Leu Gln Leu Lys Val

195

200

205

Glu Cys Ile Val Gly Thr Asn Pro Ala Glu Ala Gly Phe
 210 215 220

<210> 195

<211> 409

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(409)

<223> FRXA01637

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cgccggggaac ccggaamccg scaggraamc agtggtggaa gtg cgg gag gcg agc 115
 Val Arg Glu Ala Ser
 1 5

gtc gaa aag cag cct gca agc agt gat ccc ctc gaa acc att cga agc 163
 Val Glu Lys Gln Pro Ala Ser Ser Asp Pro Leu Glu Thr Ile Arg Ser
 10 15 20

cgc tgg tca gag ctg cgc aac atc gtg gaa aaa caa agt gtg cgc acc 211
 Arg Trp Ser Glu Leu Arg Asn Ile Val Glu Lys Gln Ser Val Arg Thr
 25 30 35

tca atc atg ctg acc gaa gcg cga gtt ttg gga ctg cga ggc gat acc 259
 Ser Ile Met Leu Thr Glu Ala Arg Val Leu Gly Leu Arg Gly Asp Thr
 40 45 50

ctc gtg ctc ggt cac agc acc ggg gcg ttg gct gcg cgt ttg aac gct 307
 Leu Val Leu Gly His Ser Thr Gly Ala Leu Ala Ala Arg Leu Asn Ala
 55 60 65

gct gat cac aac gga att ttg gtc aag gtg ttg gct gag gaa act ggt 355
 Ala Asp His Asn Gly Ile Leu Val Lys Val Leu Ala Glu Glu Thr Gly
 70 75 80 85

ctg cag ctc aag gtc gaa tgc att gtg ggc acg aac cca gcc gaa gct 403
 Leu Gln Leu Lys Val Glu Cys Ile Val Gly Thr Asn Pro Ala Glu Ala
 90 95 100

gga ttt 409
 Gly Phe

<210> 196

<211> 103

<212> PRT

<213> Corynebacterium glutamicum

<400> 196

Val Arg Glu Ala Ser Val Glu Lys Gln Pro Ala Ser Ser Asp Pro Leu
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Glu Thr Ile Arg Ser Arg Trp Ser Glu Leu Arg Asn Ile Val Glu Lys
 20 25 30
 Gln Ser Val Arg Thr Ser Ile Met Leu Thr Glu Ala Arg Val Leu Gly
 35 40 45
 Leu Arg Gly Asp Thr Leu Val Leu Gly His Ser Thr Gly Ala Leu Ala
 50 55 60
 Ala Arg Leu Asn Ala Ala Asp His Asn Gly Ile Leu Val Lys Val Leu
 65 70 75 80
 Ala Glu Glu Thr Gly Leu Gln Leu Lys Val Glu Cys Ile Val Gly Thr
 85 90 95
 Asn Pro Ala Glu Ala Gly Phe
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<210> 197
 <211> 1683
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1660)
 <223> RXA00212

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 cgcgtgatcg aagatatccc gcaccagctt cagggcactg atg aat atc ctg tgc 115
 Met Asn Ile Leu Cys
 1 5
 ctg ctg tgc tgg aaa ttc gcg gtg agg tgt tca tca ctg tgg agg att 163
 Leu Leu Cys Trp Lys Phe Ala Val Arg Cys Ser Ser Leu Trp Arg Ile
 10 15 20
 tcc cag gag gtc aac gcg cag cgc att gct gat ggt ggc aag ccg ttt 211
 Ser Gln Glu Val Asn Ala Gln Arg Ile Ala Asp Gly Gly Lys Pro Phe
 25 30 35
 gcc aac ccg cgt aat gct gcg gct ggt tct ctg cgt cag aaa aat att 259
 Ala Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu Arg Gln Lys Asn Ile
 40 45 50
 gag gac gtg aag aag cgc cgc ctg cgg atg atc agc cat ggc atc ggt 307
 Glu Asp Val Lys Lys Arg Arg Leu Arg Met Ile Ser His Gly Ile Gly
 55 60 65
 ttc act gaa ggc ttt agc cct gcg tct cag cat gat gcg tat ctg gca 355
 Phe Thr Glu Gly Phe Ser Pro Ala Ser Gln His Asp Ala Tyr Leu Ala
 70 75 80 85
 ttg gct gcc tgg ggt ttg ccc acc tcg ccg tac aca gag gct gtg act 403
 Leu Ala Ala Trp Gly Leu Pro Thr Ser Pro Tyr Thr Glu Ala Val Thr
 90 95 100
 gat cca gaa gat gtg gtg aaa aag gtc agc tac tgg gct gat cac cgc 451

Asp	Pro	Glu	Asp	Val	Val	Lys	Lys	Val	Ser	Tyr	Trp	Ala	Asp	His	Arg		
			105					110					115				
cac	gac	gca	ctc	cat	gag	atg	gat	ggc	ctg	gtg	att	aag	gtc	gat	gac	499	
His	Asp	Ala	Leu	His	Glu	Met	Asp	Gly	Leu	Val	Ile	Lys	Val	Asp	Asp		
		120					125					130					
atc	gca	tct	cag	cgt	gct	ttg	ggc	tcc	acc	agc	cgc	gcg	cct	cgc	tgg	547	
Ile	Ala	Ser	Gln	Arg	Ala	Leu	Gly	Ser	Thr	Ser	Arg	Ala	Pro	Arg	Trp		
	135					140					145						
gcc	att	gcg	tac	aag	tac	cct	ccg	gag	gag	gtc	acc	acc	aag	ctg	ctt	595	
Ala	Ile	Ala	Tyr	Lys	Tyr	Pro	Pro	Glu	Glu	Val	Thr	Thr	Lys	Leu	Leu		
150					155					160				165			
gat	att	cag	gtt	ggc	gtt	ggc	cgc	acc	ggc	cgt	gtc	acc	cca	ttc	gcg	643	
Asp	Ile	Gln	Val	Gly	Val	Gly	Arg	Thr	Gly	Arg	Val	Thr	Pro	Phe	Ala		
				170					175					180			
gtc	atg	gag	ccg	gtt	ctt	gtt	gca	gga	tca	acg	gtg	tct	atg	gcg	acg	691	
Val	Met	Glu	Pro	Val	Leu	Val	Ala	Gly	Ser	Thr	Val	Ser	Met	Ala	Thr		
			185					190					195				
ctg	cat	aac	cag	agc	gaa	gtc	aag	cgt	aaa	ggc	gtg	ctc	atc	ggc	gac	739	
Leu	His	Asn	Gln	Ser	Glu	Val	Lys	Arg	Lys	Gly	Val	Leu	Ile	Gly	Asp		
		200					205					210					
acc	gtg	gtt	atc	cgc	aag	gcg	ggc	gag	gtt	atc	cca	gag	gtg	ctt	ggc	787	
Thr	Val	Val	Ile	Arg	Lys	Ala	Gly	Glu	Val	Ile	Pro	Glu	Val	Leu	Gly		
	215					220					225						
cct	gtc	gta	gag	ctt	cgt	gac	ggc	aca	gag	cgc	gag	tac	atc	ttc	cca	835	
Pro	Val	Val	Glu	Leu	Arg	Asp	Gly	Thr	Glu	Arg	Glu	Tyr	Ile	Phe	Pro		
230					235					240					245		
acg	ctg	tgc	cct	gaa	tgc	ggc	acc	cgt	ctg	gcg	ccc	gcg	aag	gcc	gat	883	
Thr	Leu	Cys	Pro	Glu	Cys	Gly	Thr	Arg	Leu	Ala	Pro	Ala	Lys	Ala	Asp		
				250					255					260			
gac	gtg	gat	tgg	cgt	tgc	ccc	aac	atg	caa	agc	tgt	cca	ggc	cag	ctg	931	
Asp	Val	Asp	Trp	Arg	Cys	Pro	Asn	Met	Gln	Ser	Cys	Pro	Gly	Gln	Leu		
			265					270					275				
tcc	acg	cgt	ttg	acc	tac	ctt	gct	ggc	cgt	ggc	gct	ttt	gat	att	gaa	979	
Ser	Thr	Arg	Leu	Thr	Tyr	Leu	Ala	Gly	Arg	Gly	Ala	Phe	Asp	Ile	Glu		
		280					285					290					
gca	ttg	ggc	gaa	aag	ggc	gct	gaa	gac	ctc	att	cgc	acc	ggc	att	ttg	1027	
Ala	Leu	Gly	Glu	Lys	Gly	Ala	Glu	Asp	Leu	Ile	Arg	Thr	Gly	Ile	Leu		
	295					300					305						
ctt	gac	gag	tct	ggc	ctg	ttc	gac	ctc	aca	gag	gac	gat	ctg	ctg	agc	1075	
Leu	Asp	Glu	Ser	Gly	Leu	Phe	Asp	Leu	Thr	Glu	Asp	Asp	Leu	Leu	Ser		
310					315					320					325		
tcc	aat	gtc	tac	acc	acc	aac	gcc	ggc	aaa	gta	aat	gcc	agc	ggc	aag	1123	
Ser	Asn	Val	Tyr	Thr	Thr	Asn	Ala	Gly	Lys	Val	Asn	Ala	Ser	Gly	Lys		
				330					335					340			
aaa	ctg	ctg	gac	aac	ctg	caa	aaa	tcc	aag	cag	acc	gac	ctc	tgg	cga	1171	
Lys	Leu	Leu	Asp	Asn	Leu	Gln	Lys	Ser	Lys	Gln	Thr	Asp	Leu	Trp	Arg		

345	350	355	
gtc ctc gtg gca tta tct atc agg cac gta ggc ccc acc gca gcg cgc			1219
Val Leu Val Ala Leu Ser Ile Arg His Val Gly Pro Thr Ala Ala Arg			
360	365	370	
gcc ctt gca ggt cgc tac cac tcc atc cag gcg ctt atc gac gcc ccc			1267
Ala Leu Ala Gly Arg Tyr His Ser Ile Gln Ala Leu Ile Asp Ala Pro			
375	380	385	
ctc gag gaa ctc tcc gaa acc gat gga gta ggt acc atc att gcc caa			1315
Leu Glu Glu Leu Ser Glu Thr Asp Gly Val Gly Thr Ile Ile Ala Gln			
390	395	400	405
tcc ttc aag gac tgg ttc gag gtt gat tgg cac aag gcc atc gtg gac			1363
Ser Phe Lys Asp Trp Phe Glu Val Asp Trp His Lys Ala Ile Val Asp			
410	415	420	
aag tgg gca gcc gct ggt gtg act atg gag gaa gaa gta ggg gag gtc			1411
Lys Trp Ala Ala Ala Gly Val Thr Met Glu Glu Glu Val Gly Glu Val			
425	430	435	
gct gaa caa acc ctt gaa ggc cta acc atc gtg gtc acc gga ggg ttg			1459
Ala Glu Gln Thr Leu Glu Gly Leu Thr Ile Val Val Thr Gly Gly Leu			
440	445	450	
gaa ggc ttc acc aga gat tcg gtg aag gaa gcc atc atc tcc cgt ggc			1507
Glu Gly Phe Thr Arg Asp Ser Val Lys Glu Ala Ile Ile Ser Arg Gly			
455	460	465	
gga aaa gcc tct gga tct gtc tcg aag aaa act gac tac gtg gtg att			1555
Gly Lys Ala Ser Gly Ser Val Ser Lys Lys Thr Asp Tyr Val Val Ile			
470	475	480	485
ggt gaa aac gca ggt tcc aag gcc acc aag gca gaa gaa cta ggg ctg			1603
Gly Glu Asn Ala Gly Ser Lys Ala Thr Lys Ala Glu Glu Leu Gly Leu			
490	495	500	
cgc att ctg gat gag gca gga ttc gtc cgt ttg ctc aat acc ggc tca			1651
Arg Ile Leu Asp Glu Ala Gly Phe Val Arg Leu Leu Asn Thr Gly Ser			
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Ala Asp Glu			
520			

<210> 198

<211> 520

<212> PRT

<213> Corynebacterium glutamicum

<400> 198

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	20						25						30		

Gly	Gly	Lys	Pro	Phe	Ala	Asn	Pro	Arg	Asn	Ala	Ala	Ala	Gly	Ser	Leu
	35						40					45			

Arg Gln Lys Asn Ile Glu Asp Val Lys Lys Arg Arg Leu Arg Met Ile
50 55 60

Ser His Gly Ile Gly Phe Thr Glu Gly Phe Ser Pro Ala Ser Gln His
65 70 75 80

Asp Ala Tyr Leu Ala Leu Ala Ala Trp Gly Leu Pro Thr Ser Pro Tyr
85 90 95

Thr Glu Ala Val Thr Asp Pro Glu Asp Val Val Lys Lys Val Ser Tyr
100 105 110

Trp Ala Asp His Arg His Asp Ala Leu His Glu Met Asp Gly Leu Val
115 120 125

Ile Lys Val Asp Asp Ile Ala Ser Gln Arg Ala Leu Gly Ser Thr Ser
130 135 140

Arg Ala Pro Arg Trp Ala Ile Ala Tyr Lys Tyr Pro Pro Glu Glu Val
145 150 155 160

Thr Thr Lys Leu Leu Asp Ile Gln Val Gly Val Gly Arg Thr Gly Arg
165 170 175

Val Thr Pro Phe Ala Val Met Glu Pro Val Leu Val Ala Gly Ser Thr
180 185 190

Val Ser Met Ala Thr Leu His Asn Gln Ser Glu Val Lys Arg Lys Gly
195 200 205

Val Leu Ile Gly Asp Thr Val Val Ile Arg Lys Ala Gly Glu Val Ile
210 215 220

Pro Glu Val Leu Gly Pro Val Val Glu Leu Arg Asp Gly Thr Glu Arg
225 230 235 240

Glu Tyr Ile Phe Pro Thr Leu Cys Pro Glu Cys Gly Thr Arg Leu Ala
245 250 255

Pro Ala Lys Ala Asp Asp Val Asp Trp Arg Cys Pro Asn Met Gln Ser
260 265 270

Cys Pro Gly Gln Leu Ser Thr Arg Leu Thr Tyr Leu Ala Gly Arg Gly
275 280 285

Ala Phe Asp Ile Glu Ala Leu Gly Glu Lys Gly Ala Glu Asp Leu Ile
290 295 300

Arg Thr Gly Ile Leu Leu Asp Glu Ser Gly Leu Phe Asp Leu Thr Glu
305 310 315 320

Asp Asp Leu Leu Ser Ser Asn Val Tyr Thr Thr Asn Ala Gly Lys Val
325 330 335

Asn Ala Ser Gly Lys Lys Leu Leu Asp Asn Leu Gln Lys Ser Lys Gln
340 345 350

Thr Asp Leu Trp Arg Val Leu Val Ala Leu Ser Ile Arg His Val Gly
355 360 365

Pro Thr Ala Ala Arg Ala Leu Ala Gly Arg Tyr His Ser Ile Gln Ala
 370 375 380

Leu Ile Asp Ala Pro Leu Glu Glu Leu Ser Glu Thr Asp Gly Val Gly
 385 390 395 400

Thr Ile Ile Ala Gln Ser Phe Lys Asp Trp Phe Glu Val Asp Trp His
 405 410 415

Lys Ala Ile Val Asp Lys Trp Ala Ala Ala Gly Val Thr Met Glu Glu
 420 425 430

Glu Val Gly Glu Val Ala Glu Gln Thr Leu Glu Gly Leu Thr Ile Val
 435 440 445

Val Thr Gly Gly Leu Glu Gly Phe Thr Arg Asp Ser Val Lys Glu Ala
 450 455 460

Ile Ile Ser Arg Gly Gly Lys Ala Ser Gly Ser Val Ser Lys Lys Thr
 465 470 475 480

Asp Tyr Val Val Ile Gly Glu Asn Ala Gly Ser Lys Ala Thr Lys Ala
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Glu Glu Leu Gly Leu Arg Ile Leu Asp Glu Ala Gly Phe Val Arg Leu
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Leu Asn Thr Gly Ser Ala Asp Glu
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<211> 696

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(673)

<223> RXA00213

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 Val Thr Glu Asp Asn
 1 5

gct caa ctg cgt aga acg tgg aac gac tta gcc gag aag gtt cgt tat 163
 Ala Gln Leu Arg Arg Thr Trp Asn Asp Leu Ala Glu Lys Val Arg Tyr
 10 15 20

cac cga gat cgt tat tac aac gaa cag cca gag atc cct gat gct gat 211
 His Arg Asp Arg Tyr Tyr Asn Glu Gln Pro Glu Ile Pro Asp Ala Asp
 25 30 35

ttt gat gcg ctt ttt aag cag ctt cag cag ttg gaa gaa gac cac ccg 259
 Phe Asp Ala Leu Phe Lys Gln Leu Gln Gln Leu Glu Glu Asp His Pro
 40 45 50

gag ctc gcc gtc cct gat agc ccc acc atg gtt gtg ggc gct ccg gtg 307

Glu	Leu	Ala	Val	Pro	Asp	Ser	Pro	Thr	Met	Val	Val	Gly	Ala	Pro	Val		
55						60						65					
gca	gag	caa	tca	agc	ttt	gac	aat	gtt	gag	cac	ttg	gag	cga	atg	ctc	355	
Ala	Glu	Gln	Ser	Ser	Phe	Asp	Asn	Val	Glu	His	Leu	Glu	Arg	Met	Leu	85	
70					75					80							
agc	ttg	gac	aat	gtt	ttt	gat	gag	cag	gag	ttg	cgt	gat	tgg	ttg	ggc	403	
Ser	Leu	Asp	Asn	Val	Phe	Asp	Glu	Gln	Glu	Leu	Arg	Asp	Trp	Leu	Gly	100	
				90					95								
agg	acg	cca	gcc	aag	cag	tat	ttg	acg	gag	ttg	aaa	att	gat	ggc	ttg	451	
Arg	Thr	Pro	Ala	Lys	Gln	Tyr	Leu	Thr	Glu	Leu	Lys	Ile	Asp	Gly	Leu	115	
			105					110									
tcc	atc	gac	ttg	gtg	tat	cgc	aat	ggc	cag	tta	gag	cgt	gcc	gct	act	499	
Ser	Ile	Asp	Leu	Val	Tyr	Arg	Asn	Gly	Gln	Leu	Glu	Arg	Ala	Ala	Thr	130	
			120				125										
cgt	ggt	gat	ggt	cgc	gtg	ggc	gag	gac	atc	acg	gcc	aat	gct	cgc	gtg	547	
Arg	Gly	Asp	Gly	Arg	Val	Gly	Glu	Asp	Ile	Thr	Ala	Asn	Ala	Arg	Val	145	
			135			140											
atc	gaa	gat	atc	ccg	cac	cag	ctt	cag	ggc	act	gat	gaa	tat	cct	gtg	595	
Ile	Glu	Asp	Ile	Pro	His	Gln	Leu	Gln	Gly	Thr	Asp	Glu	Tyr	Pro	Val	165	
					155					160							
cct	gct	gtg	ctg	gaa	att	cgc	ggt	gag	gtg	ttc	atc	act	gtg	gag	gat	643	
Pro	Ala	Val	Leu	Glu	Ile	Arg	Gly	Glu	Val	Phe	Ile	Thr	Val	Glu	Asp	180	
				170					175								
ttc	cca	gga	ggt	caa	cgc	gca	gcg	cat	tgc	tgat	ggt	ggc	aag	ccg	tttg	693	
Phe	Pro	Gly	Gly	Gln	Arg	Ala	Ala	His	Cys								
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cca																696	

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<211> 191

<212> PRT

<213> Corynebacterium glutamicum

<400> 200

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Glu	Lys	Val	Arg	Tyr	His	Arg	Asp	Arg	Tyr	Tyr	Asn	Glu	Gln	Pro	Glu
		20						25					30		

Ile	Pro	Asp	Ala	Asp	Phe	Asp	Ala	Leu	Phe	Lys	Gln	Leu	Gln	Gln	Leu
		35					40					45			

Glu	Glu	Asp	His	Pro	Glu	Leu	Ala	Val	Pro	Asp	Ser	Pro	Thr	Met	Val
	50					55					60				

Val	Gly	Ala	Pro	Val	Ala	Glu	Gln	Ser	Ser	Phe	Asp	Asn	Val	Glu	His
	65				70					75					80

Leu	Glu	Arg	Met	Leu	Ser	Leu	Asp	Asn	Val	Phe	Asp	Glu	Gln	Glu	Leu
				85					90					95	

Arg Asp Trp Leu Gly Arg Thr Pro Ala Lys Gln Tyr Leu Thr Glu Leu
 100 105 110

Lys Ile Asp Gly Leu Ser Ile Asp Leu Val Tyr Arg Asn Gly Gln Leu
 115 120 125

Glu Arg Ala Ala Thr Arg Gly Asp Gly Arg Val Gly Glu Asp Ile Thr
 130 135 140

Ala Asn Ala Arg Val Ile Glu Asp Ile Pro His Gln Leu Gln Gly Thr
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Asp Glu Tyr Pro Val Pro Ala Val Leu Glu Ile Arg Gly Glu Val Phe
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Ile Thr Val Glu Asp Phe Pro Gly Gly Gln Arg Ala Ala His Cys
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 <223> RXA00789

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gcacccagca agcaaaactaa aaacttagga gaatgaagaa atg acc aat cca gat 115
 Met Thr Asn Pro Asp
 1 5

atc gtc ggt tcc ggc caa ggc aac gat tcc ttc gag cca gtc gcc caa 163
 Ile Val Gly Ser Gly Gln Gly Asn Asp Ser Phe Glu Pro Val Ala Gln
 10 15 20

tta tcc tac gag cgt gca cgc gat gaa ctc gtt gaa att gta aaa att 211
 Leu Ser Tyr Glu Arg Ala Arg Asp Glu Leu Val Glu Ile Val Lys Ile
 25 30 35

ttg gag ctc ggc caa atg ggc ctc gac gaa tcc ctc aaa tac tgg gag 259
 Leu Glu Leu Gly Gln Met Gly Leu Asp Glu Ser Leu Lys Tyr Trp Glu
 40 45 50

cgc ggc gaa gcc cta gca aag cgc tgc gaa gag cac ctg gcc ggc gcc 307
 Arg Gly Glu Ala Leu Ala Lys Arg Cys Glu Glu His Leu Ala Gly Ala
 55 60 65

tca gcg cgc gtc gag caa gca tta aac cag gca gaa taatgctttt 353
 Ser Ala Arg Val Glu Gln Ala Leu Asn Gln Ala Glu
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cgacgcatcc ctc 366

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 <213> Corynebacterium glutamicum

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Glu	Pro	Val	Ala	Gln	Leu	Ser	Tyr	Glu	Arg	Ala	Arg	Asp	Glu	Leu	Val
			20					25					30		
Glu	Ile	Val	Lys	Ile	Leu	Glu	Leu	Gly	Gln	Met	Gly	Leu	Asp	Glu	Ser
		35					40					45			
Leu	Lys	Tyr	Trp	Glu	Arg	Gly	Glu	Ala	Leu	Ala	Lys	Arg	Cys	Glu	Glu
	50					55					60				
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Glu

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<223> RXN00790

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				Met Ser Val Gln Leu		
				1	5	
acc tgc ccg acg gac att atc cgc aat cgc ccc aca ccg ctc aag gat						163
Thr Cys Pro Thr Asp Ile Ile Arg Asn Arg Pro Thr Pro Leu Lys Asp						
	10		15		20	
ggc gac cgc gtg att gtg tac ggc aag ccc gcg ttt tat gca ggc cgc						211
Gly Asp Arg Val Ile Val Tyr Gly Lys Pro Ala Phe Tyr Ala Gly Arg						
	25		30		35	
ggc act ttt tcg ctg tgg gtg act gat atc cgt ccc gtg ggt att ggt						259
Gly Thr Phe Ser Leu Trp Val Thr Asp Ile Arg Pro Val Gly Ile Gly						
	40		45		50	
gag ttg ctg gcg cgc att gag gag ctg cgt aaa agg ctt gcc gcg gag						307
Glu Leu Leu Ala Arg Ile Glu Glu Leu Arg Lys Arg Leu Ala Ala Glu						
	55		60		65	
ggt ctt ttt gat cca gct cgg aag aag cga ctg cca ttt ctg ccc aac						355
Gly Leu Phe Asp Pro Ala Arg Lys Lys Arg Leu Pro Phe Leu Pro Asn						
	70		75		80	85

cgc gtt ggt ttg atc acg gga cgt ggt tca gcg gct gag cgc gat gtg	403
Arg Val Gly Leu Ile Thr Gly Arg Gly Ser Ala Ala Glu Arg Asp Val	
90 95 100	
ctg agc gtg gct aag gat cgc tgg ccg gaa gtg cag ttt gag gtg atc	451
Leu Ser Val Ala Lys Asp Arg Trp Pro Glu Val Gln Phe Glu Val Ile	
105 110 115	
aac acg gca gtt cag ggc gct tca gct gtt cct gaa atc atc gaa gcg	499
Asn Thr Ala Val Gln Gly Ala Ser Ala Val Pro Glu Ile Ile Glu Ala	
120 125 130	
ttg cgg gtt tta gat cag gac cct cgc gtg gat gtc atc atc att gcc	547
Leu Arg Val Leu Asp Gln Asp Pro Arg Val Asp Val Ile Ile Ile Ala	
135 140 145	
cgc ggc ggc ggt tct gtg gag gat ctg ctc ccc ttc tct gag gag gcc	595
Arg Gly Gly Gly Ser Val Glu Asp Leu Leu Pro Phe Ser Glu Glu Ala	
150 155 160 165	
ttg cag cgc gca gtc gcg gca gcg cag acg ccc gtg gtg tcc gcg att	643
Leu Gln Arg Ala Val Ala Ala Ala Gln Thr Pro Val Val Ser Ala Ile	
170 175 180	
ggc cac gaa cca gat acg ccg gtg ttg gac aat gtc gcc gac ctt cgc	691
Gly His Glu Pro Asp Thr Pro Val Leu Asp Asn Val Ala Asp Leu Arg	
185 190 195	
gcg gcg acc ccg acc gat gca gca aag cgc gtg gtg cct gat gtg gca	739
Ala Ala Thr Pro Thr Asp Ala Ala Lys Arg Val Val Pro Asp Val Ala	
200 205 210	
gaa gaa cgc atg ttg atc aat cag ctt cgc agt cgt agt gcc gcg gcg	787
Glu Glu Arg Met Leu Ile Asn Gln Leu Arg Ser Arg Ser Ala Ala Ala	
215 220 225	
ttg cgc ggt tgg gtg cag cgc gag cag cag gcg ttg gca gcg att cgc	835
Leu Arg Gly Trp Val Gln Arg Glu Gln Gln Ala Leu Ala Ala Ile Arg	
230 235 240 245	
acc agg ccg gtg ctg gct gat ccg atg acc ccg att aac cgc cga cgt	883
Thr Arg Pro Val Leu Ala Asp Pro Met Thr Pro Ile Asn Arg Arg Arg	
250 255 260	
gat gag att gcc cag gct gtg ggc ttg att agg cgc gat gtc acc cat	931
Asp Glu Ile Ala Gln Ala Val Gly Leu Ile Arg Arg Asp Val Thr His	
265 270 275	
ctc gtc cgc acc gag caa gca ctg gtg gcg tcg ttg cgc gca cag gtt	979
Leu Val Arg Thr Glu Gln Ala Leu Val Ala Ser Leu Arg Ala Gln Val	
280 285 290	
tcc gcg ctc ggc ccg tcc gca acc ttg gcg cgc ggt tat tcc gtg gtg	1027
Ser Ala Leu Gly Pro Ser Ala Thr Leu Ala Arg Gly Tyr Ser Val Val	
295 300 305	
cag gtt att cct cgc gac ggc agc gcc ccg gaa gtg gtc acc acc atc	1075
Gln Val Ile Pro Arg Asp Gly Ser Ala Pro Glu Val Val Thr Thr Ile	
310 315 320 325	
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Thr	Pro	Leu	Lys 20	Asp	Gly	Asp	Arg	Val 25	Ile	Val	Tyr	Gly	Lys 30	Pro	Ala
Phe	Tyr	Ala 35	Gly	Arg	Gly	Thr	Phe 40	Ser	Leu	Trp	Val	Thr 45	Asp	Ile	Arg
Pro	Val 50	Gly	Ile	Gly	Glu	Leu 55	Leu	Ala	Arg	Ile	Glu 60	Glu	Leu	Arg	Lys
Arg 65	Leu	Ala	Ala	Glu	Gly 70	Leu	Phe	Asp	Pro	Ala 75	Arg	Lys	Lys	Arg	Leu 80
Pro	Phe	Leu	Pro	Asn 85	Arg	Val	Gly	Leu	Ile 90	Thr	Gly	Arg	Gly	Ser 95	Ala
Ala	Glu	Arg	Asp 100	Val	Leu	Ser	Val	Ala 105	Lys	Asp	Arg	Trp	Pro 110	Glu	Val
Gln	Phe	Glu 115	Val	Ile	Asn	Thr	Ala 120	Val	Gln	Gly	Ala	Ser 125	Ala	Val	Pro
Glu 130	Ile	Ile	Glu	Ala	Leu	Arg 135	Val	Leu	Asp	Gln	Asp 140	Pro	Arg	Val	Asp
Val 145	Ile	Ile	Ile	Ala	Arg 150	Gly	Gly	Gly	Ser	Val 155	Glu	Asp	Leu	Leu	Pro 160
Phe	Ser	Glu	Glu	Ala 165	Leu	Gln	Arg	Ala	Val 170	Ala	Ala	Ala	Gln	Thr 175	Pro
Val	Val	Ser	Ala 180	Ile	Gly	His	Glu	Pro 185	Asp	Thr	Pro	Val	Leu 190	Asp	Asn
Val	Ala	Asp 195	Leu	Arg	Ala	Ala	Thr 200	Pro	Thr	Asp	Ala	Ala 205	Lys	Arg	Val
Val 210	Pro	Asp	Val	Ala	Glu	Glu 215	Arg	Met	Leu	Ile	Asn 220	Gln	Leu	Arg	Ser
Arg 225	Ser	Ala	Ala	Ala	Leu 230	Arg	Gly	Trp	Val	Gln 235	Arg	Glu	Gln	Gln	Ala 240

Leu Ala Ala Ile Arg Thr Arg Pro Val Leu Ala Asp Pro Met Thr Pro
 245 250 255
 Ile Asn Arg Arg Arg Asp Glu Ile Ala Gln Ala Val Gly Leu Ile Arg
 260 265 270
 Arg Asp Val Thr His Leu Val Arg Thr Glu Gln Ala Leu Val Ala Ser
 275 280 285
 Leu Arg Ala Gln Val Ser Ala Leu Gly Pro Ser Ala Thr Leu Ala Arg
 290 295 300
 Gly Tyr Ser Val Val Gln Val Ile Pro Arg Asp Gly Ser Ala Pro Glu
 305 310 315 320
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 Arg Val Ala Asp Gly Ser Ile Thr Ala Ala Ser Met Gly Thr Gln Gln
 340 345 350

Ala Asn

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 <223> FRXA00790

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 ggc aag ccc gcg ttt tat gca ggc cgc ggc act ttt tcg ctg tgg gtg 96
 Gly Lys Pro Ala Phe Tyr Ala Gly Arg Gly Thr Phe Ser Leu Trp Val
 20 25 30
 act gat atc cgt ccc gtg ggt att ggt gag ttg ctg gcg cgc att gag 144
 Thr Asp Ile Arg Pro Val Gly Ile Gly Glu Leu Leu Ala Arg Ile Glu
 35 40 45
 gag ctg cgt aaa agg ctt gcc gcg gag ggt ctt ttt gat cca gct cgg 192
 Glu Leu Arg Lys Arg Leu Ala Ala Glu Gly Leu Phe Asp Pro Ala Arg
 50 55 60
 aag aag cga ctg cca ttt ctg ccc aac cgc gtt ggt ttg atc acg gga 240
 Lys Lys Arg Leu Pro Phe Leu Pro Asn Arg Val Gly Leu Ile Thr Gly
 65 70 75 80
 cgt ggt tca gcg gct gag cgc gat gtg ctg agc gtg gct aag gat cgc 288
 Arg Gly Ser Ala Ala Glu Arg Asp Val Leu Ser Val Ala Lys Asp Arg
 85 90 95
 tgg ccg gaa gtg cag ttt gag gtg atc aac acg gca gtt cag ggc gct 336

Trp	Pro	Glu	Val	Gln	Phe	Glu	Val	Ile	Asn	Thr	Ala	Val	Gln	Gly	Ala	
			100					105					110			
tca	gct	gtt	cct	gaa	atc	atc	gaa	gcg	ttg	cgg	gtt	tta	gat	cag	gac	384
Ser	Ala	Val	Pro	Glu	Ile	Ile	Glu	Ala	Leu	Arg	Val	Leu	Asp	Gln	Asp	
		115					120					125				
cct	cgc	gtg	gat	gtc	atc	atc	att	gcc	cgc	ggc	ggc	ggg	tct	gtg	gag	432
Pro	Arg	Val	Asp	Val	Ile	Ile	Ile	Ala	Arg	Gly	Gly	Gly	Ser	Val	Glu	
	130					135					140					
gat	ctg	ctc	ccc	ttc	tct	gag	gag	gcc	ttg	cag	cgc	gca	gtc	gcg	gca	480
Asp	Leu	Leu	Pro	Phe	Ser	Glu	Glu	Ala	Leu	Gln	Arg	Ala	Val	Ala	Ala	
145					150					155					160	
gcg	cag	acg	ccc	gtg	gtg	tcc	gcg	att	ggc	cac	gaa	cca	gat	acg	ccg	528
Ala	Gln	Thr	Pro	Val	Val	Ser	Ala	Ile	Gly	His	Glu	Pro	Asp	Thr	Pro	
				165					170					175		
gtg	ttg	gac	aat	gtc	gcc	gac	ctt	cgc	gcg	gcg	acc	ccg	acc	gat	gca	576
Val	Leu	Asp	Asn	Val	Ala	Asp	Leu	Arg	Ala	Ala	Thr	Pro	Thr	Asp	Ala	
			180					185					190			
gca	aag	cgc	gtg	gtg	cct	gat	gtg	gca	gaa	gaa	cgc	atg	ttg	atc	aat	624
Ala	Lys	Arg	Val	Val	Pro	Asp	Val	Ala	Glu	Glu	Arg	Met	Leu	Ile	Asn	
		195					200					205				
cag	ctt	cgc	agt	cgt	agt	gcc	gcg	gcg	ttg	cgc	ggg	tgg	gtg	cag	cgc	672
Gln	Leu	Arg	Ser	Arg	Ser	Ala	Ala	Ala	Leu	Arg	Gly	Trp	Val	Gln	Arg	
	210					215					220					
gag	cag	cag	gcg	ttg	gca	gcg	att	cgc	acc	agg	ccg	gtg	ctg	gct	gat	720
Glu	Gln	Gln	Ala	Leu	Ala	Ala	Ile	Arg	Thr	Arg	Pro	Val	Leu	Ala	Asp	
225					230				235					240		
ccg	atg	acc	ccg	att	aac	cgc	cga	cgt	gat	gag	att	gcc	cag	gct	gtg	768
Pro	Met	Thr	Pro	Ile	Asn	Arg	Arg	Arg	Asp	Glu	Ile	Ala	Gln	Ala	Val	
				245					250					255		
ggc	ttg	att	agg	cgc	gat	gtc	acc	cat	ctc	gtc	cgc	acc	gag	caa	gca	816
Gly	Leu	Ile	Arg	Arg	Asp	Val	Thr	His	Leu	Val	Arg	Thr	Glu	Gln	Ala	
			260					265					270			
ctg	gtg	gcg	tcg	ttg	cgc	gca	cag	gtt	tcc	gcg	ctc	ggc	ccg	tcc	gca	864
Leu	Val	Ala	Ser	Leu	Arg	Ala	Gln	Val	Ser	Ala	Leu	Gly	Pro	Ser	Ala	
		275					280					285				
acc	ttg	gcg	cgc	ggg	tat	tcc	gtg	gtg	cag	gtt	att	cct	cgc	gac	ggc	912
Thr	Leu	Ala	Arg	Gly	Tyr	Ser	Val	Val	Gln	Val	Ile	Pro	Arg	Asp	Gly	
	290					295					300					
agc	gcc	ccg	gaa	gtg	gtc	acc	acc	atc	gag	caa	tca	ccg	ccc	ggc	agc	960
Ser	Ala	Pro	Glu	Val	Val											

340

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<211> 342

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 206

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Thr	Asp	Ile	Arg	Pro	Val	Gly	Ile	Gly	Glu	Leu	Leu	Ala	Arg	Ile	Glu
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Glu	Leu	Arg	Lys	Arg	Leu	Ala	Ala	Glu	Gly	Leu	Phe	Asp	Pro	Ala	Arg
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Lys	Lys	Arg	Leu	Pro	Phe	Leu	Pro	Asn	Arg	Val	Gly	Leu	Ile	Thr	Gly
	65				70					75					80
Arg	Gly	Ser	Ala	Ala	Glu	Arg	Asp	Val	Leu	Ser	Val	Ala	Lys	Asp	Arg
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Trp	Pro	Glu	Val	Gln	Phe	Glu	Val	Ile	Asn	Thr	Ala	Val	Gln	Gly	Ala
			100					105					110		
Ser	Ala	Val	Pro	Glu	Ile	Ile	Glu	Ala	Leu	Arg	Val	Leu	Asp	Gln	Asp
		115					120					125			
Pro	Arg	Val	Asp	Val	Ile	Ile	Ile	Ala	Arg	Gly	Gly	Gly	Ser	Val	Glu
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Asp	Leu	Leu	Pro	Phe	Ser	Glu	Glu	Ala	Leu	Gln	Arg	Ala	Val	Ala	Ala
	145				150					155				160	
Ala	Gln	Thr	Pro	Val	Val	Ser	Ala	Ile	Gly	His	Glu	Pro	Asp	Thr	Pro
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Val	Leu	Asp	Asn	Val	Ala	Asp	Leu	Arg	Ala	Ala	Thr	Pro	Thr	Asp	Ala
			180					185						190	
Ala	Lys	Arg	Val	Val	Pro	Asp	Val	Ala	Glu	Glu	Arg	Met	Leu	Ile	Asn
		195					200						205		
Gln	Leu	Arg	Ser	Arg	Ser	Ala	Ala	Ala	Leu	Arg	Gly	Trp	Val	Gln	Arg
	210					215					220				
Glu	Gln	Gln	Ala	Leu	Ala	Ala	Ile	Arg	Thr	Arg	Pro	Val	Leu	Ala	Asp
	225				230					235				240	
Pro	Met	Thr	Pro	Ile	Asn	Arg	Arg	Arg	Asp	Glu	Ile	Ala	Gln	Ala	Val
			245						250					255	
Gly	Leu	Ile	Arg	Arg	Asp	Val	Thr	His	Leu	Val	Arg	Thr	Glu	Gln	Ala
			260					265					270		
Leu	Val	Ala	Ser	Leu	Arg	Ala	Gln	Val	Ser	Ala	Leu	Gly	Pro	Ser	Ala

ggc cgc gaa atc gca gat cct cac tac gac tac aaa ctg cgc tgg cta 499

Gly	Arg	Glu	Ile	Ala	Asp	Pro	His	Tyr	Asp	Tyr	Lys	Leu	Arg	Trp	Leu		
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ttc	tcc	ctg	cgc	aac	tac	gtg	atc	gac	acc	ttg	gaa	tac	cgc	ccc	gag	547	
Phe	Ser	Leu	Arg	Asn	Tyr	Val	Ile	Asp	Thr	Leu	Glu	Tyr	Arg	Pro	Glu		
	135					140				145							
gaa	aaa	ctg	gtg	ttg	ctc	ggc	gac	ttc	aac	atc	gcg	ccc	aca	gac	atc	595	
Glu	Lys	Leu	Val	Leu	Leu	Gly	Asp	Phe	Asn	Ile	Ala	Pro	Thr	Asp	Ile		
150					155					160					165		
gac	gtc	tgg	gac	atc	gca	gcc	ttc	gaa	gga	aaa	acc	cac	gtc	acc	gaa	643	
Asp	Val	Trp	Asp	Ile	Ala	Ala	Phe	Glu	Gly	Lys	Thr	His	Val	Thr	Glu		
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cca	gaa	cgt	gca	gct	ttc	gac	ggc	ctc	atc	gaa	gcc	gga	ctc	aaa	gaa	691	
Pro	Glu	Arg	Ala	Ala	Phe	Asp	Gly	Leu	Ile	Glu	Ala	Gly	Leu	Lys	Glu		
			185					190					195				
acc	acc	ccc	gga	cct	ggt	acc	tac	acc	tac	tgg	gat	tac	aaa	ggc	gca	739	
Thr	Thr	Pro	Gly	Pro	Gly	Thr	Tyr	Thr	Tyr	Trp	Asp	Tyr	Lys	Gly	Ala		
		200					205					210					
cgc	ttc	ctc	aaa	ggc	gaa	ggc	atg	cgc	atc	gat	ttc	cag	ctc	gca	tcc	787	
Arg	Phe	Leu	Lys	Gly	Glu	Gly	Met	Arg	Ile	Asp	Phe	Gln	Leu	Ala	Ser		
	215					220					225						
ccg	gcc	ctt	gct	gca	acc	gcg	ggt	gaa	acc	ttt	gtg	gac	gtt	gaa	gaa	835	
Pro	Ala	Leu	Ala	Ala	Thr	Ala	Gly	Glu	Thr	Phe	Val	Asp	Val	Glu	Glu		
230					235					240					245		
cgc	agc	gga	acc	ggc	gcc	tct	gac	cac	gca	cca	gtc	atc	gtt	gat	tac	883	
Arg	Ser	Gly	Thr	Gly	Ala	Ser	Asp	His	Ala	Pro	Val	Ile	Val	Asp	Tyr		
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Lys	Val																

<210> 208

<211> 263

<212> PRT

<213> Corynebacterium glutamicum

<400> 208

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Arg	Met	Val	Asp	Phe	Leu	Leu	Arg	His	Asp	Val	Asp	Val	Leu	Ala	Val		
			20					25					30				

Gln	Glu	Thr	Lys	Cys	Lys	Asp	Glu	Gln	Phe	Pro	Thr	Glu	Arg	Phe	Thr		
		35					40						45				

Glu	Ile	Gly	Tyr	Glu	Val	Ala	His	Phe	Gly	Leu	Asn	Gln	Trp	Asn	Gly		
	50					55					60						

Val	Ala	Ile	Ile	Ser	Arg	Val	Gly	Ile	Glu	Asn	Val	Glu	Thr	His	Phe		
65					70					75					80		

Pro Ala Gln Pro Gly Phe Asn Lys Asp Ile Thr Lys Glu Gln Ser Ile
85 90 95

Glu Ala Arg Ala Ile Gly Ala Arg Cys Gly Gly Val Gln Val Trp Ser
100 105 110

Leu Tyr Val Pro Asn Gly Arg Glu Ile Ala Asp Pro His Tyr Asp Tyr
115 120 125

Lys Leu Arg Trp Leu Phe Ser Leu Arg Asn Tyr Val Ile Asp Thr Leu
130 135 140

Glu Tyr Arg Pro Glu Glu Lys Leu Val Leu Leu Gly Asp Phe Asn Ile
145 150 155 160

Ala Pro Thr Asp Ile Asp Val Trp Asp Ile Ala Ala Phe Glu Gly Lys
165 170 175

Thr His Val Thr Glu Pro Glu Arg Ala Ala Phe Asp Gly Leu Ile Glu
180 185 190

Ala Gly Leu Lys Glu Thr Thr Pro Gly Pro Gly Thr Tyr Thr Tyr Trp
195 200 205

Asp Tyr Lys Gly Ala Arg Phe Leu Lys Gly Glu Gly Met Arg Ile Asp
210 215 220

Phe Gln Leu Ala Ser Pro Ala Leu Ala Ala Thr Ala Gly Glu Thr Phe
225 230 235 240

Val Asp Val Glu Glu Arg Ser Gly Thr Gly Ala Ser Asp His Ala Pro
245 250 255

Val Ile Val Asp Tyr Lys Val
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<210> 209

<211> 806

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(783)

<223> RXN03175

<400> 209

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Val Arg Ala Ser Glu Lys Asp Thr Ala Thr Ala Leu Gln Pro Ala Leu
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Asp Asn Gly Trp His Tyr Ile Gly Ala Pro Ala Ala Ala Lys Gly Arg
20 25 30

gcc ggt gtc ggc att ttg tct agg cat gaa ctt gaa gat gtg aac atc 144
Ala Gly Val Gly Ile Leu Ser Arg His Glu Leu Glu Asp Val Asn Ile
35 40 45

ggg ttt gga tct ttc ctt gac tcc ggc cgc tac att gaa gca acc atc 192

Gly	Phe	Gly	Ser	Phe	Leu	Asp	Ser	Gly	Arg	Tyr	Ile	Glu	Ala	Thr	Ile	
	50					55					60					
aaa	gac	acc	acc	ctg	gat	gtg	cca	gta	acc	gtg	gca	tct	ctt	tac	ctc	240
Lys	Asp	Thr	Thr	Leu	Asp	Val	Pro	Val	Thr	Val	Ala	Ser	Leu	Tyr	Leu	
65					70				75						80	
ccc	tca	ggt	tca	gcg	ggc	acc	gac	aag	cag	gat	gaa	aag	tac	cgc	ttc	288
Pro	Ser	Gly	Ser	Ala	Gly	Thr	Asp	Lys	Gln	Asp	Glu	Lys	Tyr	Arg	Phe	
				85				90						95		
ctc	gat	gaa	ttc	gaa	ggg	ttc	ctg	gac	cag	cgc	gct	aaa	gaa	cgc	tcc	336
Leu	Asp	Glu	Phe	Glu	Gly	Phe	Leu	Asp	Gln	Arg	Ala	Lys	Glu	Arg	Ser	
			100				105						110			
cac	atg	gtc	atc	ggg	ggc	gac	tgg	aac	atc	tgc	cac	cgc	cgc	gaa	gac	384
His	Met	Val	Ile	Gly	Gly	Asp	Trp	Asn	Ile	Cys	His	Arg	Arg	Glu	Asp	
		115					120					125				
ctg	aaa	aac	tgg	aaa	acc	aac	caa	aag	aaa	tcc	ggg	ttc	ctt	ccc	gac	432
Leu	Lys	Asn	Trp	Lys	Thr	Asn	Gln	Lys	Lys	Ser	Gly	Phe	Leu	Pro	Asp	
	130					135					140					
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Glu	Arg	Ala	Phe	Met	Asp	Ser	Val	Phe	Gly	Thr	Phe	Pro	Asp	Glu	Ala	
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acc	cag	gtt	gca	ggg	gcc	ggc	gac	ttc	ttc	ggg	gcc	gtg	gac	tat	gaa	528
Thr	Gln	Val	Ala	Gly	Ala	Gly	Asp	Phe	Phe	Gly	Ala	Val	Asp	Tyr	Glu	
				165				170						175		
gga	acg	agg	cgt	cga	gaa	gca	act	acg	gac	cct	gcg	tgg	ttc	gac	gtt	576
Gly	Thr	Arg	Arg	Arg	Glu	Ala	Thr	Thr	Asp	Pro	Ala	Trp	Phe	Asp	Val	
			180					185					190			
gca	cgt	cgc	ctg	caa	cct	gaa	ggc	gac	ggc	ccc	tac	act	tgg	tgg	acc	624
Ala	Arg	Arg	Leu	Gln	Pro	Glu	Gly	Asp	Gly	Pro	Tyr	Thr	Trp	Trp	Thr	
		195				200						205				
tac	cgc	gga	aaa	gcc	ttc	gac	acc	ggc	gcc	gga	tgg	cgc	atc	gac	tac	672
Tyr	Arg	Gly	Lys	Ala	Phe	Asp	Thr	Gly	Ala	Gly	Trp	Arg	Ile	Asp	Tyr	
	210					215					220					
caa	gca	gca	acc	gca	gcg	atg	ctc	gaa	cgc	gca	gaa	cgc	tcc	tgg	gta	720
Gln	Ala	Ala	Thr	Ala	Ala	Met	Leu	Glu	Arg	Ala	Glu	Arg	Ser	Trp	Val	
225					230					235					240	
gac	aaa	gcc	gct	gca	tac	gat	ttg	cgc	tgg	tca	gat	cac	tca	cca	ctg	768
Asp	Lys	Ala	Ala	Ala	Tyr	Asp	Leu	Arg	Trp	Ser	Asp	His	Ser	Pro	Leu	
				245				250					255			
aac	gtg	atc	tac	tcc	taaa	atgctg	ctgaca	attc	tat							806
Asn	Val	Ile	Tyr	Ser												
			260													

<210> 210

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 210

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Asp	Asn	Gly	Trp	His	Tyr	Ile	Gly	Ala	Pro	Ala	Ala	Ala	Lys	Gly	Arg
		20					25						30		
Ala	Gly	Val	Gly	Ile	Leu	Ser	Arg	His	Glu	Leu	Glu	Asp	Val	Asn	Ile
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Gly	Phe	Gly	Ser	Phe	Leu	Asp	Ser	Gly	Arg	Tyr	Ile	Glu	Ala	Thr	Ile
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Lys	Asp	Thr	Thr	Leu	Asp	Val	Pro	Val	Thr	Val	Ala	Ser	Leu	Tyr	Leu
65					70					75					80
Pro	Ser	Gly	Ser	Ala	Gly	Thr	Asp	Lys	Gln	Asp	Glu	Lys	Tyr	Arg	Phe
				85					90					95	
Leu	Asp	Glu	Phe	Glu	Gly	Phe	Leu	Asp	Gln	Arg	Ala	Lys	Glu	Arg	Ser
		100						105					110		
His	Met	Val	Ile	Gly	Gly	Asp	Trp	Asn	Ile	Cys	His	Arg	Arg	Glu	Asp
		115					120					125			
Leu	Lys	Asn	Trp	Lys	Thr	Asn	Gln	Lys	Lys	Ser	Gly	Phe	Leu	Pro	Asp
	130					135					140				
Glu	Arg	Ala	Phe	Met	Asp	Ser	Val	Phe	Gly	Thr	Phe	Pro	Asp	Glu	Ala
145					150					155					160
Thr	Gln	Val	Ala	Gly	Ala	Gly	Asp	Phe	Phe	Gly	Ala	Val	Asp	Tyr	Glu
			165					170						175	
Gly	Thr	Arg	Arg	Arg	Glu	Ala	Thr	Thr	Asp	Pro	Ala	Trp	Phe	Asp	Val
		180						185					190		
Ala	Arg	Arg	Leu	Gln	Pro	Glu	Gly	Asp	Gly	Pro	Tyr	Thr	Trp	Trp	Thr
		195					200					205			
Tyr	Arg	Gly	Lys	Ala	Phe	Asp	Thr	Gly	Ala	Gly	Trp	Arg	Ile	Asp	Tyr
	210					215					220				
Gln	Ala	Ala	Thr	Ala	Ala	Met	Leu	Glu	Arg	Ala	Glu	Arg	Ser	Trp	Val
225					230					235					240
Asp	Lys	Ala	Ala	Ala	Tyr	Asp	Leu	Arg	Trp	Ser	Asp	His	Ser	Pro	Leu
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Asn	Val	Ile	Tyr	Ser											
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<210> 211

<211> 1035

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1012)

<223> FRXA02883

<400> 211

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ggatggagga tttccccaag caccactag tgtgacaagc atg agt ttt cac atc 115
Met Ser Phe His Ile
1 5

aca tcc gtc aat gtc aac ggc att agg gca gcg gtc aaa cag cga agc 163
Thr Ser Val Asn Val Asn Gly Ile Arg Ala Ala Val Lys Gln Arg Ser
10 15 20

gaa aca aac cta ggt ttc ctt ccg tgg ctt gaa gaa act cgc ccg gac 211
Glu Thr Asn Leu Gly Phe Leu Pro Trp Leu Glu Glu Thr Arg Pro Asp
25 30 35

gtt gtc ctc ctc caa gaa gtc cgc gca agc gaa aaa gac acc gcc acc 259
Val Val Leu Leu Gln Glu Val Arg Ala Ser Glu Lys Asp Thr Ala Thr
40 45 50

gca ctg caa ccc gcc tta gat aac gga tgg cac tac att ggt gcc cca 307
Ala Leu Gln Pro Ala Leu Asp Asn Gly Trp His Tyr Ile Gly Ala Pro
55 60 65

gca gct gcc aag gga cgt gcc ggt gtc ggc att ttg tct agg cat gaa 355
Ala Ala Ala Lys Gly Arg Ala Gly Val Gly Ile Leu Ser Arg His Glu
70 75 80 85

ctt gaa gat gtg aac atc ggt ttt gga tct ttc ctt gac tcc ggc cgc 403
Leu Glu Asp Val Asn Ile Gly Phe Gly Ser Phe Leu Asp Ser Gly Arg
90 95 100

tac att gaa gca acc atc aaa gac acc acc ctg gat gtg cca gta acc 451
Tyr Ile Glu Ala Thr Ile Lys Asp Thr Thr Leu Asp Val Pro Val Thr
105 110 115

gtg gca tct ctt tac ctc ccc tca ggt tca gcg ggc acc gac aag cag 499
Val Ala Ser Leu Tyr Leu Pro Ser Gly Ser Ala Gly Thr Asp Lys Gln
120 125 130

gat gaa aag tac cgc ttc ctc gat gaa ttc gaa ggg ttc ctg gac cag 547
Asp Glu Lys Tyr Arg Phe Leu Asp Glu Phe Glu Gly Phe Leu Asp Gln
135 140 145

cgc gct aaa gaa cgc tcc cac atg gtc atc ggt ggc gac tgg aac atc 595
Arg Ala Lys Glu Arg Ser His Met Val Ile Gly Gly Asp Trp Asn Ile
150 155 160 165

tgc cac cgc cgc gaa gac ctg aaa aac tgg aaa acc aac caa aag aaa 643
Cys His Arg Arg Glu Asp Leu Lys Asn Trp Lys Thr Asn Gln Lys Lys
170 175 180

tcc ggt ttc ctt ccc gac gaa cgc gca ttc atg gat tca gtc ttt ggc 691
Ser Gly Phe Leu Pro Asp Glu Arg Ala Phe Met Asp Ser Val Phe Gly
185 190 195

acc ttc cca gat gag gca acc cag gtt gca ggg gcc ggc gac ttc ttc 739
Thr Phe Pro Asp Glu Ala Thr Gln Val Ala Gly Ala Gly Asp Phe Phe
200 205 210

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ggt gcc gtg gac tat gaa gga acg agg cgt cga gaa gca act acg gac 787
 Gly Ala Val Asp Tyr Glu Gly Thr Arg Arg Arg Glu Ala Thr Thr Asp
 215 220 225

cct gcg tgg ttc gac gtt gca cgt cgc ctg caa cct gaa ggc gac ggc 835
 Pro Ala Trp Phe Asp Val Ala Arg Arg Leu Gln Pro Glu Gly Asp Gly
 230 235 240 245

ccc tac act tgg tgg acc tac cgc gga aaa gcc ttc gac acc ggc gcc 883
 Pro Tyr Thr Trp Trp Thr Tyr Arg Gly Lys Ala Phe Asp Thr Gly Ala
 250 255 260

gga tgg cgc atc gac tac caa gca gca acc gca gcg atg ctc gaa cgc 931
 Gly Trp Arg Ile Asp Tyr Gln Ala Ala Thr Ala Ala Met Leu Glu Arg
 265 270 275

gca gaa cgc tcc tgg gta gac aaa gcc gct gca tac gat ttg cgc tgg 979
 Ala Glu Arg Ser Trp Val Asp Lys Ala Ala Ala Tyr Asp Leu Arg Trp
 280 285 290

tca gat cac tca cca ctg aac gtg atc tac tcc taaaatgctg ctgacaattc 1032
 Ser Asp His Ser Pro Leu Asn Val Ile Tyr Ser
 295 300

tat 1035

<210> 212
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 212
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 Glu Thr Arg Pro Asp Val Val Leu Leu Gln Glu Val Arg Ala Ser Glu
 35 40 45
 Lys Asp Thr Ala Thr Ala Leu Gln Pro Ala Leu Asp Asn Gly Trp His
 50 55 60
 Tyr Ile Gly Ala Pro Ala Ala Ala Lys Gly Arg Ala Gly Val Gly Ile
 65 70 75 80
 Leu Ser Arg His Glu Leu Glu Asp Val Asn Ile Gly Phe Gly Ser Phe
 85 90 95
 Leu Asp Ser Gly Arg Tyr Ile Glu Ala Thr Ile Lys Asp Thr Thr Leu
 100 105 110
 Asp Val Pro Val Thr Val Ala Ser Leu Tyr Leu Pro Ser Gly Ser Ala
 115 120 125
 Gly Thr Asp Lys Gln Asp Glu Lys Tyr Arg Phe Leu Asp Glu Phe Glu
 130 135 140
 Gly Phe Leu Asp Gln Arg Ala Lys Glu Arg Ser His Met Val Ile Gly

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<222> (101) .. (1507)
<223> RXA00341
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Met Lys Leu Tyr Ala																
1 5																
gca gtc ctc gac ttt gaa cca gtg gca caa gag ttc ggt gtg gag cga																163
Ala Val Leu Asp Phe Glu Pro Val Ala Gln Glu Phe Gly Val Glu Arg																
10 15 20																
ggt ttt gac cct cat atc cac gac gaa gcc gcg tca agt gtc gat agg																211
Gly Phe Asp Pro His Ile His Asp Glu Ala Ala Ser Ser Val Asp Arg																
25 30 35																
tat gcg caa gag cgg gaa gat ctc ctg cac atg ccc ttt gtc acc atc																259
Tyr Ala Gln Glu Arg Glu Asp Leu Leu His Met Pro Phe Val Thr Ile																
40 45 50																

gat	ccc	gta	ggt	tcc	aga	gac	ctc	gat	caa	gct	gtg	ctg	att	gag	gag	307
Asp	Pro	Val	Gly	Ser	Arg	Asp	Leu	Asp	Gln	Ala	Val	Leu	Ile	Glu	Glu	
	55					60					65					
atc	gac	agc	gga	ttt	cgg	gtg	cat	tac	gcg	att	gca	gat	gtc	gca	gcc	355
Ile	Asp	Ser	Gly	Phe	Arg	Val	His	Tyr	Ala	Ile	Ala	Asp	Val	Ala	Ala	
	70				75					80					85	
ttc	gtg	gag	ccg	ggc	agt	gaa	ttg	gaa	aag	att	tcc	ctt	cac	cgc	ggg	403
Phe	Val	Glu	Pro	Gly	Ser	Glu	Leu	Glu	Lys	Ile	Ser	Leu	His	Arg	Gly	
				90					95					100		
cag	act	att	tat	ctg	ccg	gat	tcc	cca	gcg	cga	ctg	cac	cct	gag	gaa	451
Gln	Thr	Ile	Tyr	Leu	Pro	Asp	Ser	Pro	Ala	Arg	Leu	His	Pro	Glu	Glu	
			105					110					115			
tta	tcc	gaa	gat	gcg	gca	agc	ctg	ctg	gag	gga	caa	acg	aga	cca	gcg	499
Leu	Ser	Glu	Asp	Ala	Ala	Ser	Leu	Leu	Glu	Gly	Gln	Thr	Arg	Pro	Ala	
		120					125					130				
gtt	gtg	tgg	tcg	att	gat	cta	gat	gaa	cgt	ggc	gaa	gtc	aca	gcc	acc	547
Val	Val	Trp	Ser	Ile	Asp	Leu	Asp	Glu	Arg	Gly	Glu	Val	Thr	Ala	Thr	
		135				140					145					
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Lys	Val	Arg	Arg	Gly	Leu	Val	Lys	Ser	Arg	Ala	Arg	Leu	Asp	Tyr	Asp	
	150				155					160					165	
cag	gct	caa	ata	gat	gcc	gag	aat	ggt	cgg	ttg	cat	ccg	tcg	ata	agc	643
Gln	Ala	Gln	Ile	Asp	Ala	Glu	Asn	Gly	Arg	Leu	His	Pro	Ser	Ile	Ser	
				170					175					180		
tta	ttg	ccc	aag	gtc	ggg	cag	ctg	agg	cag	gaa	agc	gcg	cta	cgg	cgc	691
Leu	Leu	Pro	Lys	Val	Gly	Gln	Leu	Arg	Gln	Glu	Ser	Ala	Leu	Arg	Arg	
			185					190					195			
gaa	gcc	gtg	aat	ctt	tct	att	ccc	agc	cag	cga	gtg	gtg	aaa	gtg	ccc	739
Glu	Ala	Val	Asn	Leu	Ser	Ile	Pro	Ser	Gln	Arg	Val	Val	Lys	Val	Pro	
		200					205					210				
aat	gat	gac	gcc	ggt	gaa	cac	tat	gaa	att	gtc	atc	gag	cca	cgc	ccg	787
Asn	Asp	Asp	Ala	Gly	Glu	His	Tyr	Glu	Ile	Val	Ile	Glu	Pro	Arg	Pro	
	215					220					225					
cac	atc	atg	gat	tac	aat	tcc	gag	att	tcc	ctg	ctc	aca	ggc	atg	gta	835
His	Ile	Met	Asp	Tyr	Asn	Ser	Glu	Ile	Ser	Leu	Leu	Thr	Gly	Met	Val	
	230				235					240					245	
gcg	ggg	gag	atg	atg	gtg	aaa	gcg	ggg	cac	ggt	ttg	ctg	cgt	aca	ctc	883
Ala	Gly	Glu	Met	Met	Val	Lys	Ala	Gly	His	Gly	Leu	Leu	Arg	Thr	Leu	
				250					255					260		
gcc	ccg	gcg	acc	aaa	gaa	tcc	gaa	gct	act	ttc	aga	tca	gag	gcg	caa	931
Ala	Pro	Ala	Thr	Lys	Glu	Ser	Glu	Ala	Thr	Phe	Arg	Ser	Glu	Ala	Gln	
			265					270					275			
gcc	ctt	ggt	ttt	gag	atc	gcg	ccc	gaa	caa	ccc	atc	ggt	gag	ttt	ctt	979
Ala	Leu	Gly	Phe	Glu	Ile	Ala	Pro	Glu	Gln	Pro	Ile	Gly	Glu	Phe	Leu	
		280					285					290				

caa agt gtg gat ccc aat acg ccc aaa ggg atg gcc att cag agg gaa 1027
 Gln Ser Val Asp Pro Asn Thr Pro Lys Gly Met Ala Ile Gln Arg Glu
 295 300 305

gca cag aaa ctc ttg cgg ggc tcc ggc tac gcc agc gtg aaa aat ggg 1075
 Ala Gln Lys Leu Leu Arg Gly Ser Gly Tyr Ala Ser Val Lys Asn Gly
 310 315 320 325

gac tcg gaa gtg cat tcc ggt gtt ggt ggt tac tat gct cac gtc acc 1123
 Asp Ser Glu Val His Ser Gly Val Gly Gly Tyr Tyr Ala His Val Thr
 330 335 340

gca ccg ctg cgc cga ctt atc gac cgt ttc gcc acc gaa cat tgc ctt 1171
 Ala Pro Leu Arg Arg Leu Ile Asp Arg Phe Ala Thr Glu His Cys Leu
 345 350 355

gcg att gcc tcc gga acg gac gtt cct gaa tgg gtg acc agg gtg gaa 1219
 Ala Ile Ala Ser Gly Thr Asp Val Pro Glu Trp Val Thr Arg Val Glu
 360 365 370

gag caa gtt ctc gac acc atg aaa tac tcc tcc att ttg gcc agc caa 1267
 Glu Gln Val Leu Asp Thr Met Lys Tyr Ser Ser Ile Leu Ala Ser Gln
 375 380 385

gtg gat aat gcc tgc ctc gac ctc aca gaa gcc acc gtg ttg aaa tac 1315
 Val Asp Asn Ala Cys Leu Asp Leu Thr Glu Ala Thr Val Leu Lys Tyr
 390 395 400 405

tgg gag ggc caa aac ttc aac gcg gtg gtt gta gcg agc gaa cct gaa 1363
 Trp Glu Gly Gln Asn Phe Asn Ala Val Val Val Ala Ser Glu Pro Glu
 410 415 420

aag aac tct gct cga ctt ttt gtg tac aaa ccg cca gtg ttg gca aag 1411
 Lys Asn Ser Ala Arg Leu Phe Val Tyr Lys Pro Pro Val Leu Ala Lys
 425 430 435

tgt att ggc gcc cca gaa cag gga aca aac caa gat gtc aca ctg gtg 1459
 Cys Ile Gly Ala Pro Glu Gln Gly Thr Asn Gln Asp Val Thr Leu Val
 440 445 450

act gcg aac ttg aag aag cgt gaa gtt ttg ttt gcg tgg ccg gct gac 1507
 Thr Ala Asn Leu Lys Lys Arg Glu Val Leu Phe Ala Trp Pro Ala Asp
 455 460 465

taagcatgca ggctgggttaa gta 1530

<210> 214

<211> 469

<212> PRT

<213> Corynebacterium glutamicum

<400> 214

Met Lys Leu Tyr Ala Ala Val Leu Asp Phe Glu Pro Val Ala Gln Glu
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Phe Gly Val Glu Arg Gly Phe Asp Pro His Ile His Asp Glu Ala Ala
 20 25 30

Ser Ser Val Asp Arg Tyr Ala Gln Glu Arg Glu Asp Leu Leu His Met
 35 40 45

Pro	Phe	Val	Thr	Ile	Asp	Pro	Val	Gly	Ser	Arg	Asp	Leu	Asp	Gln	Ala
50						55					60				
Val	Leu	Ile	Glu	Glu	Ile	Asp	Ser	Gly	Phe	Arg	Val	His	Tyr	Ala	Ile
65					70					75					80
Ala	Asp	Val	Ala	Ala	Phe	Val	Glu	Pro	Gly	Ser	Glu	Leu	Glu	Lys	Ile
				85					90					95	
Ser	Leu	His	Arg	Gly	Gln	Thr	Ile	Tyr	Leu	Pro	Asp	Ser	Pro	Ala	Arg
			100					105					110		
Leu	His	Pro	Glu	Glu	Leu	Ser	Glu	Asp	Ala	Ala	Ser	Leu	Leu	Glu	Gly
		115					120					125			
Gln	Thr	Arg	Pro	Ala	Val	Val	Trp	Ser	Ile	Asp	Leu	Asp	Glu	Arg	Gly
130						135					140				
Glu	Val	Thr	Ala	Thr	Lys	Val	Arg	Arg	Gly	Leu	Val	Lys	Ser	Arg	Ala
145					150					155					160
Arg	Leu	Asp	Tyr	Asp	Gln	Ala	Gln	Ile	Asp	Ala	Glu	Asn	Gly	Arg	Leu
				165					170					175	
His	Pro	Ser	Ile	Ser	Leu	Leu	Pro	Lys	Val	Gly	Gln	Leu	Arg	Gln	Glu
			180					185					190		
Ser	Ala	Leu	Arg	Arg	Glu	Ala	Val	Asn	Leu	Ser	Ile	Pro	Ser	Gln	Arg
		195					200					205			
Val	Val	Lys	Val	Pro	Asn	Asp	Asp	Ala	Gly	Glu	His	Tyr	Glu	Ile	Val
		210				215						220			
Ile	Glu	Pro	Arg	Pro	His	Ile	Met	Asp	Tyr	Asn	Ser	Glu	Ile	Ser	Leu
225					230					235					240
Leu	Thr	Gly	Met	Val	Ala	Gly	Glu	Met	Met	Val	Lys	Ala	Gly	His	Gly
				245					250					255	
Leu	Leu	Arg	Thr	Leu	Ala	Pro	Ala	Thr	Lys	Glu	Ser	Glu	Ala	Thr	Phe
			260					265					270		
Arg	Ser	Glu	Ala	Gln	Ala	Leu	Gly	Phe	Glu	Ile	Ala	Pro	Glu	Gln	Pro
		275					280					285			
Ile	Gly	Glu	Phe	Leu	Gln	Ser	Val	Asp	Pro	Asn	Thr	Pro	Lys	Gly	Met
		290				295					300				
Ala	Ile	Gln	Arg	Glu	Ala	Gln	Lys	Leu	Leu	Arg	Gly	Ser	Gly	Tyr	Ala
305					310					315					320
Ser	Val	Lys	Asn	Gly	Asp	Ser	Glu	Val	His	Ser	Gly	Val	Gly	Gly	Tyr
				325					330					335	
Tyr	Ala	His	Val	Thr	Ala	Pro	Leu	Arg	Arg	Leu	Ile	Asp	Arg	Phe	Ala
			340					345					350		
Thr	Glu	His	Cys	Leu	Ala	Ile	Ala	Ser	Gly	Thr	Asp	Val	Pro	Glu	Trp
		355					360					365			

Val Thr Arg Val Glu Glu Gln Val Leu Asp Thr Met Lys Tyr Ser Ser
 370 375 380

Ile Leu Ala Ser Gln Val Asp Asn Ala Cys Leu Asp Leu Thr Glu Ala
 385 390 395 400

Thr Val Leu Lys Tyr Trp Glu Gly Gln Asn Phe Asn Ala Val Val Val
 405 410 415

Ala Ser Glu Pro Glu Lys Asn Ser Ala Arg Leu Phe Val Tyr Lys Pro
 420 425 430

Pro Val Leu Ala Lys Cys Ile Gly Ala Pro Glu Gln Gly Thr Asn Gln
 435 440 445

Asp Val Thr Leu Val Thr Ala Asn Leu Lys Lys Arg Glu Val Leu Phe
 450 455 460

Ala Trp Pro Ala Asp
 465

<210> 215
 <211> 519
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(496)
 <223> RXA02077

<400> 215
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 tggcagatat cgctcgcgaa attgatcttg gcaaccacat atg ctg ggc aaa ggc 115
 Met Leu Gly Lys Gly
 1 5

gaa ttg ctc acc gaa ggt cgc agt aag gat tcc att ctt gcg gac acc 163
 Glu Leu Leu Thr Glu Gly Arg Ser Lys Asp Ser Ile Leu Ala Asp Thr
 10 15 20

aca gag gcg ttg ttc ggc gcg att ttc cgc cag cac ggt ttt gaa acc 211
 Thr Glu Ala Leu Phe Gly Ala Ile Phe Arg Gln His Gly Phe Glu Thr
 25 30 35

gcc cgc gac gta att ttg cgc ctg ttt gcc tac aag atc gat aac gca 259
 Ala Arg Asp Val Ile Leu Arg Leu Phe Ala Tyr Lys Ile Asp Asn Ala
 40 45 50

tcg gcc agg ggc att cac cag gac tgg aag acc acg ctg cag gag gaa 307
 Ser Ala Arg Gly Ile His Gln Asp Trp Lys Thr Thr Leu Gln Glu Glu
 55 60 65

ctt gct cag cgc aag cgc ccc atg gct gaa tat tcc gcc acc tca gtc 355
 Leu Ala Gln Arg Lys Arg Pro Met Ala Glu Tyr Ser Ala Thr Ser Val
 70 75 80 85

ggg ccg gat cac gat cta gtg ttc acc gcc atc gtg acg ctg gaa ggt 403
 Gly Pro Asp His Asp Leu Val Phe Thr Ala Ile Val Thr Leu Glu Gly

90

95

100

gaa gaa atg ggt cgg gga gaa ggc ccg aac aag aag ctg gcc gag cag 451
 Glu Glu Met Gly Arg Gly Glu Gly Pro Asn Lys Lys Leu Ala Glu Gln
 105 110 115

gaa gca gcg cac cag gca ttc cga aag ctt cgg gag tcc cgt gcc 496
 Glu Ala Ala His Gln Ala Phe Arg Lys Leu Arg Glu Ser Arg Ala
 120 125 130

tgaactgcct gaagttgagg tgg 519

<210> 216

<211> 132

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

Met Leu Gly Lys Gly Glu Leu Leu Thr Glu Gly Arg Ser Lys Asp Ser
 1 5 10 15

Ile Leu Ala Asp Thr Thr Glu Ala Leu Phe Gly Ala Ile Phe Arg Gln
 20 25 30

His Gly Phe Glu Thr Ala Arg Asp Val Ile Leu Arg Leu Phe Ala Tyr
 35 40 45

Lys Ile Asp Asn Ala Ser Ala Arg Gly Ile His Gln Asp Trp Lys Thr
 50 55 60

Thr Leu Gln Glu Glu Leu Ala Gln Arg Lys Arg Pro Met Ala Glu Tyr
 65 70 75 80

Ser Ala Thr Ser Val Gly Pro Asp His Asp Leu Val Phe Thr Ala Ile
 85 90 95

Val Thr Leu Glu Gly Glu Glu Met Gly Arg Gly Glu Gly Pro Asn Lys
 100 105 110

Lys Leu Ala Glu Gln Glu Ala Ala His Gln Ala Phe Arg Lys Leu Arg
 115 120 125

Glu Ser Arg Ala
 130

<210> 217

<211> 1332

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1309)

<223> RXN01563

<400> 217

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ccagagggcg tcaccgaact acgaaggtag attggacacc atg gtt tcc gat etc 115

	Met	Val	Ser	Asp	Leu	
	1				5	
ctt caa ccc cgc gac ggc att ccg cct ttg cta tct acc cct ggt gag 163						
Leu Gln Pro Arg Asp Gly Ile Pro Pro Leu Leu Ser Thr Pro Gly Glu						
	10				20	
ttc act gct gcg gca gat ctc ttg gct agc gga act ggg ccc ttc gcc 211						
Phe Thr Ala Ala Ala Asp Leu Leu Ala Ser Gly Thr Gly Pro Phe Ala						
	25				35	
att gat acg gaa cgc gcg tcc ggt ttt aga tac gat gac cgc gca ttt 259						
Ile Asp Thr Glu Arg Ala Ser Gly Phe Arg Tyr Asp Asp Arg Ala Phe						
	40				50	
ttg att cag atc cgg cgc cgt ggc agc gga act ctc cta ttc gac ccg 307						
Leu Ile Gln Ile Arg Arg Arg Gly Ser Gly Thr Leu Leu Phe Asp Pro						
	55				65	
gag cag ttc cgt cct gaa tta act cag gcg tta aag ccg gtg ctc aat 355						
Glu Gln Phe Arg Pro Glu Leu Thr Gln Ala Leu Lys Pro Val Leu Asn						
	70				80	
ggt caa gag tgg atc att cac gca gca agc acc gat ttg ccg agc ctt 403						
Gly Gln Glu Trp Ile Ile His Ala Ala Ser Thr Asp Leu Pro Ser Leu						
	90				100	
gcg tgg ctt gat ctt cac ccc gga tta ctc ttt gat aca gaa ctt gct 451						
Ala Trp Leu Asp Leu His Pro Gly Leu Leu Phe Asp Thr Glu Leu Ala						
	105				115	
ggc cgc tta gcc gga ttt gat cac gtt aat ctc gct gcc atg gtg gaa 499						
Gly Arg Leu Ala Gly Phe Asp His Val Asn Leu Ala Ala Met Val Glu						
	120				130	
cag att ttt gat ctc cac ttg ctc aaa ggc cac cgt tcg gaa gat tgg 547						
Gln Ile Phe Asp Leu His Leu Leu Lys Gly His Arg Ser Glu Asp Trp						
	135				145	
tcc aag cgt cct ctg ccg gaa tct tgg ctc aac tac gca gca ctc gat 595						
Ser Lys Arg Pro Leu Pro Glu Ser Trp Leu Asn Tyr Ala Ala Leu Asp						
	150				160	
gtg gag atg ctg ctg gag ctt gcc gat gtc atg gct gaa atc ctg gat 643						
Val Glu Met Leu Leu Glu Leu Ala Asp Val Met Ala Glu Ile Leu Asp						
	170				180	
cag cag gga aaa ctc ccc tgg gct gaa cag gaa ttt gtc cat att gtg 691						
Gln Gln Gly Lys Leu Pro Trp Ala Glu Gln Glu Phe Val His Ile Val						
	185				195	
gat caa ttc gcc acg atg acc gaa cct tcc gaa acg tcc tgg cag gac 739						
Asp Gln Phe Ala Thr Met Thr Glu Pro Ser Glu Thr Ser Trp Gln Asp						
	200				210	
ctt aaa ggg ctg tcc act ctc aaa cga cca gac caa tta gtt gtg gcc 787						
Leu Lys Gly Leu Ser Thr Leu Lys Arg Pro Asp Gln Leu Val Val Ala						
	215				225	
cgt gaa atg tgg ttg gaa cgc gac tct ttc gca gcc tcc cgc gac ctg 835						
Arg Glu Met Trp Leu Glu Arg Asp Ser Phe Ala Ala Ser Arg Asp Leu						

230	235	240	245	
gcg ccc ggt aaa gtg ctg tcc aac aaa gtc atc gtg gaa gtc gcc cgt				883
Ala Pro Gly Lys Val Leu Ser Asn Lys Val Ile Val Glu Val Ala Arg	250	255	260	
gtt ctc ccc cgc acc ccg gca gaa tta gcg cag gtc aag gga ttc ccc				931
Val Leu Pro Arg Thr Pro Ala Glu Leu Ala Gln Val Lys Gly Phe Pro	265	270	275	
ggt cga tcc cag ggt gcc acc aaa cgc tgg ttc cgc atc atc acc cgg				979
Gly Arg Ser Gln Gly Ala Thr Lys Arg Trp Phe Arg Ile Ile Thr Arg	280	285	290	
gcg ctc aaa tcc cct cgc agg aac tgg cca aag cct cag cag cgc aag				1027
Ala Leu Lys Ser Pro Arg Asn Trp Pro Lys Pro Gln Gln Arg Lys	295	300	305	
gac ggc atc ccc gat cgt cgc gcg tgg gcg tcc tac tac cca gaa gag				1075
Asp Gly Ile Pro Asp Arg Arg Ala Trp Ala Ser Tyr Tyr Pro Glu Glu	310	315	320	325
cac gaa gtg ctc caa gag att aga gcg ctt atc gac gac ctc gcc gcc				1123
His Glu Val Leu Gln Glu Ile Arg Ala Leu Ile Asp Asp Leu Ala Ala	330	335	340	
gat atc aac gtt ccc ggc gag aat atc ctt cag cct tca act ctg cga				1171
Asp Ile Asn Val Pro Gly Glu Asn Ile Leu Gln Pro Ser Thr Leu Arg	345	350	355	
gta gct gtg tgg atg gct aaa cac acc ggc gag atc cat aat gct gaa				1219
Val Ala Val Trp Met Ala Lys His Thr Gly Glu Ile His Asn Ala Glu	360	365	370	
aca ctc aac gct gta ctt cgc gat tat ggt gcc cgc cag tgg caa att				1267
Thr Leu Asn Ala Val Leu Arg Asp Tyr Gly Ala Arg Gln Trp Gln Ile	375	380	385	
gac cag act ttt ccg att ctg tcc gcc aac ttg ctg aag ctc				1309
Asp Gln Thr Phe Pro Ile Leu Ser Ala Asn Leu Leu Lys Leu	390	395	400	
taaacctaaa gcccgcggt aag				1332

<210> 218

<211> 403

<212> PRT

<213> Corynebacterium glutamicum

<400> 218

Met Val Ser Asp Leu Leu Gln Pro Arg Asp Gly Ile Pro Pro Leu Leu
 1 5 10 15

Ser Thr Pro Gly Glu Phe Thr Ala Ala Ala Asp Leu Leu Ala Ser Gly
 20 25 30

Thr Gly Pro Phe Ala Ile Asp Thr Glu Arg Ala Ser Gly Phe Arg Tyr
 35 40 45

Asp Asp Arg Ala Phe Leu Ile Gln Ile Arg Arg Arg Gly Ser Gly Thr

50					55					60					
Leu	Leu	Phe	Asp	Pro	Glu	Gln	Phe	Arg	Pro	Glu	Leu	Thr	Gln	Ala	Leu
65					70					75					80
Lys	Pro	Val	Leu	Asn	Gly	Gln	Glu	Trp	Ile	Ile	His	Ala	Ala	Ser	Thr
			85						90					95	
Asp	Leu	Pro	Ser	Leu	Ala	Trp	Leu	Asp	Leu	His	Pro	Gly	Leu	Leu	Phe
			100					105					110		
Asp	Thr	Glu	Leu	Ala	Gly	Arg	Leu	Ala	Gly	Phe	Asp	His	Val	Asn	Leu
		115					120					125			
Ala	Ala	Met	Val	Glu	Gln	Ile	Phe	Asp	Leu	His	Leu	Leu	Lys	Gly	His
		130					135					140			
Arg	Ser	Glu	Asp	Trp	Ser	Lys	Arg	Pro	Leu	Pro	Glu	Ser	Trp	Leu	Asn
145					150					155					160
Tyr	Ala	Ala	Leu	Asp	Val	Glu	Met	Leu	Leu	Glu	Leu	Ala	Asp	Val	Met
			165						170					175	
Ala	Glu	Ile	Leu	Asp	Gln	Gln	Gly	Lys	Leu	Pro	Trp	Ala	Glu	Gln	Glu
			180					185					190		
Phe	Val	His	Ile	Val	Asp	Gln	Phe	Ala	Thr	Met	Thr	Glu	Pro	Ser	Glu
		195					200					205			
Thr	Ser	Trp	Gln	Asp	Leu	Lys	Gly	Leu	Ser	Thr	Leu	Lys	Arg	Pro	Asp
		210				215					220				
Gln	Leu	Val	Val	Ala	Arg	Glu	Met	Trp	Leu	Glu	Arg	Asp	Ser	Phe	Ala
225					230					235					240
Ala	Ser	Arg	Asp	Leu	Ala	Pro	Gly	Lys	Val	Leu	Ser	Asn	Lys	Val	Ile
			245						250					255	
Val	Glu	Val	Ala	Arg	Val	Leu	Pro	Arg	Thr	Pro	Ala	Glu	Leu	Ala	Gln
			260					265					270		
Val	Lys	Gly	Phe	Pro	Gly	Arg	Ser	Gln	Gly	Ala	Thr	Lys	Arg	Trp	Phe
		275					280					285			
Arg	Ile	Ile	Thr	Arg	Ala	Leu	Lys	Ser	Pro	Arg	Arg	Asn	Trp	Pro	Lys
	290					295					300				
Pro	Gln	Gln	Arg	Lys	Asp	Gly	Ile	Pro	Asp	Arg	Arg	Ala	Trp	Ala	Ser
305					310					315					320
Tyr	Tyr	Pro	Glu	Glu	His	Glu	Val	Leu	Gln	Glu	Ile	Arg	Ala	Leu	Ile
			325						330					335	
Asp	Asp	Leu	Ala	Ala	Asp	Ile	Asn	Val	Pro	Gly	Glu	Asn	Ile	Leu	Gln
			340					345					350		
Pro	Ser	Thr	Leu	Arg	Val	Ala	Val	Trp	Met	Ala	Lys	His	Thr	Gly	Glu
		355					360					365			
Ile	His	Asn	Ala	Glu	Thr	Leu	Asn	Ala	Val	Leu	Arg	Asp	Tyr	Gly	Ala
		370				375					380				

Arg Gln Trp Gln Ile Asp Gln Thr Phe Pro Ile Leu Ser Ala Asn Leu
 385 390 395 400

Leu Lys Leu

<210> 219

<211> 833

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(810)

<223> FRXA01563

<400> 219

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Gln Ile Phe Asp Leu His Leu Leu Lys Gly His Gly Ser Glu Asp Trp	
1 5 10 15	
tcc aag cgt cct ctg ccg gaa tct tgg ctc aac tac gca gca ctc gat	96
Ser Lys Arg Pro Leu Pro Glu Ser Trp Leu Asn Tyr Ala Ala Leu Asp	
20 25 30	
gtg gag atg ctg ctg gag ctt gcc gat gtc atg gct gaa atc ctg gat	144
Val Glu Met Leu Leu Glu Leu Ala Asp Val Met Ala Glu Ile Leu Asp	
35 40 45	
cag cag gga aaa ctc ccc tgg gct gaa cag gaa ttt gtc cat att gtg	192
Gln Gln Gly Lys Leu Pro Trp Ala Glu Gln Glu Phe Val His Ile Val	
50 55 60	
gat caa ttc gcc acg atg acc gaa cct tcc gaa acg tcc tgg cag gac	240
Asp Gln Phe Ala Thr Met Thr Glu Pro Ser Glu Thr Ser Trp Gln Asp	
65 70 75 80	
ctt aaa ggg ctg tcc act ctc aaa cga cca gac caa tta gtt gtg gcc	288
Leu Lys Gly Leu Ser Thr Leu Lys Arg Pro Asp Gln Leu Val Val Ala	
85 90 95	
cgt gaa atg tgg ttg gaa cgc gac tct ttc gca gcc tcc cgc gac ctg	336
Arg Glu Met Trp Leu Glu Arg Asp Ser Phe Ala Ala Ser Arg Asp Leu	
100 105 110	
gcg ccc ggt aaa gtg ctg tcc aac aaa gtc atc gtg gaa gtc gcc cgt	384
Ala Pro Gly Lys Val Leu Ser Asn Lys Val Ile Val Glu Val Ala Arg	
115 120 125	
gtt ctc ccc cgc acc ccg gca gaa tta gcg cag gtc aag gga ttc ccc	432
Val Leu Pro Arg Thr Pro Ala Glu Leu Ala Gln Val Lys Gly Phe Pro	
130 135 140	
ggt cga tcc cag ggt gcc acc aaa cgc tgg ttc cgc atc atc acc cgg	480
Gly Arg Ser Gln Gly Ala Thr Lys Arg Trp Phe Arg Ile Ile Thr Arg	
145 150 155 160	
gcg ctc aaa tcc cct cgc agg aac tgg cca aag cct cag cag cgc aag	528
Ala Leu Lys Ser Pro Arg Arg Asn Trp Pro Lys Pro Gln Gln Arg Lys	

	165	170	175	
gac ggc atc ccc gat cgt cgc gcg tgg gcg tcc tac tac cca gaa gag				576
Asp Gly Ile Pro Asp Arg Arg Ala Trp Ala Ser Tyr Tyr Pro Glu Glu				
	180	185	190	
cac gaa gtg ctc caa gag att aga gcg ctt atc gac gac ctc gcc gcc				624
His Glu Val Leu Gln Glu Ile Arg Ala Leu Ile Asp Asp Leu Ala Ala				
	195	200	205	
gat atc aac gtt ccc ggc gag aat atc ctt cag cct tca act ctg cga				672
Asp Ile Asn Val Pro Gly Glu Asn Ile Leu Gln Pro Ser Thr Leu Arg				
	210	215	220	
gta gct gtg tgg atg gct aaa cac acc ggc gag atc cat aat gct gaa				720
Val Ala Val Trp Met Ala Lys His Thr Gly Glu Ile His Asn Ala Glu				
	225	230	235	240
aca ctc aac gct gta ctt cgc gat tat ggt gcc cgc cag tgg caa att				768
Thr Leu Asn Ala Val Leu Arg Asp Tyr Gly Ala Arg Gln Trp Gln Ile				
	245	250	255	
gac cag act ttt ccg att ctg tcc gcc aac ttg ctg aag ctc				810
Asp Gln Thr Phe Pro Ile Leu Ser Ala Asn Leu Leu Lys Leu				
	260	265	270	
taaacctaaa gcccgcggt aag				833
<210> 220				
<211> 270				
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<213> Corynebacterium glutamicum				
<400> 220				
Gln Ile Phe Asp Leu His Leu Leu Lys Gly His Gly Ser Glu Asp Trp				
1 5 10 15				
Ser Lys Arg Pro Leu Pro Glu Ser Trp Leu Asn Tyr Ala Ala Leu Asp				
20 25 30				
Val Glu Met Leu Leu Glu Leu Ala Asp Val Met Ala Glu Ile Leu Asp				
35 40 45				
Gln Gln Gly Lys Leu Pro Trp Ala Glu Gln Glu Phe Val His Ile Val				
50 55 60				
Asp Gln Phe Ala Thr Met Thr Glu Pro Ser Glu Thr Ser Trp Gln Asp				
65 70 75 80				
Leu Lys Gly Leu Ser Thr Leu Lys Arg Pro Asp Gln Leu Val Val Ala				
85 90 95				
Arg Glu Met Trp Leu Glu Arg Asp Ser Phe Ala Ala Ser Arg Asp Leu				
100 105 110				
Ala Pro Gly Lys Val Leu Ser Asn Lys Val Ile Val Glu Val Ala Arg				
115 120 125				
Val Leu Pro Arg Thr Pro Ala Glu Leu Ala Gln Val Lys Gly Phe Pro				
130 135 140				

Gly Arg Ser Gln Gly Ala Thr Lys Arg Trp Phe Arg Ile Ile Thr Arg
145 150 155 160

Ala Leu Lys Ser Pro Arg Arg Asn Trp Pro Lys Pro Gln Gln Arg Lys
165 170 175

Asp Gly Ile Pro Asp Arg Arg Ala Trp Ala Ser Tyr Tyr Pro Glu Glu
180 185 190

His Glu Val Leu Gln Glu Ile Arg Ala Leu Ile Asp Asp Leu Ala Ala
195 200 205

Asp Ile Asn Val Pro Gly Glu Asn Ile Leu Gln Pro Ser Thr Leu Arg
210 215 220

Val Ala Val Trp Met Ala Lys His Thr Gly Glu Ile His Asn Ala Glu
225 230 235 240

Thr Leu Asn Ala Val Leu Arg Asp Tyr Gly Ala Arg Gln Trp Gln Ile
245 250 255

Asp Gln Thr Phe Pro Ile Leu Ser Ala Asn Leu Leu Lys Leu
260 265 270

<210> 221

<211> 454

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(454)

<223> FRXA01713

<400> 221

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ccagagggcg tcaccgaact acgaaggtag attggacacc atg gtt tcc gat ctc 115
Met Val Ser Asp Leu
1 5

ctt caa ccc cgc gac ggc att ccg cct ttg cta tct acc cct ggt gag 163
Leu Gln Pro Arg Asp Gly Ile Pro Pro Leu Leu Ser Thr Pro Gly Glu
10 15 20

ttc act gct gcg gca gat ctc ttg gct agc gga act ggg ccc ttc gcc 211
Phe Thr Ala Ala Ala Asp Leu Leu Ala Ser Gly Thr Gly Pro Phe Ala
25 30 35

att gat acg gaa cgc gcg tcc ggt ttt aga tac gat gac cgc gca ttt 259
Ile Asp Thr Glu Arg Ala Ser Gly Phe Arg Tyr Asp Asp Arg Ala Phe
40 45 50

ttg att cag atc cgg cgc cgt ggc agc gga act ctc cta ttc gac ccg 307
Leu Ile Gln Ile Arg Arg Arg Gly Ser Gly Thr Leu Leu Phe Asp Pro
55 60 65

gag cag ttc cgt cct gaa tta act cag gcg tta aag ccg gtg ctc aat 355
Glu Gln Phe Arg Pro Glu Leu Thr Gln Ala Leu Lys Pro Val Leu Asn

70	75	80	85		
ggt	caa	gag	tgg	atc att cac gca gca agc acc gat ttg ccg agc ctt	403
Gly	Gln	Glu	Trp	Ile Ile His Ala Ala Ser Thr Asp Leu Pro Ser Leu	
	90			95	100
gcg	tgg	ctt	gat	ctt cac ccc gga tta ctc ttt gat aca gaa ctt gct	451
Ala	Trp	Leu	Asp	Leu His Pro Gly Leu Leu Phe Asp Thr Glu Leu Ala	
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ggc					454
Gly					

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 222
 Met Val Ser Asp Leu Leu Gln Pro Arg Asp Gly Ile Pro Pro Leu Leu
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 Ser Thr Pro Gly Glu Phe Thr Ala Ala Ala Asp Leu Leu Ala Ser Gly
 20 25 30
 Thr Gly Pro Phe Ala Ile Asp Thr Glu Arg Ala Ser Gly Phe Arg Tyr
 35 40 45
 Asp Asp Arg Ala Phe Leu Ile Gln Ile Arg Arg Arg Gly Ser Gly Thr
 50 55 60
 Leu Leu Phe Asp Pro Glu Gln Phe Arg Pro Glu Leu Thr Gln Ala Leu
 65 70 75 80
 Lys Pro Val Leu Asn Gly Gln Glu Trp Ile Ile His Ala Ala Ser Thr
 85 90 95
 Asp Leu Pro Ser Leu Ala Trp Leu Asp Leu His Pro Gly Leu Leu Phe
 100 105 110
 Asp Thr Glu Leu Ala Gly
 115

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 <211> 2412
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(2389)
 <223> RXA02369

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 Val Pro Asn Asn Lys

1

5

gca gta gaa gca gaa atc tct ccc tcg gct gtg ctg gcc gcg gaa ttt	163
Ala Val Glu Ala Glu Ile Ser Pro Ser Ala Val Leu Ala Ala Glu Phe	
10 15 20	
gat cga gat tca ttg agc gaa aaa acc cgc gta cat caa ctg gcc aaa	211
Asp Arg Asp Ser Leu Ser Glu Lys Thr Arg Val His Gln Leu Ala Lys	
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cga ctt gga atg gtt tcc aag gac gtc gtt gtt gcg ctc gat ggc atc	259
Arg Leu Gly Met Val Ser Lys Asp Val Val Val Ala Leu Asp Gly Ile	
40 45 50	
ggc ctg gtc aag gtt gcg cag tca aac ctg agc aaa gaa gaa gta gaa	307
Gly Leu Val Lys Val Ala Gln Ser Asn Leu Ser Lys Glu Glu Val Glu	
55 60 65	
aag ctt ctc gac gcc ctg tct cag ccc gta ctc aac gct gcc cca gct	355
Lys Leu Leu Asp Ala Leu Ser Gln Pro Val Leu Asn Ala Ala Pro Ala	
70 75 80 85	
gcc gtc ccc gac gtt gaa ccg gtg gag aag att cgt cga cgc gtt gag	403
Ala Val Pro Asp Val Glu Pro Val Glu Lys Ile Arg Arg Arg Val Glu	
90 95 100	
aag aat gtg gaa aat gaa atc cac caa atc gaa gaa aaa gta gag cgc	451
Lys Asn Val Glu Asn Glu Ile His Gln Ile Glu Glu Lys Val Glu Arg	
105 110 115	
gaa ctc gcg gca gtc gcg caa cct act gac ttc gag gcg gca gcc cgc	499
Glu Leu Ala Ala Val Ala Gln Pro Thr Asp Phe Glu Ala Ala Ala Arg	
120 125 130	
gaa gaa gcc act gca gaa ctg ctg gaa gat atc gtc cca gag atc acc	547
Glu Glu Ala Thr Ala Glu Leu Leu Glu Asp Ile Val Pro Glu Ile Thr	
135 140 145	
ccg gcg ccg gtg gaa gca tct gtg tac acg ccg atc ttt gtg gca cct	595
Pro Ala Pro Val Glu Ala Ser Val Tyr Thr Pro Ile Phe Val Ala Pro	
150 155 160 165	
gca gtt gta cct act gaa aac gtc caa gac acc gac gat gaa cag gtc	643
Ala Val Val Pro Thr Glu Asn Val Gln Asp Thr Asp Asp Glu Gln Val	
170 175 180	
cgc gaa cgc acg gcg cgg aag cgc cgt ggg cgt cgt ggc acc ggc cgc	691
Arg Glu Arg Thr Ala Arg Lys Arg Arg Gly Arg Arg Gly Thr Gly Arg	
185 190 195	
gga cgt gga gct gaa gct gaa acc gtc acc gaa gtg agt gag gag gcg	739
Gly Arg Gly Ala Glu Ala Glu Thr Val Thr Glu Val Ser Glu Glu Ala	
200 205 210	
tcg aca agc gaa gta gaa gag gta aac gag cca atc gga att aag ggc	787
Ser Thr Ser Glu Val Glu Glu Val Asn Glu Pro Ile Gly Ile Lys Gly	
215 220 225	
tcc act cgc ttg gag gcg caa cgc cgc cgt cgc acg gaa atg cgc gaa	835
Ser Thr Arg Leu Glu Ala Gln Arg Arg Arg Arg Thr Glu Met Arg Glu	
230 235 240 245	

gaa aac aaa aaa cgc cgc cat gtg gtc agc acc cag gag ttc atg gaa 883
 Glu Asn Lys Lys Arg Arg His Val Val Ser Thr Gln Glu Phe Met Glu
 250 255 260

cgc cgt gaa tcg atg gaa cgt cgc atg att gtg cgc gag cgc caa cgc 931
 Arg Arg Glu Ser Met Glu Arg Arg Met Ile Val Arg Glu Arg Gln Arg
 265 270 275

cac gat cac cca ggt ctg gtc act cag gtt ggt gtg ctg gaa gac gat 979
 His Asp His Pro Gly Leu Val Thr Gln Val Gly Val Leu Glu Asp Asp
 280 285 290

cag ctg gtt gag cag ttt gtt acc tct gat gcg cag atg tct atg gtg 1027
 Gln Leu Val Glu Gln Phe Val Thr Ser Asp Ala Gln Met Ser Met Val
 295 300 305

ggc aat att tat ctg ggg cgc gtt caa aat gtg ctg cca agc atg gaa 1075
 Gly Asn Ile Tyr Leu Gly Arg Val Gln Asn Val Leu Pro Ser Met Glu
 310 315 320 325

gct gcc ttc att gac att gga aaa ggt cgc aac ggt gtg ttg tat gcc 1123
 Ala Ala Phe Ile Asp Ile Gly Lys Gly Arg Asn Gly Val Leu Tyr Ala
 330 335 340

ggc gaa gtc gac tgg aaa gct gct gga ctt ggc gga cgt gga cgt cgc 1171
 Gly Glu Val Asp Trp Lys Ala Ala Gly Leu Gly Gly Arg Gly Arg Arg
 345 350 355

att gag cag gcg ctg aaa gcc ggc gac cag gtt ctc gtc cag gtc tcc 1219
 Ile Glu Gln Ala Leu Lys Ala Gly Asp Gln Val Leu Val Gln Val Ser
 360 365 370

aag gat cca ttg ggc cat aag ggt gcg cgt ttg acc acc caa att tcc 1267
 Lys Asp Pro Leu Gly His Lys Gly Ala Arg Leu Thr Thr Gln Ile Ser
 375 380 385

ctg gcg gga cgt tac ctg gtg tac gtt cca ggt ggt cgc agc gct ggc 1315
 Leu Ala Gly Arg Tyr Leu Val Tyr Val Pro Gly Gly Arg Ser Ala Gly
 390 395 400 405

att tcc cgc aaa ctg cct gga cct gag cgc aag cgt ctg aag gaa atc 1363
 Ile Ser Arg Lys Leu Pro Gly Pro Glu Arg Lys Arg Leu Lys Glu Ile
 410 415 420

ctt ggc cgc gtt gtc cca gcg cag ggt gga acc atc atc cga act gct 1411
 Leu Gly Arg Val Val Pro Ala Gln Gly Gly Thr Ile Ile Arg Thr Ala
 425 430 435

gct gaa ggt gtg tcg gaa gaa aac atc gca gct gac gtg aac cgt ctg 1459
 Ala Glu Gly Val Ser Glu Glu Asn Ile Ala Ala Asp Val Asn Arg Leu
 440 445 450

cac acc ctg tgg gag cag atc aag gaa cgc act gcg gag gaa aag aag 1507
 His Thr Leu Trp Glu Gln Ile Lys Glu Arg Thr Ala Glu Glu Lys Lys
 455 460 465

tcc cgc ggt tct aag ccg atc acc atg tat gaa gag cca gac atg ctg 1555
 Ser Arg Gly Ser Lys Pro Ile Thr Met Tyr Glu Glu Pro Asp Met Leu
 470 475 480 485

gtg aag gtg atc cgt gac ctc ttc aat gaa gat ttc acc tca ctg atc	1603
Val Lys Val Ile Arg Asp Leu Phe Asn Glu Asp Phe Thr Ser Leu Ile	
490 495 500	
gtt gac ggc gac cgt gcc tgg aac acc gtg cgt gcc tac atc caa tca	1651
Val Asp Gly Asp Arg Ala Trp Asn Thr Val Arg Ala Tyr Ile Gln Ser	
505 510 515	
gtc gct cct gat ttg gtg tcc cgc gtg gaa cac ttc aat cgc gca gac	1699
Val Ala Pro Asp Leu Val Ser Arg Val Glu His Phe Asn Arg Ala Asp	
520 525 530	
ttt gac ggc aag gat gct ttc gaa gca ttc gac ctg aac acc cag ctt	1747
Phe Asp Gly Lys Asp Ala Phe Glu Ala Phe Asp Leu Asn Thr Gln Leu	
535 540 545	
gag gaa gcg ctg tcc cga aag gtg aac ctg cca tcg ggt gga tcg ctg	1795
Glu Glu Ala Leu Ser Arg Lys Val Asn Leu Pro Ser Gly Gly Ser Leu	
550 555 560 565	
atc atc gac cgc acc gaa gcc atg acg gtg atc gat gtg aac acc gga	1843
Ile Ile Asp Arg Thr Glu Ala Met Thr Val Ile Asp Val Asn Thr Gly	
570 575 580	
cgc tac acc ggc aag ggt ggt ggc aac ttg gaa gaa acc gtc acg ctc	1891
Arg Tyr Thr Gly Lys Gly Gly Gly Asn Leu Glu Glu Thr Val Thr Leu	
585 590 595	
aac aac att gaa gct gcc gaa gaa atc gtg cgc caa atg cgc ctg cgg	1939
Asn Asn Ile Glu Ala Ala Glu Glu Ile Val Arg Gln Met Arg Leu Arg	
600 605 610	
gat ctc ggt ggc atg atc gtt gtc gac ttc atc gat atg gtg ctg cca	1987
Asp Leu Gly Gly Met Ile Val Val Asp Phe Ile Asp Met Val Leu Pro	
615 620 625	
gaa aac caa gaa ttg gtc ctg cgc cga ctc aat gaa gcg cta gaa aac	2035
Glu Asn Gln Glu Leu Val Leu Arg Arg Leu Asn Glu Ala Leu Glu Asn	
630 635 640 645	
gat cgc acc cgc cac caa gtc tct gag gta acc tca ctg gga ctt gtt	2083
Asp Arg Thr Arg His Gln Val Ser Glu Val Thr Ser Leu Gly Leu Val	
650 655 660	
cag atg acc cgc aaa cgc atc ggc gcg ggc ctg ctg gaa acc ttc tct	2131
Gln Met Thr Arg Lys Arg Ile Gly Ala Gly Leu Leu Glu Thr Phe Ser	
665 670 675	
tca ccg tgt gag cac tgt gaa ggc cga ggc atc atc gtt cat gtt gat	2179
Ser Pro Cys Glu His Cys Glu Gly Arg Gly Ile Ile Val His Val Asp	
680 685 690	
cca gta gac acc gtt gac gag cgc gtt gag gcg aaa gcg gaa gag cgt	2227
Pro Val Asp Thr Val Asp Glu Arg Val Glu Ala Lys Ala Glu Glu Arg	
695 700 705	
agc cgt cgt cac cag cgt tcc aat agc act aac aag gca gct gcg gag	2275
Ser Arg Arg His Gln Arg Ser Asn Ser Thr Asn Lys Ala Ala Glu	
710 715 720 725	
cac ccg atg gtt gtt gcc atg cgt gat ctc gtg gaa agc gat gaa cac	2323

His Pro Met Val Val Ala Met Arg Asp Leu Val Glu Ser Asp Glu His
730 735 740

gat ctg gat caa gaa ttt gag gaa ctc gct gca tca atg atc gtt ctc 2371
Asp Leu Asp Gln Glu Phe Glu Glu Leu Ala Ala Ser Met Ile Val Leu
745 750 755

gat gac tcc gat cta tta tgatgtggac aacgacaagc tcg 2412
Asp Asp Ser Asp Leu Leu
760

<210> 224

<211> 763

<212> PRT

<213> Corynebacterium glutamicum

<400> 224

Val Pro Asn Asn Lys Ala Val Glu Ala Glu Ile Ser Pro Ser Ala Val
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Leu Ala Ala Glu Phe Asp Arg Asp Ser Leu Ser Glu Lys Thr Arg Val
20 25 30

His Gln Leu Ala Lys Arg Leu Gly Met Val Ser Lys Asp Val Val Val
35 40 45

Ala Leu Asp Gly Ile Gly Leu Val Lys Val Ala Gln Ser Asn Leu Ser
50 55 60

Lys Glu Glu Val Glu Lys Leu Leu Asp Ala Leu Ser Gln Pro Val Leu
65 70 75 80

Asn Ala Ala Pro Ala Ala Val Pro Asp Val Glu Pro Val Glu Lys Ile
85 90 95

Arg Arg Arg Val Glu Lys Asn Val Glu Asn Glu Ile His Gln Ile Glu
100 105 110

Glu Lys Val Glu Arg Glu Leu Ala Ala Val Ala Gln Pro Thr Asp Phe
115 120 125

Glu Ala Ala Ala Arg Glu Glu Ala Thr Ala Glu Leu Leu Glu Asp Ile
130 135 140

Val Pro Glu Ile Thr Pro Ala Pro Val Glu Ala Ser Val Tyr Thr Pro
145 150 155 160

Ile Phe Val Ala Pro Ala Val Val Pro Thr Glu Asn Val Gln Asp Thr
165 170 175

Asp Asp Glu Gln Val Arg Glu Arg Thr Ala Arg Lys Arg Arg Gly Arg
180 185 190

Arg Gly Thr Gly Arg Gly Arg Gly Ala Glu Ala Glu Thr Val Thr Glu
195 200 205

Val Ser Glu Glu Ala Ser Thr Ser Glu Val Glu Glu Val Asn Glu Pro
210 215 220

Ile Gly Ile Lys Gly Ser Thr Arg Leu Glu Ala Gln Arg Arg Arg Arg

225		230		235		240
Thr Glu Met Arg	Glu Glu Asn Lys Lys Arg Arg His Val Val Ser Thr					
	245			250		255
Gln Glu Phe Met	Glu Arg Arg Glu Ser Met Glu Arg Arg Met Ile Val					
	260		265			270
Arg Glu Arg Gln Arg His Asp His	Pro Gly Leu Val Thr Gln Val Gly					
	275		280			285
Val Leu Glu Asp Asp Gln Leu Val Glu Gln Phe Val Thr Ser Asp Ala						
	290		295			300
Gln Met Ser Met Val Gly Asn Ile Tyr Leu Gly Arg Val Gln Asn Val						
305		310		315		320
Leu Pro Ser Met Glu Ala Ala Phe Ile Asp Ile Gly Lys Gly Arg Asn						
	325		330			335
Gly Val Leu Tyr Ala Gly Glu Val Asp Trp Lys Ala Ala Gly Leu Gly						
	340		345			350
Gly Arg Gly Arg Arg Ile Glu Gln Ala Leu Lys Ala Gly Asp Gln Val						
	355		360			365
Leu Val Gln Val Ser Lys Asp Pro Leu Gly His Lys Gly Ala Arg Leu						
	370		375			380
Thr Thr Gln Ile Ser Leu Ala Gly Arg Tyr Leu Val Tyr Val Pro Gly						
385		390		395		400
Gly Arg Ser Ala Gly Ile Ser Arg Lys Leu Pro Gly Pro Glu Arg Lys						
	405		410			415
Arg Leu Lys Glu Ile Leu Gly Arg Val Val Pro Ala Gln Gly Gly Thr						
	420		425			430
Ile Ile Arg Thr Ala Ala Glu Gly Val Ser Glu Glu Asn Ile Ala Ala						
	435		440			445
Asp Val Asn Arg Leu His Thr Leu Trp Glu Gln Ile Lys Glu Arg Thr						
	450		455			460
Ala Glu Glu Lys Lys Ser Arg Gly Ser Lys Pro Ile Thr Met Tyr Glu						
465		470		475		480
Glu Pro Asp Met Leu Val Lys Val Ile Arg Asp Leu Phe Asn Glu Asp						
	485		490			495
Phe Thr Ser Leu Ile Val Asp Gly Asp Arg Ala Trp Asn Thr Val Arg						
	500		505			510
Ala Tyr Ile Gln Ser Val Ala Pro Asp Leu Val Ser Arg Val Glu His						
	515		520			525
Phe Asn Arg Ala Asp Phe Asp Gly Lys Asp Ala Phe Glu Ala Phe Asp						
	530		535			540
Leu Asn Thr Gln Leu Glu Glu Ala Leu Ser Arg Lys Val Asn Leu Pro						
545		550		555		560

Ser Gly Gly Ser Leu Ile Ile Asp Arg Thr Glu Ala Met Thr Val Ile
 565 570 575
 Asp Val Asn Thr Gly Arg Tyr Thr Gly Lys Gly Gly Gly Asn Leu Glu
 580 585 590
 Glu Thr Val Thr Leu Asn Asn Ile Glu Ala Ala Glu Glu Ile Val Arg
 595 600 605
 Gln Met Arg Leu Arg Asp Leu Gly Gly Met Ile Val Val Asp Phe Ile
 610 615 620
 Asp Met Val Leu Pro Glu Asn Gln Glu Leu Val Leu Arg Arg Leu Asn
 625 630 635 640
 Glu Ala Leu Glu Asn Asp Arg Thr Arg His Gln Val Ser Glu Val Thr
 645 650 655
 Ser Leu Gly Leu Val Gln Met Thr Arg Lys Arg Ile Gly Ala Gly Leu
 660 665 670
 Leu Glu Thr Phe Ser Ser Pro Cys Glu His Cys Glu Gly Arg Gly Ile
 675 680 685
 Ile Val His Val Asp Pro Val Asp Thr Val Asp Glu Arg Val Glu Ala
 690 695 700
 Lys Ala Glu Glu Arg Ser Arg Arg His Gln Arg Ser Asn Ser Thr Asn
 705 710 715 720
 Lys Ala Ala Ala Glu His Pro Met Val Val Ala Met Arg Asp Leu Val
 725 730 735
 Glu Ser Asp Glu His Asp Leu Asp Gln Glu Phe Glu Glu Leu Ala Ala
 740 745 750
 Ser Met Ile Val Leu Asp Asp Ser Asp Leu Leu
 755 760

<210> 225

<211> 915

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(892)

<223> RXN02370

<400> 225

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caagaatttg aggaactcgc tgcataatg atcggttctcg atg act ccg atc tat 115
 Met Thr Pro Ile Tyr
 1 5

gat gat gtg gac aac gac aag ctc gac gag cct gag cgc att ctt gct 163
 Asp Asp Val Asp Asn Asp Lys Leu Asp Glu Pro Glu Arg Ile Leu Ala
 10 15 20

gaa Glu	tcc Ser	acc Thr	gtg Val 25	gaa Glu	cgc Pro	gag Glu	gaa Glu	gga Gly 30	cca Pro	cgc Arg	atg Met	agg Arg	gcc Ala 35	cgc Arg	cgt Arg	211
caa Gln	cgt Arg	cag Gln 40	gaa Glu	tct Ser	gct Ala	gcg Ala	gat Asp 45	gat Asp	att Ile	gcc Ala	gcg Ala	att Ile 50	gca Ala	gct Ala	gct Ala	259
gcc Ala	gtg Val 55	gac Asp	att Ile	gct Ala	tct Ser	gaa Glu 60	gaa Glu	gac Asp	cct Pro	gat Asp	gag Glu 65	cct Pro	tcg Ser	gga Gly	tcg Ser	307
tcg Ser 70	tat Tyr	gtg Val	tct Ser	gac Asp	ttt Phe 75	gag Glu	gca Ala	gag Glu	cct Pro	att Ile 80	gca Ala	cct Pro	gta Val	gtt Val	gag Glu 85	355
aag Lys	gct Ala	gct Ala	gaa Glu	cct Pro 90	gtg Val	gct Ala	gag Glu	cca Pro	acc Thr 95	gct Ala	gat Asp	tat Tyr	gaa Glu	aag Lys 100	gca Ala	403
cgt Arg	gcc Ala	gaa Glu	ttt Phe 105	gag Glu	gca Ala	agc Ser	cca Pro	cgc Arg 110	agg Arg	cgc Arg	cgc Arg	aag Lys	act Thr 115	cgt Arg	ggc Gly	451
aat Asn	tca Ser	cgt Arg 120	tcg Ser	gat Asp	cat His	gct Ala	cca Pro 125	aag Lys	cca Pro	gag Glu	gat Asp	ttc Phe 130	gca Ala	cct Pro	gta Val	499
gtt Val	gaa Glu 135	gag Glu	gtt Val	gct Ala	gag Glu	act Thr 140	cca Pro	gtg Val	aag Lys	aca Thr	cct Pro 145	gcg Ala	cgg Arg	aag Lys	gct Ala	547
cca Pro 150	cgc Arg	cgt Arg	aac Asn	cgt Arg	cca Pro 155	agt Ser	gag Glu	ctc Leu	agt Ser	tcc Ser 160	ggg Gly	gcg Ala	cgc Pro	tcc Ser	tct Ser 165	595
gca Ala	cca Pro	tcg Ser	acc Thr	agg Arg 170	aac Asn	cgt Arg	cgc Arg	cgc Arg	gca Ala 175	gtg Val	cgc Arg	cgt Arg	caa Gln	ctg Leu 180	gtg Val	643
gaa Glu	gct Ala	cct Pro	gag Glu 185	acc Thr	gtc Val	gtt Val	gag Glu	ata Ile 190	gca Ala	cct Pro	gaa Glu	gca Ala	gca Ala 195	cca Pro	gaa Glu	691
cag Gln	gtt Val	gca Ala 200	gag Glu	cct Pro	cag Gln	gtt Val	gaa Glu 205	ttc Phe	gac Asp	cag Gln	cca Pro	gac Asp 210	aac Asn	cgc Arg	cga Arg	739
aag Lys	cgt Arg 215	cgt Arg	cgt Arg	gct Ala	gtg Val	cgc Arg 220	gtg Val	aca Thr	gcg Ala	gcg Ala	ccg Pro 225	gtg Val	gag Glu	aag Lys	aag Lys	787
gtg Val 230	gcg Ala	tcg Ser	aca Thr	agc Ser	aat Asn 235	gcg Ala	cgg Arg	gcg Ala	ccg Pro	aag Lys 240	aag Lys	gaa Glu	cct Pro	cag Gln	gcg Ala 245	835
gcg Ala	agc Ser	acc Thr	acc Thr	aac Asn 250	cca Pro	ggc Gly	cgc Arg	cgt Arg	agg Arg 255	cgg Arg	gct Ala	acc Thr	cga Arg	cga Arg	ggc Gly	883

915

[illegible]

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<220>
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 <223> FRXA02370

<400> 227

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caagaatttg aggaactcgc tgcataatg atcggttctcg atg act ccg atc tat 115
                               Met Thr Pro Ile Tyr
                               1 5

tat gat gtg gac aac gac aag ctc gac gag cct gag cgc att ctt gct 163
Tyr Asp Val Asp Asn Asp Lys Leu Asp Glu Pro Glu Arg Ile Leu Ala
                               10 15 20

gaa tcc acc gtg gaa ccg gag gaa gga cca cgc atg agg gcc cgc cgt 211
Glu Ser Thr Val Glu Pro Glu Glu Gly Pro Arg Met Arg Ala Arg Arg
                               25 30 35

caa cgt cag gaa tct gct gcg gat gat att gcc gcg att gca gct gct 259
Gln Arg Gln Glu Ser Ala Ala Asp Asp Ile Ala Ala Ile Ala Ala Ala
                               40 45 50

gcc gtg gac att gct tct gaa gaa gac cct gat gag cct tcg gga tcg 307
Ala Val Asp Ile Ala Ser Glu Glu Asp Pro Asp Glu Pro Ser Gly Ser
                               55 60 65

tcg tat gtg tct gac ttt gag gca gag cct att gca cct gta gtt gag 355
Ser Tyr Val Ser Asp Phe Glu Ala Glu Pro Ile Ala Pro Val Val Glu
                               70 75 80 85

aag gct gct gaa cct gtg gct gag cca acc gct gat tat gaa aag gca 403
Lys Ala Ala Glu Pro Val Ala Glu Pro Thr Ala Asp Tyr Glu Lys Ala
                               90 95 100

cgt gcc gaa ttt gag gca agc cca cgc agg cgc cgc aag act cgt ggc 451
Arg Ala Glu Phe Glu Ala Ser Pro Arg Arg Arg Arg Lys Thr Arg Gly
                               105 110 115

aat tca cgt tcg gat cat gct cca aag cca gag gat ttc gca cct gta 499
Asn Ser Arg Ser Asp His Ala Pro Lys Pro Glu Asp Phe Ala Pro Val
                               120 125 130

gtt gaa gag gtt gct gag act cca gtg aag aca cct gcg cgg aag gct 547
Val Glu Glu Val Ala Glu Thr Pro Val Lys Thr Pro Ala Arg Lys Ala
                               135 140 145

cca cgc cgt aac cgt cca agt gag ctc agt tcc ggt gcg ccg tcc tct 595
Pro Arg Arg Asn Arg Pro Ser Glu Leu Ser Ser Gly Ala Pro Ser Ser
                               150 155 160 165

gca cca tcg acc agg aac cgt cgc cgc gca gtg cgc cgt caa ctg gtg 643
Ala Pro Ser Thr Arg Asn Arg Arg Arg Ala Val Arg Arg Gln Leu Val

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	170	175	180	
	gaa gct cct gag acc gtc gtt gag ata gca cct gaa gca gca cca gaa			691
	Glu Ala Pro Glu Thr Val Val Glu Ile Ala Pro Glu Ala Ala Pro Glu			
	185	190	195	
	cag gtt gca gag cct cag gtt gaa ttc gac cag cca gac aac cgc cga			739
	Gln Val Ala Glu Pro Gln Val Glu Phe Asp Gln Pro Asp Asn Arg Arg			
	200	205	210	
	aag cgt cgt cgt gct gtg cgc gtg aca gcg gcg ccg gtg gag aag aag			787
	Lys Arg Arg Arg Ala Val Arg Val Thr Ala Ala Pro Val Glu Lys Lys			
	215	220	225	
	gtg gcg tcg aca agc aat gcg cgg gcg ccg aag aag gaa cct cag gcg			835
	Val Ala Ser Thr Ser Asn Ala Arg Ala Pro Lys Lys Glu Pro Gln Ala			
	230	235	240	245
	gcg agc acc acc aac cca ggc cgc cgt agg cgg gct acc cga cga ggc			883
	Ala Ser Thr Thr Asn Pro Gly Arg Arg Arg Arg Ala Thr Arg Arg Gly			
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	cca cga agc taggggtataa gggcggtttg tgt			915
	Pro Arg Ser			

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<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 228

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20 25 30	

Met Arg Ala Arg Arg Gln Arg Gln Glu Ser Ala Ala Asp Asp Ile Ala	
35 40 45	

Ala Ile Ala Ala Ala Ala Val Asp Ile Ala Ser Glu Glu Asp Pro Asp	
50 55 60	

Glu Pro Ser Gly Ser Ser Tyr Val Ser Asp Phe Glu Ala Glu Pro Ile	
65 70 75 80	

Ala Pro Val Val Glu Lys Ala Ala Glu Pro Val Ala Glu Pro Thr Ala	
85 90 95	

Asp Tyr Glu Lys Ala Arg Ala Glu Phe Glu Ala Ser Pro Arg Arg Arg	
100 105 110	

Arg Lys Thr Arg Gly Asn Ser Arg Ser Asp His Ala Pro Lys Pro Glu	
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Pro Ala Arg Lys Ala Pro Arg Arg Asn Arg Pro Ser Glu Leu Ser Ser

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<210> 229
<211> 750
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(727)  
<223> RXA01356
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<400> 229																
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aatgcgacgc ttaaagcatc tacggacctt tgaggtcacc						115										
				ttg	tca	cgc	aac	ggg								
				Leu	Ser	Arg	Asn	Gly								
				1				5								
cta ggg ccc gtt gca gga gta gac gaa gct gga cgc ggt gcc tgc tgc																163
Leu	Gly	Pro	Val	Ala	Gly	Val	Asp	Glu	Ala	Gly	Arg	Gly	Ala	Cys	Cys	
				10				15					20			
gga ccc att tca att gcc gca tgc ata ctc ccg gac aaa ccc atc cag																211
Gly	Pro	Ile	Ser	Ile	Ala	Ala	Cys	Ile	Leu	Pro	Asp	Lys	Pro	Ile	Gln	
			25					30					35			
gag cta gcc gca ctg aca gac tcc aaa aag ctc agt gcc agc acc cgc																259
Glu	Leu	Ala	Ala	Leu	Thr	Asp	Ser	Lys	Lys	Leu	Ser	Ala	Ser	Thr	Arg	
		40					45					50				
gaa aaa ctc atg cca ctg atc aaa aaa cac gca ctc gct tgg tca gtc																307
Glu	Lys	Leu	Met	Pro	Leu	Ile	Lys	Lys	His	Ala	Leu	Ala	Trp	Ser	Val	
	55					60					65					
atc gtg atc tcc gcc caa gac atc gac cga ttt ggc atc caa cac gca																355
Ile	Val	Ile	Ser	Ala	Gln	Asp	Ile	Asp	Arg	Phe	Gly	Ile	Gln	His	Ala	
70					75					80					85	

aac atc tcc ggc atg cga cga gcc gta gcc gcc cta ggc acc caa ccc 403
 Asn Ile Ser Gly Met Arg Arg Ala Val Ala Ala Leu Gly Thr Gln Pro
 90 95 100

ggc tac gta ctt acc gac gcc atg aaa gtc ccc ggc ttc aca gtc cca 451
 Gly Tyr Val Leu Thr Asp Ala Met Lys Val Pro Gly Phe Thr Val Pro
 105 110 115

tac cta ccc atc atc ggc gga gac gcc tcc gcc cga tgc atc gcc gcc 499
 Tyr Leu Pro Ile Ile Gly Gly Asp Ala Ser Ala Arg Cys Ile Ala Ala
 120 125 130

gca agt gta tta gcc aaa caa acc cgc gac gac atc atg acc gac atg 547
 Ala Ser Val Leu Ala Lys Gln Thr Arg Asp Asp Ile Met Thr Asp Met
 135 140 145

gcc aac gac tac ccg cac tac ggt ctc gaa att cac aaa ggc tac agt 595
 Ala Asn Asp Tyr Pro His Tyr Gly Leu Glu Ile His Lys Gly Tyr Ser
 150 155 160 165

acg aag atc cac atg gat gcg gtg cgc cac cac ggc gca agt ccc gag 643
 Thr Lys Ile His Met Asp Ala Val Arg His His Gly Ala Ser Pro Glu
 170 175 180

cac aga tat agt tat gca aat gtg gcc aag gca cac caa gaa tgg cta 691
 His Arg Tyr Ser Tyr Ala Asn Val Ala Lys Ala His Gln Glu Trp Leu
 185 190 195

cac gct gca gat aat gac acg acg gaa ggt gga gca tgagcgctga 737
 His Ala Ala Asp Asn Asp Thr Thr Glu Gly Gly Ala
 200 205

agaactcgac aac 750

<210> 230

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 230

Leu Ser Arg Asn Gly Leu Gly Pro Val Ala Gly Val Asp Glu Ala Gly
 1 5 10 15

Arg Gly Ala Cys Cys Gly Pro Ile Ser Ile Ala Ala Cys Ile Leu Pro
 20 25 30

Asp Lys Pro Ile Gln Glu Leu Ala Ala Leu Thr Asp Ser Lys Lys Leu
 35 40 45

Ser Ala Ser Thr Arg Glu Lys Leu Met Pro Leu Ile Lys Lys His Ala
 50 55 60

Leu Ala Trp Ser Val Ile Val Ile Ser Ala Gln Asp Ile Asp Arg Phe
 65 70 75 80

Gly Ile Gln His Ala Asn Ile Ser Gly Met Arg Arg Ala Val Ala Ala
 85 90 95

Leu Gly Thr Gln Pro Gly Tyr Val Leu Thr Asp Ala Met Lys Val Pro
 100 105 110

Gly Phe Thr Val Pro Tyr Leu Pro Ile Ile Gly Gly Asp Ala Ser Ala
 115 120 125

Arg Cys Ile Ala Ala Ala Ser Val Leu Ala Lys Gln Thr Arg Asp Asp
 130 135 140

Ile Met Thr Asp Met Ala Asn Asp Tyr Pro His Tyr Gly Leu Glu Ile
 145 150 155 160

His Lys Gly Tyr Ser Thr Lys Ile His Met Asp Ala Val Arg His His
 165 170 175

Gly Ala Ser Pro Glu His Arg Tyr Ser Tyr Ala Asn Val Ala Lys Ala
 180 185 190

His Gln Glu Trp Leu His Ala Ala Asp Asn Asp Thr Thr Glu Gly Gly
 195 200 205

Ala

<210> 231
 <211> 807
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(784)
 <223> RXN01786

<400> 231
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ttccagcttt tctcgttttg atggccgcgc acaggatcag atg cgt gcc gcc aaa 115
 Met Arg Ala Ala Lys
 1 5

atc acc cgt gga ttt act tcc aac cct gca ggc agc gtg ctt gta gaa 163
 Ile Thr Arg Gly Phe Thr Ser Asn Pro Ala Gly Ser Val Leu Val Glu
 10 15 20

ttc ggc aat act cgt gtc atg tgc acc gct tct gtg gaa ttg ggt gtg 211
 Phe Gly Asn Thr Arg Val Met Cys Thr Ala Ser Val Glu Leu Gly Val
 25 30 35

cct cgt ttc aag cgt gat tca ggt gaa ggc tgg ttg acc gca gag tac 259
 Pro Arg Phe Lys Arg Asp Ser Gly Glu Gly Trp Leu Thr Ala Glu Tyr
 40 45 50

gcg atg ctt cct gct gcg act gcg gag cgt aac cgt cgt gaa tcc atg 307
 Ala Met Leu Pro Ala Ala Thr Ala Glu Arg Asn Arg Arg Glu Ser Met
 55 60 65

gcc ggc aag gtc aag gga cgc act cat gaa att tct cgt ctg att ggt 355
 Ala Gly Lys Val Lys Gly Arg Thr His Glu Ile Ser Arg Leu Ile Gly
 70 75 80 85

cgt tct ttg cgt gca gct gtg gat ctt tcc cag ctg ggt gag aac acc 403

Arg Ser Leu Arg Ala Ala Val Asp Leu Ser Gln Leu Gly Glu Asn Thr
 90 95 100
 att gcg att gac tgc gat gtt ctg caa gct gac ggc ggt act cgt act 451
 Ile Ala Ile Asp Cys Asp Val Leu Gln Ala Asp Gly Gly Thr Arg Thr
 105 110 115
 gca tcg atc acc ggt gcg tat gtg gcg ctg gct gat gcc atc aag gtt 499
 Ala Ser Ile Thr Gly Ala Tyr Val Ala Leu Ala Asp Ala Ile Lys Val
 120 125 130
 ctg cag gag cgc ggg gtt gtt cca ggc agc cca ctt ctt gca cca gtt 547
 Leu Gln Glu Arg Gly Val Val Pro Gly Ser Pro Leu Leu Ala Pro Val
 135 140 145
 gct gct gtt tcc gtt ggt ctg gtc gac ggt aat gta tgc ctt gac ttg 595
 Ala Ala Val Ser Val Gly Leu Val Asp Gly Asn Val Cys Leu Asp Leu
 150 155 160 165
 cca tat gaa gaa gat tcc cgc gcc gat gtt gac ctc aac gtt gtt atg 643
 Pro Tyr Glu Glu Asp Ser Arg Ala Asp Val Asp Leu Asn Val Val Met
 170 175 180
 acc gaa cac ggt gaa ttc gtg gaa att cag ggc acc ggc gaa gaa act 691
 Thr Glu His Gly Glu Phe Val Glu Ile Gln Gly Thr Gly Glu Glu Thr
 185 190 195
 acc ttc acc cgc gcg cag ctc aac gac atg ctt gac cac gct gaa aag 739
 Thr Phe Thr Arg Ala Gln Leu Asn Asp Met Leu Asp His Ala Glu Lys
 200 205 210
 ggc tgc cgc gaa ttg gtt gct gcc caa aaa gct gca ctg gga atc 784
 Gly Cys Arg Glu Leu Val Ala Ala Gln Lys Ala Ala Leu Gly Ile
 215 220 225
 taaaaccaca acagagttaa gga 807

<210> 232

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Met Arg Ala Ala Lys Ile Thr Arg Gly Phe Thr Ser Asn Pro Ala Gly
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 Ser Val Leu Val Glu Phe Gly Asn Thr Arg Val Met Cys Thr Ala Ser
 20 25 30
 Val Glu Leu Gly Val Pro Arg Phe Lys Arg Asp Ser Gly Glu Gly Trp
 35 40 45
 Leu Thr Ala Glu Tyr Ala Met Leu Pro Ala Ala Thr Ala Glu Arg Asn
 50 55 60
 Arg Arg Glu Ser Met Ala Gly Lys Val Lys Gly Arg Thr His Glu Ile
 65 70 75 80
 Ser Arg Leu Ile Gly Arg Ser Leu Arg Ala Ala Val Asp Leu Ser Gln
 85 90 95

Leu Gly Glu Asn Thr Ile Ala Ile Asp Cys Asp Val Leu Gln Ala Asp
 100 105 110
 Gly Gly Thr Arg Thr Ala Ser Ile Thr Gly Ala Tyr Val Ala Leu Ala
 115 120 125
 Asp Ala Ile Lys Val Leu Gln Glu Arg Gly Val Val Pro Gly Ser Pro
 130 135 140
 Leu Leu Ala Pro Val Ala Ala Val Ser Val Gly Leu Val Asp Gly Asn
 145 150 155 160
 Val Cys Leu Asp Leu Pro Tyr Glu Glu Asp Ser Arg Ala Asp Val Asp
 165 170 175
 Leu Asn Val Val Met Thr Glu His Gly Glu Phe Val Glu Ile Gln Gly
 180 185 190
 Thr Gly Glu Glu Thr Thr Phe Thr Arg Ala Gln Leu Asn Asp Met Leu
 195 200 205
 Asp His Ala Glu Lys Gly Cys Arg Glu Leu Val Ala Ala Gln Lys Ala
 210 215 220
 Ala Leu Gly Ile
 225

<210> 233
 <211> 541
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(541)
 <223> FRXA01786

<400> 233
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 Met Arg Ala Ala Lys
 1 5
 atc acc cgt gga ttt act tcc aac cct gca ggc agc gtg ctt gta gaa 163
 Ile Thr Arg Gly Phe Thr Ser Asn Pro Ala Gly Ser Val Leu Val Glu
 10 15 20
 ttc ggc aat act cgt gtc atg tgc acc gct tct gtg gaa ttg ggt gtg 211
 Phe Gly Asn Thr Arg Val Met Cys Thr Ala Ser Val Glu Leu Gly Val
 25 30 35
 cct cgt ttc aag cgt gat tca ggt gaa ggc tgg ttg acc gca gag tac 259
 Pro Arg Phe Lys Arg Asp Ser Gly Glu Gly Trp Leu Thr Ala Glu Tyr
 40 45 50
 gcg atg ctt cct gct gcg act gcg gag cgt aac cgt cgt gaa tcc atg 307
 Ala Met Leu Pro Ala Ala Thr Ala Glu Arg Asn Arg Arg Glu Ser Met
 55 60 65

gcc ggc aag gtc aag gga cgc act cat gaa att tct cgt ctg att ggt 355
 Ala Gly Lys Val Lys Gly Arg Thr His Glu Ile Ser Arg Leu Ile Gly
 70 75 80 85

cgt tct ttg cgt gca gct gtg gat ctt tcc cag ctg ggt gag aac acc 403
 Arg Ser Leu Arg Ala Ala Val Asp Leu Ser Gln Leu Gly Glu Asn Thr
 90 95 100

att gcg att gac tgc gat gtt ctg caa gct gac ggc ggt act cgt act 451
 Ile Ala Ile Asp Cys Asp Val Leu Gln Ala Asp Gly Gly Thr Arg Thr
 105 110 115

gca tcg atc acc ggt gcg tat gtg gcg ctg gct gat gcc atc aag gtt 499
 Ala Ser Ile Thr Gly Ala Tyr Val Ala Leu Ala Asp Ala Ile Lys Val
 120 125 130

ctg cag gag cgc ggg gtt gtt cca ggc agc cca ctt ctt gca 541
 Leu Gln Glu Arg Gly Val Val Pro Gly Ser Pro Leu Leu Ala
 135 140 145

<210> 234

<211> 147

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 234

Met Arg Ala Ala Lys Ile Thr Arg Gly Phe Thr Ser Asn Pro Ala Gly
 1 5 10 15

Ser Val Leu Val Glu Phe Gly Asn Thr Arg Val Met Cys Thr Ala Ser
 20 25 30

Val Glu Leu Gly Val Pro Arg Phe Lys Arg Asp Ser Gly Glu Gly Trp
 35 40 45

Leu Thr Ala Glu Tyr Ala Met Leu Pro Ala Ala Thr Ala Glu Arg Asn
 50 55 60

Arg Arg Glu Ser Met Ala Gly Lys Val Lys Gly Arg Thr His Glu Ile
 65 70 75 80

Ser Arg Leu Ile Gly Arg Ser Leu Arg Ala Ala Val Asp Leu Ser Gln
 85 90 95

Leu Gly Glu Asn Thr Ile Ala Ile Asp Cys Asp Val Leu Gln Ala Asp
 100 105 110

Gly Gly Thr Arg Thr Ala Ser Ile Thr Gly Ala Tyr Val Ala Leu Ala
 115 120 125

Asp Ala Ile Lys Val Leu Gln Glu Arg Gly Val Val Pro Gly Ser Pro
 130 135 140

Leu Leu Ala
 145

<210> 235

<211> 741

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(718)

<223> RXN00163

<400> 235

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cactgggaat	ctaaaaccac	aacagagtta	aggacaccgg	atg	aaa	ctt	ctt	ctt	115
				Met	Lys	Leu	Leu	Leu	
				1				5	

gca	tcc	aac	aac	gca	aag	aaa	ctc	aaa	gaa	ctc	cag	cgg	att	ttg	gat	163
Ala	Ser	Asn	Asn	Ala	Lys	Lys	Leu	Lys	Glu	Leu	Gln	Arg	Ile	Leu	Asp	
				10					15					20		

caa	gca	ggc	ctg	gat	tcc	gtt	gaa	ttg	ctt	gcg	ctg	cgt	gat	gtc	gag	211
Gln	Ala	Gly	Leu	Asp	Ser	Val	Glu	Leu	Leu	Ala	Leu	Arg	Asp	Val	Glu	
			25					30					35			

gca	tac	gac	gag	ccg	atc	gaa	gac	ggc	cgc	act	ttt	gcc	gac	aac	gca	259
Ala	Tyr	Asp	Glu	Pro	Ile	Glu	Asp	Gly	Arg	Thr	Phe	Ala	Asp	Asn	Ala	
			40				45					50				

cag	atc	aaa	gcg	cgc	gcc	ggg	gta	acc	cac	aca	ggc	atc	gcc	acg	atc	307
Gln	Ile	Lys	Ala	Arg	Ala	Gly	Val	Thr	His	Thr	Gly	Ile	Ala	Thr	Ile	
		55				60					65					

gcc	gat	gat	tcc	ggc	atc	gct	gtc	gaa	gaa	ctc	aac	gga	atg	ccc	ggc	355
Ala	Asp	Asp	Ser	Gly	Ile	Ala	Val	Glu	Glu	Leu	Asn	Gly	Met	Pro	Gly	
	70				75					80					85	

gtt	ttg	tcc	gca	cgc	tgg	tcc	ggc	gca	cac	ggc	aac	gac	acc	gcc	aac	403
Val	Leu	Ser	Ala	Arg	Trp	Ser	Gly	Ala	His	Gly	Asn	Asp	Thr	Ala	Asn	
			90					95						100		

aac	gag	ctg	ctt	ctt	gcc	caa	atg	gaa	cat	gtt	ccc	gac	gag	cgc	cgc	451
Asn	Glu	Leu	Leu	Leu	Ala	Gln	Met	Glu	His	Val	Pro	Asp	Glu	Arg	Arg	
		105						110					115			

aac	gca	gcc	ttc	gtg	tcc	gta	tgc	gtg	ctt	gca	ctt	ccg	gac	ggc	caa	499
Asn	Ala	Ala	Phe	Val	Ser	Val	Cys	Val	Leu	Ala	Leu	Pro	Asp	Gly	Gln	
		120					125					130				

gaa	ttt	gtt	cag	gaa	ggc	cgt	tgg	gaa	ggc	caa	ctc	cta	cgc	gga	cct	547
Glu	Phe	Val	Gln	Glu	Gly	Arg	Trp	Glu	Gly	Gln	Leu	Leu	Arg	Gly	Pro	
	135					140					145					

aag	ggc	gaa	aac	ggt	ttc	gga	tac	gat	cca	ctg	ttc	att	cca	gca	gag	595
Lys	Gly	Glu	Asn	Gly	Phe	Gly	Tyr	Asp	Pro	Leu	Phe	Ile	Pro	Ala	Glu	
	150				155					160					165	

gaa	atc	gat	gga	caa	gga	cgc	agc	tcc	gct	gaa	ctt	tcc	gca	gag	gaa	643
Glu	Ile	Asp	Gly	Gln	Gly	Arg	Ser	Ser	Ala	Glu	Leu	Ser	Ala	Glu	Glu	
			170						175					180		

aag	gac	gct	ttg	tcc	cac	cga	ggt	caa	gcg	ctg	cgc	gga	ttg	gtt	gag	691
Lys	Asp	Ala	Leu	Ser	His	Arg	Gly	Gln	Ala	Leu	Arg	Gly	Leu	Val	Glu	

BGI-130CP
 Corynebacterium glutamicum
 RXN00163
 (101)..(718)
 CDS
 DNA
 - 435 -

185 190 195
aag atc gca cag gta gct gcg gct agc taaggcctta aggaaaacta 738
Lys Ile Ala Gln Val Ala Ala Ala Ser
200 205

aaa 741

<210> 236
<211> 206
<212> PRT
<213> Corynebacterium glutamicum

<400> 236
Met Lys Leu Leu Leu Ala Ser Asn Asn Ala Lys Lys Leu Lys Glu Leu
1 5 10 15
Gln Arg Ile Leu Asp Gln Ala Gly Leu Asp Ser Val Glu Leu Leu Ala
20 25 30
Leu Arg Asp Val Glu Ala Tyr Asp Glu Pro Ile Glu Asp Gly Arg Thr
35 40 45
Phe Ala Asp Asn Ala Gln Ile Lys Ala Arg Ala Gly Val Thr His Thr
50 55 60
Gly Ile Ala Thr Ile Ala Asp Asp Ser Gly Ile Ala Val Glu Glu Leu
65 70 75 80
Asn Gly Met Pro Gly Val Leu Ser Ala Arg Trp Ser Gly Ala His Gly
85 90 95
Asn Asp Thr Ala Asn Asn Glu Leu Leu Leu Ala Gln Met Glu His Val
100 105 110
Pro Asp Glu Arg Arg Asn Ala Ala Phe Val Ser Val Cys Val Leu Ala
115 120 125
Leu Pro Asp Gly Gln Glu Phe Val Gln Glu Gly Arg Trp Glu Gly Gln
130 135 140
Leu Leu Arg Gly Pro Lys Gly Glu Asn Gly Phe Gly Tyr Asp Pro Leu
145 150 155 160
Phe Ile Pro Ala Glu Glu Ile Asp Gly Gln Gly Arg Ser Ser Ala Glu
165 170 175
Leu Ser Ala Glu Glu Lys Asp Ala Leu Ser His Arg Gly Gln Ala Leu
180 185 190
Arg Gly Leu Val Glu Lys Ile Ala Gln Val Ala Ala Ala Ser
195 200 205

<210> 237
<211> 641
<212> DNA
<213> Corynebacterium glutamicum
<220>

<221> CDS
 <222> (58)..(618)
 <223> FRXA00163

<400> 237

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                                         Leu
                                         1

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Asp Gln Ala Gly Leu Asp Ser Val Glu Leu Leu Ala Leu Arg Asp Val
                    5                      10                      15

gag gca tac gac gag ccg atc gaa gac ggc cgc act ttt gcc gac aac 156
Glu Ala Tyr Asp Glu Pro Ile Glu Asp Gly Arg Thr Phe Ala Asp Asn
                    20                      25                      30

gca cag atc aaa gcg cgc gcc ggg gta acc cac aca gcc atc gcc acg 204
Ala Gln Ile Lys Ala Arg Ala Gly Val Thr His Thr Gly Ile Ala Thr
                    35                      40                      45

atc gcc gat gat tcc ggc atc gct gtc gaa gaa ctc aac gga atg ccc 252
Ile Ala Asp Asp Ser Gly Ile Ala Val Glu Glu Leu Asn Gly Met Pro
                    50                      55                      60                      65

ggc gtt ttg tcc gca cgc tgg tcc ggc gca cac ggc aac gac acc gcc 300
Gly Val Leu Ser Ala Arg Trp Ser Gly Ala His Gly Asn Asp Thr Ala
                    70                      75                      80

aac aac gag ctg ctt ctt gcc caa atg gaa cat gtt ccc gac gag cgc 348
Asn Asn Glu Leu Leu Leu Ala Gln Met Glu His Val Pro Asp Glu Arg
                    85                      90                      95

cgc aac gca gcc ttc gtg tcc gta tgc gtg ctt gca ctt ccg gac ggc 396
Arg Asn Ala Ala Phe Val Ser Val Cys Val Leu Ala Leu Pro Asp Gly
                    100                      105                      110

caa gaa ttt gtt cag gaa ggc cgt tgg gaa ggc caa ctc cta cgc gga 444
Gln Glu Phe Val Gln Glu Gly Arg Trp Glu Gly Gln Leu Leu Arg Gly
                    115                      120                      125

cct aag ggc gaa aac ggt ttc gga tac gat cca ctg ttc att cca gca 492
Pro Lys Gly Glu Asn Gly Phe Gly Tyr Asp Pro Leu Phe Ile Pro Ala
                    130                      135                      140                      145

gag gaa atc gat gga caa gga cgc agc tcc gct gaa ctt tcc gca gag 540
Glu Glu Ile Asp Gly Gln Gly Arg Ser Ser Ala Glu Leu Ser Ala Glu
                    150                      155                      160

gaa aag gac gct ttg tcc cac cga ggt caa gcg ctg cgc gga ttg gtt 588
Glu Lys Asp Ala Leu Ser His Arg Gly Gln Ala Leu Arg Gly Leu Val
                    165                      170                      175

gag aag atc gca cag gta gct gcg gct agc taaggcctta aggaaaacta 638
Glu Lys Ile Ala Gln Val Ala Ala Ala Ser
                    180                      185

aaa 641

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<210> 238

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<211> 187
<212> PRT
<213> Corynebacterium glutamicum
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<400> 238

Leu Asp Gln Ala Gly Leu Asp Ser Val Glu Leu Leu Ala Leu Arg Asp
1 5 10 15

Val Glu Ala Tyr Asp Glu Pro Ile Glu Asp Gly Arg Thr Phe Ala Asp
20 25 30

Asn Ala Gln Ile Lys Ala Arg Ala Gly Val Thr His Thr Gly Ile Ala
35 40 45

Thr Ile Ala Asp Asp Ser Gly Ile Ala Val Glu Glu Leu Asn Gly Met
50 55 60

Pro Gly Val Leu Ser Ala Arg Trp Ser Gly Ala His Gly Asn Asp Thr
65 70 75 80

Ala Asn Asn Glu Leu Leu Leu Ala Gln Met Glu His Val Pro Asp Glu
85 90 95

Arg Arg Asn Ala Ala Phe Val Ser Val Cys Val Leu Ala Leu Pro Asp
100 105 110

Gly Gln Glu Phe Val Gln Glu Gly Arg Trp Glu Gly Gln Leu Leu Arg
115 120 125

Gly Pro Lys Gly Glu Asn Gly Phe Gly Tyr Asp Pro Leu Phe Ile Pro
130 135 140

Ala Glu Glu Ile Asp Gly Gln Gly Arg Ser Ser Ala Glu Leu Ser Ala
145 150 155 160

Glu Glu Lys Asp Ala Leu Ser His Arg Gly Gln Ala Leu Arg Gly Leu
165 170 175

Val Glu Lys Ile Ala Gln Val Ala Ala Ala Ser
180 185

<210> 239

<211> 432

<212> DNA

<213> Corynebacterium glutamicum

 $\langle 220 \rangle$

<221> CDS

<222> (101) .. (409)

<223> RXA01424

<400> 239

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gatgaggaaa gggcgctcgcg ctggcagtaa aactgtcgtt gtg cac ctg tgg gat 115
Val His Leu Trp Asp
1 5

agt gcc gaa tcg ttg gat ggc acc gaa aaa cag ggc gaa gtc gcc tca 163
Ser Ala Glu Ser Leu Asp Gly Thr Glu Lys Gln Gly Glu Val Ala Ser

	10	15	20	
ttc ggt ggt ccg cgg ttc ggc ctt gtc gtt tct aag gcc gtc gga aat				211
Phe Gly Gly Pro Arg Phe Gly Leu Val Val Ser Lys Ala Val Gly Asn				
	25	30	35	
gcg gtg gtt cgt cac cgc acc tcc cga cgg ctt cgt cat atc tgt gca				259
Ala Val Val Arg His Arg Thr Ser Arg Arg Leu Arg His Ile Cys Ala				
	40	45	50	
agc att gca gaa aaa tca cca gag cta ctc tcc ccc act cat cac gtg				307
Ser Ile Ala Glu Lys Ser Pro Glu Leu Leu Ser Pro Thr His His Val				
	55	60	65	
gtg atc cgc gcg ttg gcg ggg gct ggg aat gca acc tcg gcg gaa ctt				355
Val Ile Arg Ala Leu Ala Gly Ala Gly Asn Ala Thr Ser Ala Glu Leu				
	70	75	80	85
gaa cga gac atc cgc tac ggg ttg ggg aaa gct agc cgt gtg cgc acc				403
Glu Arg Asp Ile Arg Tyr Gly Leu Gly Lys Ala Ser Arg Val Arg Thr				
	90	95	100	
aac aag tgatgatcct ttcgacatcc cag				432
Asn Lys				

<210> 240

<211> 103

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

Val His Leu Trp Asp Ser Ala Glu Ser Leu Asp Gly Thr Glu Lys Gln
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Gly Glu Val Ala Ser Phe Gly Gly Pro Arg Phe Gly Leu Val Val Ser
20 25 30

Lys Ala Val Gly Asn Ala Val Val Arg His Arg Thr Ser Arg Arg Leu
35 40 45

Arg His Ile Cys Ala Ser Ile Ala Glu Lys Ser Pro Glu Leu Leu Ser
50 55 60

Pro Thr His His Val Val Ile Arg Ala Leu Ala Gly Ala Gly Asn Ala
65 70 75 80

Thr Ser Ala Glu Leu Glu Arg Asp Ile Arg Tyr Gly Leu Gly Lys Ala
85 90 95

Ser Arg Val Arg Thr Asn Lys
100

<210> 241

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (101)..(592)
 <223> RXA01481

<400> 241

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tcacttttagc ccgtcccttt agtgtgccta tattggttgt atg  caa  aac  agc  aag      115
                               Met Gln Asn Ser  Lys
                               1      5

aag acc ctc ggc gga gtg ctc gga gtc atc gtt gtc ctc gct gct gca      163
Lys Thr Leu Gly Gly Val Leu Gly Val Ile Val Val Leu Ala Ala Ala
                               10      15      20

tgg ttt gga att gat ctg tcc act tca ggt gaa gcc acc agc caa gca      211
Trp Phe Gly Ile Asp Leu Ser Thr Ser Gly Glu Ala Thr Ser Gln Ala
                               25      30      35

tca agc tca gca act act acc act att act agc tct aac act cca aca      259
Ser Ser Ser Ala Thr Thr Thr Thr Ile Thr Ser Ser Asn Thr Pro Thr
                               40      45      50

tct gag tcc atc tcc agc aac agc gac tta gac ggt gac agc tgc tcc      307
Ser Glu Ser Ile Ser Ser Asn Ser Asp Leu Asp Gly Asp Ser Cys Ser
                               55      60      65

atg agt gag ctg cca caa gaa gct gat gag gtg gtc gac gat atc ctc      355
Met Ser Glu Leu Pro Gln Glu Ala Asp Glu Val Val Asp Asp Ile Leu
                               70      75      80      85

gcc ggt ggt cct ttt gat tac cca gac aat gac ggc gtg cgc ttt gga      403
Ala Gly Gly Pro Phe Asp Tyr Pro Asp Asn Asp Gly Val Arg Phe Gly
                               90      95      100

aac tac gaa ggc gta cta ccg aaa gag tcc agc aac tac tac cgc gaa      451
Asn Tyr Glu Gly Val Leu Pro Lys Glu Ser Ser Asn Tyr Tyr Arg Glu
                               105      110      115

tac acc gtg gaa acc cca gga ctt agc cac cgc ggt cca ctg cgc att      499
Tyr Thr Val Glu Thr Pro Gly Leu Ser His Arg Gly Pro Leu Arg Ile
                               120      125      130

gtc acc ggt gga tca aac cca act gat cca gag gtg tgg tac tac acc      547
Val Thr Gly Gly Ser Asn Pro Thr Asp Pro Glu Val Trp Tyr Tyr Thr
                               135      140      145

tca gat cac tat gaa act ttc tgt gcc atc acc gat gcg gag aac      592
Ser Asp His Tyr Glu Thr Phe Cys Ala Ile Thr Asp Ala Glu Asn
                               150      155      160

taaatgaata tcgtcttgca ggg      615

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<210> 242
 <211> 164
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 242

Met Gln Asn Ser Lys Lys Thr Leu Gly Gly Val Leu Gly Val Ile Val

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Val Leu Ala	Ala Ala Trp Phe Gly	Ile Asp Leu Ser Thr	Ser Gly Glu
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Ala Thr Ser	Gln Ala Ser Ser Ser	Ala Thr Thr Thr Thr	Ile Thr Ser
	35	40	45
Ser Asn Thr	Pro Thr Ser Glu Ser	Ile Ser Ser Asn Ser	Asp Leu Asp
	50	55	60
Gly Asp Ser	Cys Ser Met Ser Glu	Leu Pro Gln Glu Ala	Asp Glu Val
	65	70	75
Val Asp Asp	Ile Leu Ala Gly Gly	Pro Phe Asp Tyr Pro	Asp Asn Asp
	85	90	95
Gly Val Arg	Phe Gly Asn Tyr Glu	Gly Val Leu Pro Lys	Glu Ser Ser
	100	105	110
Asn Tyr Tyr	Arg Glu Tyr Thr Val	Glu Thr Pro Gly Leu	Ser His Arg
	115	120	125
Gly Pro Leu	Arg Ile Val Thr Gly	Gly Ser Asn Pro Thr	Asp Pro Glu
	130	135	140
Val Trp Tyr	Tyr Thr Ser Asp His	Tyr Glu Thr Phe Cys	Ala Ile Thr
	145	150	155
Asp Ala Glu	Asn		

<210> 243
 <211> 2100
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2077)
 <223> RXN00724

<400> 243
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 Val Gly Ile Gly Asp 5
 gcc act gag ggc gat ctt gtt acc atc gtg ggt cag gtc gcc ttt gcc 163
 Ala Thr Glu Gly Asp Leu Val Thr Ile Val Gly Gln Val Ala Phe Ala 20
 aag cag tcc tat acc cag tcc ggc aag atg ctg tac aag gtt aca gtc 211
 Lys Gln Ser Tyr Thr Gln Ser Gly Lys Met Leu Tyr Lys Val Thr Val 35
 ttg act gag acg gaa cgc atc ggc att tcc ttc ttc gga gcc aag cac 259
 Leu Thr Glu Thr Glu Arg Ile Gly Ile Ser Phe Phe Gly Ala Lys His 40 45 50

att ccg cgt ctt ctc cca gaa ggc act cgt gcg ctt ttt acc ggc aag	307
Ile Pro Arg Leu Leu Pro Glu Gly Thr Arg Ala Leu Phe Thr Gly Lys	
55 60 65	
gtg aag ttt ttt cgc aac gaa cct cag cta tct cat cca gag ttc att	355
Val Lys Phe Phe Arg Asn Glu Pro Gln Leu Ser His Pro Glu Phe Ile	
70 75 80 85	
gtg atc cca gat cct gga tca ggc cgc cga ctc acc gcc act ggc ggt	403
Val Ile Pro Asp Pro Gly Ser Gly Arg Arg Leu Thr Ala Thr Gly Gly	
90 95 100	
atg aaa tct ctg gct gcc tac ggc gat gtg gaa gaa gtg gca ctt cgt	451
Met Lys Ser Leu Ala Ala Tyr Gly Asp Val Glu Glu Val Ala Leu Arg	
105 110 115	
ttg gtg gat cgc gaa tac atc ccg atc tat gcc ggc acc gcc acc atg	499
Leu Val Asp Arg Glu Tyr Ile Pro Ile Tyr Ala Gly Thr Ala Thr Met	
120 125 130	
act acc tgg cgg atc atg gct gca gtg caa cgg gta ctg gaa acc atg	547
Thr Thr Trp Arg Ile Met Ala Ala Val Gln Arg Val Leu Glu Thr Met	
135 140 145	
ccg gtg atc aaa gaa cca ctg agc gtg gtg ccc gaa ggc atg ccc agt	595
Pro Val Ile Lys Glu Pro Leu Ser Val Val Pro Glu Gly Met Pro Ser	
150 155 160 165	
ttc gac gag gcc atc cgc ggc att cac gat cca ggc cat gaa tct ccc	643
Phe Asp Glu Ala Ile Arg Gly Ile His Asp Pro Gly His Glu Ser Pro	
170 175 180	
agc acg ttt atc aac cgt ctg aaa tac aac gaa gca cta tcg ctg gcc	691
Ser Thr Phe Ile Asn Arg Leu Lys Tyr Asn Glu Ala Leu Ser Leu Ala	
185 190 195	
acg gtg atg gcg atc cgg cgt gcc gat acc aag aac cgc aaa gca cca	739
Thr Val Met Ala Ile Arg Arg Ala Asp Thr Lys Asn Arg Lys Ala Pro	
200 205 210	
ccc atg ccg cgc gca ctc aaa ggg cat cag cac atg ctc atc gat gca	787
Pro Met Pro Arg Ala Leu Lys Gly His Gln His Met Leu Ile Asp Ala	
215 220 225	
ctc aac ttt cag ctc aca gtg gga cag aag caa gtg atc cgt gag atc	835
Leu Asn Phe Gln Leu Thr Val Gly Gln Lys Gln Val Ile Arg Glu Ile	
230 235 240 245	
agc gcg gac att gaa caa cgc gtt ccc atg tct cgt ctg ctc caa ggt	883
Ser Ala Asp Ile Glu Gln Arg Val Pro Met Ser Arg Leu Leu Gln Gly	
250 255 260	
gag gtt ggt tcg ggt aaa acc atc gtg tcg ttg atc gcg atg ctg cag	931
Glu Val Gly Ser Gly Lys Thr Ile Val Ser Leu Ile Ala Met Leu Gln	
265 270 275	
gca att gat tcc ggt agg cag tgc gcc atg ctc gcc ccg acg gaa gtg	979
Ala Ile Asp Ser Gly Arg Gln Cys Ala Met Leu Ala Pro Thr Glu Val	
280 285 290	

ttg gcc acc cag cat gcc cgc agc ctg agc aaa act ctc gac gac gca	1027
Leu Ala Thr Gln His Ala Arg Ser Leu Ser Lys Thr Leu Asp Asp Ala	
295 300 305	
ggc ctt gat atc aat gtt gtg ctc ttg act ggc tcg atg ccc acg gga	1075
Gly Leu Asp Ile Asn Val Val Leu Leu Thr Gly Ser Met Pro Thr Gly	
310 315 320 325	
gcc aag aag gag gct ctg ctg gaa atc atc tcc ggt gac gca gac att	1123
Ala Lys Lys Glu Ala Leu Leu Glu Ile Ile Ser Gly Asp Ala Asp Ile	
330 335 340	
gtg gtc ggc acg cat gcg ctg atc cag gac acc gtg gag ttc ttc gac	1171
Val Val Gly Thr His Ala Leu Ile Gln Asp Thr Val Glu Phe Phe Asp	
345 350 355	
ctt ggc ctc gtg gtg gtg gat gag cag cac cgt ttc ggc gtg gag caa	1219
Leu Gly Leu Val Val Val Asp Glu Gln His Arg Phe Gly Val Glu Gln	
360 365 370	
cgc gat caa ctg cgg acc aag ggc agg gaa ggc ctg acc ccg cac cta	1267
Arg Asp Gln Leu Arg Thr Lys Gly Arg Glu Gly Leu Thr Pro His Leu	
375 380 385	
ttg gtt atg act gcg acc cca att ccg cgc acc atc gcc atg acg gtg	1315
Leu Val Met Thr Ala Thr Pro Ile Pro Arg Thr Ile Ala Met Thr Val	
390 395 400 405	
ttc ggc gac ttg gcg gtg tcc acg ttg cgt gaa ctt cca ggc ggg cgc	1363
Phe Gly Asp Leu Ala Val Ser Thr Leu Arg Glu Leu Pro Gly Gly Arg	
410 415 420	
cgg ccg att caa acc tcg gtg ata ccc gat cac aaa cct ggc tgg gtt	1411
Arg Pro Ile Gln Thr Ser Val Ile Pro Asp His Lys Pro Gly Trp Val	
425 430 435	
aaa cgc ggt tgg gaa cgc atc ggt gag gaa gtc ctc gcc gga cgc caa	1459
Lys Arg Gly Trp Glu Arg Ile Gly Glu Glu Val Leu Ala Gly Arg Gln	
440 445 450	
gcc tat gtg gtg tgt ccg cgc att gaa ggc gaa ggc ggc gtg ctg gaa	1507
Ala Tyr Val Val Cys Pro Arg Ile Glu Gly Glu Gly Gly Val Leu Glu	
455 460 465	
atc cac gcc tat ctt tcc gaa cag gta tat cca gga ttg aat gtt gga	1555
Ile His Ala Tyr Leu Ser Glu Gln Val Tyr Pro Gly Leu Asn Val Gly	
470 475 480 485	
atg ctg cac ggt cgc atg gac acg gat ctc aaa gat tcg gtc atg cag	1603
Met Leu His Gly Arg Met Asp Thr Asp Leu Lys Asp Ser Val Met Gln	
490 495 500	
gaa ttc gcc caa ggt gag atc gat att ttg gtc gcc acc acg gtc att	1651
Glu Phe Ala Gln Gly Glu Ile Asp Ile Leu Val Ala Thr Thr Val Ile	
505 510 515	
gag gtc ggt att gac gtt gcc aac gcc acc gtc atg ctc atc cgc gag	1699
Glu Val Gly Ile Asp Val Ala Asn Ala Thr Val Met Leu Ile Arg Glu	
520 525 530	
gcg gaa cgc ttc ggc gtt tcc cag atc cac cag ctg cgc ggc cgt gtt	1747

Ala Glu Arg Phe Gly Val Ser Gln Ile His Gln Leu Arg Gly Arg Val
535 540 545

ggc cgt ggg cag cac gat tcc ctc tgc ctg ctg cac acc acc ttc gac 1795
Gly Arg Gly Gln His Asp Ser Leu Cys Leu Leu His Thr Thr Phe Asp
550 555 560 565

gag gac tcc cca caa ggc caa cgc ctc gcc gca att tcc acc aca acc 1843
Glu Asp Ser Pro Gln Gly Gln Arg Leu Ala Ala Ile Ser Thr Thr Thr
570 575 580

gac ggt ttt caa ctc tct gaa ctt gat ttg cag gta cgc caa gaa ggc 1891
Asp Gly Phe Gln Leu Ser Glu Leu Asp Leu Gln Val Arg Gln Glu Gly
585 590 595

gac gtg ttg ggc acc cgc cag tcc ggc agc gac acc aaa ctc cgt cac 1939
Asp Val Leu Gly Thr Arg Gln Ser Gly Ser Asp Thr Lys Leu Arg His
600 605 610

ctc tcg ttt atc agc gac caa aaa atc atc gag cgt gcg ctt atc gac 1987
Leu Ser Phe Ile Ser Asp Gln Lys Ile Ile Glu Arg Ala Leu Ile Asp
615 620 625

gcc acc gag ctg gtt gcc gcc agc cgt tcc agg gcg ctt gag ctg gtc 2035
Ala Thr Glu Leu Val Ala Ala Ser Arg Ser Arg Ala Leu Glu Leu Val
630 635 640 645

agc gac atc gca atg atc aac cag gaa tac ctg gaa aag agc 2077
Ser Asp Ile Ala Met Ile Asn Gln Glu Tyr Leu Glu Lys Ser
650 655

tgatattgat agggtttaag tca 2100

<210> 244
<211> 659
<212> PRT
<213> Corynebacterium glutamicum

<400> 244
Val Gly Ile Gly Asp Ala Thr Glu Gly Asp Leu Val Thr Ile Val Gly
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Gln Val Ala Phe Ala Lys Gln Ser Tyr Thr Gln Ser Gly Lys Met Leu
20 25 30

Tyr Lys Val Thr Val Leu Thr Glu Thr Glu Arg Ile Gly Ile Ser Phe
35 40 45

Phe Gly Ala Lys His Ile Pro Arg Leu Leu Pro Glu Gly Thr Arg Ala
50 55 60

Leu Phe Thr Gly Lys Val Lys Phe Phe Arg Asn Glu Pro Gln Leu Ser
65 70 75 80

His Pro Glu Phe Ile Val Ile Pro Asp Pro Gly Ser Gly Arg Arg Leu
85 90 95

Thr Ala Thr Gly Gly Met Lys Ser Leu Ala Ala Tyr Gly Asp Val Glu
100 105 110

Glu Val Ala Leu Arg Leu Val Asp Arg Glu Tyr Ile Pro Ile Tyr Ala
 115 120 125
 Gly Thr Ala Thr Met Thr Thr Trp Arg Ile Met Ala Ala Val Gln Arg
 130 135 140
 Val Leu Glu Thr Met Pro Val Ile Lys Glu Pro Leu Ser Val Val Pro
 145 150 155 160
 Glu Gly Met Pro Ser Phe Asp Glu Ala Ile Arg Gly Ile His Asp Pro
 165 170 175
 Gly His Glu Ser Pro Ser Thr Phe Ile Asn Arg Leu Lys Tyr Asn Glu
 180 185 190
 Ala Leu Ser Leu Ala Thr Val Met Ala Ile Arg Arg Ala Asp Thr Lys
 195 200 205
 Asn Arg Lys Ala Pro Pro Met Pro Arg Ala Leu Lys Gly His Gln His
 210 215 220
 Met Leu Ile Asp Ala Leu Asn Phe Gln Leu Thr Val Gly Gln Lys Gln
 225 230 235 240
 Val Ile Arg Glu Ile Ser Ala Asp Ile Glu Gln Arg Val Pro Met Ser
 245 250 255
 Arg Leu Leu Gln Gly Glu Val Gly Ser Gly Lys Thr Ile Val Ser Leu
 260 265 270
 Ile Ala Met Leu Gln Ala Ile Asp Ser Gly Arg Gln Cys Ala Met Leu
 275 280 285
 Ala Pro Thr Glu Val Leu Ala Thr Gln His Ala Arg Ser Leu Ser Lys
 290 295 300
 Thr Leu Asp Asp Ala Gly Leu Asp Ile Asn Val Val Leu Leu Thr Gly
 305 310 315 320
 Ser Met Pro Thr Gly Ala Lys Lys Glu Ala Leu Leu Glu Ile Ile Ser
 325 330 335
 Gly Asp Ala Asp Ile Val Val Gly Thr His Ala Leu Ile Gln Asp Thr
 340 345 350
 Val Glu Phe Phe Asp Leu Gly Leu Val Val Val Asp Glu Gln His Arg
 355 360 365
 Phe Gly Val Glu Gln Arg Asp Gln Leu Arg Thr Lys Gly Arg Glu Gly
 370 375 380
 Leu Thr Pro His Leu Leu Val Met Thr Ala Thr Pro Ile Pro Arg Thr
 385 390 395 400
 Ile Ala Met Thr Val Phe Gly Asp Leu Ala Val Ser Thr Leu Arg Glu
 405 410 415
 Leu Pro Gly Gly Arg Arg Pro Ile Gln Thr Ser Val Ile Pro Asp His
 420 425 430
 Lys Pro Gly Trp Val Lys Arg Gly Trp Glu Arg Ile Gly Glu Glu Val

435					440					445					
Leu	Ala	Gly	Arg	Gln	Ala	Tyr	Val	Val	Cys	Pro	Arg	Ile	Glu	Gly	Glu
450					455					460					
Gly	Gly	Val	Leu	Glu	Ile	His	Ala	Tyr	Leu	Ser	Glu	Gln	Val	Tyr	Pro
465					470					475					480
Gly	Leu	Asn	Val	Gly	Met	Leu	His	Gly	Arg	Met	Asp	Thr	Asp	Leu	Lys
				485					490					495	
Asp	Ser	Val	Met	Gln	Glu	Phe	Ala	Gln	Gly	Glu	Ile	Asp	Ile	Leu	Val
			500					505					510		
Ala	Thr	Thr	Val	Ile	Glu	Val	Gly	Ile	Asp	Val	Ala	Asn	Ala	Thr	Val
			515				520						525		
Met	Leu	Ile	Arg	Glu	Ala	Glu	Arg	Phe	Gly	Val	Ser	Gln	Ile	His	Gln
	530					535					540				
Leu	Arg	Gly	Arg	Val	Gly	Arg	Gly	Gln	His	Asp	Ser	Leu	Cys	Leu	Leu
545					550					555					560
His	Thr	Thr	Phe	Asp	Glu	Asp	Ser	Pro	Gln	Gly	Gln	Arg	Leu	Ala	Ala
				565					570					575	
Ile	Ser	Thr	Thr	Thr	Asp	Gly	Phe	Gln	Leu	Ser	Glu	Leu	Asp	Leu	Gln
				580				585					590		
Val	Arg	Gln	Glu	Gly	Asp	Val	Leu	Gly	Thr	Arg	Gln	Ser	Gly	Ser	Asp
			595				600					605			
Thr	Lys	Leu	Arg	His	Leu	Ser	Phe	Ile	Ser	Asp	Gln	Lys	Ile	Ile	Glu
	610					615					620				
Arg	Ala	Leu	Ile	Asp	Ala	Thr	Glu	Leu	Val	Ala	Ala	Ser	Arg	Ser	Arg
625					630					635					640
Ala	Leu	Glu	Leu	Val	Ser	Asp	Ile	Ala	Met	Ile	Asn	Gln	Glu	Tyr	Leu
				645					650					655	

Glu Lys Ser

<210> 245
 <211> 1604
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1581)
 <223> RXN01979

<400> 245
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 1 5 10 15
 gcg gga ctt gcg ccc aat att ccc gtg cta gca acc aca gcc acc gcc 96

Ala	Gly	Leu	Ala	Pro	Asn	Ile	Pro	Val	Leu	Ala	Thr	Thr	Ala	Thr	Ala	
			20					25					30			
aat	gac	cgc	gtg	gtt	gaa	gat	gtc	cgt	gcc	caa	cta	gaa	gat	ggc	aca	144
Asn	Asp	Arg	Val	Val	Glu	Asp	Val	Arg	Ala	Gln	Leu	Glu	Asp	Gly	Thr	
		35					40					45				
ggc	ttg	ttt	cgt	ggc	ggg	ata	gac	cgt	gaa	tcc	ctt	tac	cta	tca	gtg	192
Gly	Leu	Phe	Arg	Gly	Gly	Ile	Asp	Arg	Glu	Ser	Leu	Tyr	Leu	Ser	Val	
	50					55					60					
gtg	aac	ctg	ctc	aac	ccc	acc	gaa	cgc	cca	gct	tgg	ctt	gcc	acc	cac	240
Val	Asn	Leu	Leu	Asn	Pro	Thr	Glu	Arg	Pro	Ala	Trp	Leu	Ala	Thr	His	
	65				70					75					80	
ctc	aaa	gaa	ctg	acg	ggc	tcg	ggc	atc	att	tac	tgc	ctc	act	gtg	tca	288
Leu	Lys	Glu	Leu	Thr	Gly	Ser	Gly	Ile	Ile	Tyr	Cys	Leu	Thr	Val	Ser	
				85					90					95		
gct	gca	cat	gat	ctt	gcc	gat	gca	ctt	aat	tct	gtt	gga	tgg	aat	gtt	336
Ala	Ala	His	Asp	Leu	Ala	Asp	Ala	Leu	Asn	Ser	Val	Gly	Trp	Asn	Val	
			100					105					110			
gcc	gcg	tac	acc	ggc	cga	acc	gaa	gca	gga	gag	cgc	gaa	cgt	tta	gaa	384
Ala	Ala	Tyr	Thr	Gly	Arg	Thr	Glu	Ala	Gly	Glu	Arg	Glu	Arg	Leu	Glu	
		115					120					125				
cat	gcc	ttg	atc	aac	aac	gag	atc	aaa	gca	cta	gta	gca	acc	tct	gca	432
His	Ala	Leu	Ile	Asn	Asn	Glu	Ile	Lys	Ala	Leu	Val	Ala	Thr	Ser	Ala	
	130					135					140					
ctg	gga	atg	ggc	ttt	gac	aaa	cct	gac	ctt	gga	ttt	gtt	gtg	cac	atg	480
Leu	Gly	Met	Gly	Phe	Asp	Lys	Pro	Asp	Leu	Gly	Phe	Val	Val	His	Met	
	145				150					155					160	
ggc	agc	ccc	agc	tca	ccg	gtg	tct	tat	tac	cag	cag	att	ggc	cgc	gcc	528
Gly	Ser	Pro	Ser	Ser	Pro	Val	Ser	Tyr	Tyr	Gln	Gln	Ile	Gly	Arg	Ala	
				165					170					175		
ggg	cgc	ggc	acc	gct	cgt	gcc	gat	gtc	atc	ctg	ctg	cca	gga	act	gaa	576
Gly	Arg	Gly	Thr	Ala	Arg	Ala	Asp	Val	Ile	Leu	Leu	Pro	Gly	Thr	Glu	
			180					185					190			
gac	aaa	gag	atc	tgg	gag	tac	ttt	gca	tca	gta	tcg	ttc	cca	cgc	gaa	624
Asp	Lys	Glu	Ile	Trp	Glu	Tyr	Phe	Ala	Ser	Val	Ser	Phe	Pro	Arg	Glu	
		195					200					205				
gag	gta	gtc	cgc	caa	ctg	ctt	gcg	gtg	tta	acc	gat	gag	gcg	caa	tcc	672
Glu	Val	Val	Arg	Gln	Leu	Leu	Ala	Val	Leu	Thr	Asp	Glu	Ala	Gln	Ser	
	210					215					220					
act	gtc	aaa	ttg	gaa	tca	caa	gta	gat	ctt	tcc	cga	tca	cgc	ctt	gaa	720
Thr	Val	Lys	Leu	Glu	Ser	Gln	Val	Asp	Leu	Ser	Arg	Ser	Arg	Leu	Glu	
	225				230				235						240	
caa	gta	ctt	aaa	gtg	cta	gac	gta	gat	ggc	gca	gtc	aaa	cgt	gta	cgt	768
Gln	Val	Leu	Lys	Val	Leu	Asp	Val	Asp	Gly	Ala	Val	Lys	Arg	Val	Arg	
				245					250					255		
ggc	gga	tgg	gtc	tcc	acc	ggg	caa	gag	tgg	atc	tac	gat	gcg	gaa	cgc	816
Gly	Gly	Trp	Val	Ser	Thr	Gly	Gln	Glu	Trp	Ile	Tyr	Asp	Ala	Glu	Arg	

260	265	270	
tac gca gga ctt gaa caa gca agg aaa att gaa cag caa agc atg gtg Tyr Ala Gly Leu Glu Gln Ala Arg Lys Ile Glu Gln Gln Ser Met Val 275 280 285			864
aac tac cag aac acc act gag tgc cgc atg ctg tac ctc cgc aaa gaa Asn Tyr Gln Asn Thr Thr Glu Cys Arg Met Leu Tyr Leu Arg Lys Glu 290 295 300			912
cta gac gat gtg gag gca act act ccg tgc ggg cgc tgc gac aat tgc Leu Asp Asp Val Glu Ala Thr Thr Pro Cys Gly Arg Cys Asp Asn Cys 305 310 315 320			960
acg ggc aaa acg tgg ggg ctc gac acc gat gcc tcg atc act ttg aaa Thr Gly Lys Thr Trp Gly Leu Asp Thr Asp Ala Ser Ile Thr Leu Lys 325 330 335			1008
gtg gac caa cag ctt caa aca ccc gga gtg aaa ata gcc cca cga aaa Val Asp Gln Gln Leu Gln Thr Pro Gly Val Lys Ile Ala Pro Arg Lys 340 345 350			1056
atg tgg ccg act ggc att agt gtc aga gga aaa atc gca ggg cta gaa Met Trp Pro Thr Gly Ile Ser Val Arg Gly Lys Ile Ala Gly Leu Glu 355 360 365			1104
gaa gga cga gca ctg gga cga ctc aat gac att gcc cgt gga cct gca Glu Gly Arg Ala Leu Gly Arg Leu Asn Asp Ile Ala Arg Gly Pro Ala 370 375 380			1152
cta aag gcc ctg ctg gac agc gga gct tat tct gat gat cca tgg atg Leu Lys Ala Leu Leu Asp Ser Gly Ala Tyr Ser Asp Asp Pro Trp Met 385 390 395 400			1200
gca cgc atc atc gaa gtg ctg aaa aac tgg gat tgg acc aac cgg cct Ala Arg Ile Ile Glu Val Leu Lys Asn Trp Asp Trp Thr Asn Arg Pro 405 410 415			1248
gcc aac gtg gtc gct ctc ggc aat acc aac ttt gga tca act gag atg Ala Asn Val Val Ala Leu Gly Asn Thr Asn Phe Gly Ser Thr Glu Met 420 425 430			1296
atc atc cag gta gct caa tca atc gca gcg gtg gga cga atg aac ttt Ile Ile Gln Val Ala Gln Ser Ile Ala Ala Val Gly Arg Met Asn Phe 435 440 445			1344
gcg ggt gta ctt ccc gcc gcg ccg ggt gct gaa gaa gtc atg gct cag Ala Gly Val Leu Pro Ala Ala Pro Gly Ala Glu Glu Val Met Ala Gln 450 455 460			1392
aat tcc gca tac cga gta gaa gcc cta ttg aaa caa tgg gac tgg tcg Asn Ser Ala Tyr Arg Val Glu Ala Leu Leu Lys Gln Trp Asp Trp Ser 465 470 475 480			1440
caa ggc ttg caa cta gtt ccc ggt ccc att ttg ctg gtg aca gac ctt Gln Gly Leu Gln Leu Val Pro Gly Pro Ile Leu Leu Val Thr Asp Leu 485 490 495			1488
att gat act ggc tgg tcg gtg aca gtt gca gga aat ggc att gcg cag Ile Asp Thr Gly Trp Ser Val Thr Val Ala Gly Asn Gly Ile Ala Gln 500 505 510			1536

cgg acc tca gag aag gtg ctg ccg ttc gct tta gcg agt agg gga 1581
 Arg Thr Ser Glu Lys Val Leu Pro Phe Ala Leu Ala Ser Arg Gly
 515 520 525

taggtgctct gggacgagag caa 1604

<210> 246

<211> 527

<212> PRT

<213> Corynebacterium glutamicum

<400> 246

Leu Gly His Asp Phe Arg Pro Asp Tyr Arg Arg Ile Arg Asp Leu Leu
 1 5 10 15

Ala Gly Leu Ala Pro Asn Ile Pro Val Leu Ala Thr Thr Ala Thr Ala
 20 25 30

Asn Asp Arg Val Val Glu Asp Val Arg Ala Gln Leu Glu Asp Gly Thr
 35 40 45

Gly Leu Phe Arg Gly Gly Ile Asp Arg Glu Ser Leu Tyr Leu Ser Val
 50 55 60

Val Asn Leu Leu Asn Pro Thr Glu Arg Pro Ala Trp Leu Ala Thr His
 65 70 75 80

Leu Lys Glu Leu Thr Gly Ser Gly Ile Ile Tyr Cys Leu Thr Val Ser
 85 90 95

Ala Ala His Asp Leu Ala Asp Ala Leu Asn Ser Val Gly Trp Asn Val
 100 105 110

Ala Ala Tyr Thr Gly Arg Thr Glu Ala Gly Glu Arg Glu Arg Leu Glu
 115 120 125

His Ala Leu Ile Asn Asn Glu Ile Lys Ala Leu Val Ala Thr Ser Ala
 130 135 140

Leu Gly Met Gly Phe Asp Lys Pro Asp Leu Gly Phe Val Val His Met
 145 150 155 160

Gly Ser Pro Ser Ser Pro Val Ser Tyr Tyr Gln Gln Ile Gly Arg Ala
 165 170 175

Gly Arg Gly Thr Ala Arg Ala Asp Val Ile Leu Leu Pro Gly Thr Glu
 180 185 190

Asp Lys Glu Ile Trp Glu Tyr Phe Ala Ser Val Ser Phe Pro Arg Glu
 195 200 205

Glu Val Val Arg Gln Leu Leu Ala Val Leu Thr Asp Glu Ala Gln Ser
 210 215 220

Thr Val Lys Leu Glu Ser Gln Val Asp Leu Ser Arg Ser Arg Leu Glu
 225 230 235 240

Gln Val Leu Lys Val Leu Asp Val Asp Gly Ala Val Lys Arg Val Arg
 245 250 255

Gly Gly Trp Val Ser Thr Gly Gln Glu Trp Ile Tyr Asp Ala Glu Arg
 260 265 270
 Tyr Ala Gly Leu Glu Gln Ala Arg Lys Ile Glu Gln Gln Ser Met Val
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Ala Asp Leu Asp Gly Asp Ala Thr Ile Ser Thr Asn Ala Thr Glu Glu
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Gly Val Asp Ala Ala Ala Glu Lys Pro Lys Lys Lys Arg Lys Ala Pro
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Thr Asn Pro Asp Leu Ser Tyr Gln Pro Val Ser Asp Val Tyr Thr Pro
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Gln Ser Ala Asp His Lys Gly Ile Lys Thr Arg Tyr Ile Leu Thr His
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Pro Thr Pro Ala Val Val Leu Ser Glu Ser Ile Ser Asn Ala Phe His
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Gln Met Ile Asn Val Ala Asp Ile Cys Asp Tyr His Phe His Gly Tyr
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Lys Thr Val Leu Asp Asp Gly Thr Thr Ala Ser Asp Asn Thr Thr His	
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Val Tyr Tyr Arg Val Thr Val His Val Ile Ala Gly Gln Asp His Gly	
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Ser Thr Leu Leu Asp Asp Gln Gly Asn Gln Val Leu Asp Arg Asp Asp	
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Arg Gln Leu Arg Ile Leu Glu His Tyr Asp Val Pro Leu Thr Ala Tyr	
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Ser Ala Leu Phe Trp Thr Val Ser Ala Ile Lys Asn Glu Ser Met Val	
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Gln Tyr Leu Val Arg Gln Asn Met Gln Leu Thr Leu Ser Asn Leu	
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Gln	Arg	Glu	Ala	Ile	Thr	Thr	Asp	Asn	Pro	Leu	Ala	Ile	Ile	Gln	Ala	
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Thr	Asn	Ala	Ala	Ala	Asp	Asn	Ile	Thr	Ala	Lys	Asn	Asp	Lys	Val	Thr	
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Pro	Asp	His	Glu	Ile	Ser	Thr	Ile	Asp	Thr	Ile	Ile	Asn	Thr	Leu	Asp	
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Ile	Glu	Tyr	Gly	Asp	Gln	Met	Val	Thr	Ser	Asp	Tyr	Met	Ile	Gln	Leu	
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Arg	Asp	Leu	Leu	Tyr	Lys	Val	Met	Thr	Gln	Gly	Gly	Asn	Ala	Asn	Leu	
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Thr	Ala	Leu	Ser	Ile	Phe	Met	Glu	Ser	His	Ile	Glu	Ala	Phe	Ile	Ser	
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Tyr	Leu	Ile	Ile	Asp	Glu	Val	Gln	Asp	Asn	Ser	Val	Phe	Glu	Phe	Val	
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Phe	Ala	Leu	Arg	Phe	Ala	Ala	Lys	His	Asn	Thr	Ser	Leu	Tyr	Leu	Val	
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Thr Thr Asn Tyr Arg	Ser Asn Gln Glu Ile Leu	Asp Phe Ala Asn Ile	
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His Leu Ser Asp Ile	Glu Ala Asn Gln Phe	Ala Gly Ile Gln Leu	
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Ala Asn Ser Phe Asp	Ala Pro Thr Ala Asp	Ser Phe Lys Glu Lys	
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Glu Leu Asp Met His	His Val Ser Lys Gln	Ser Glu Phe Thr Asp	
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Arg Ala Ala Gln Gln	Ala Leu Ala Glu Met	Tyr Pro Ser Ile Thr	
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Arg Gln Cys Ile Leu	Asp Tyr Glu Ile Arg	Asn Asn Arg Ala Arg	
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Ile Pro Gln Leu Asp Gln Met Ile Asn Val Ala Asp Ile Cys Asp Tyr

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Val	Pro	Asp	Lys	Asp	Val	Val	Ala	Ala	Ser	Gly	Tyr	Gln	Ile	Gln	Pro
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His	Phe	Ser	Thr	Gln	Gln	Arg	Glu	Ala	Ile	Thr	Thr	Asp	Asn	Pro	Leu
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Ala	Ile	Ile	Gln	Ala	Gly	Ala	Gly	Thr	Gly	Lys	Ser	Thr	Val	Ile	Leu
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 Gly Asn Ala Asn Leu Thr Ala Leu Ser Ile Phe Met Glu Ser His Ile
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 Leu Glu Ile Ile Ile Cys Tyr Leu Leu Leu Asp Lys Leu Ile Glu Pro
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Asn Ser Ala Ile Thr Pro Gln Thr Ser Gln Lys Tyr Gln Ser Leu Leu
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Ser Tyr Leu Gly Asp Ile Gly Val Lys Lys Asn Ser Asp Thr Arg Val
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Cys Leu Leu Glu Gly Phe Asn Asn Val Pro Glu Asp Ser Ile Asn Arg	
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Tyr Gln Ser Leu Leu Ser Tyr Leu Gly Asp Ile Gly Val Lys Lys Asn
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Ile Ala Val Met His Gly Gly Leu Pro Asp Gln Glu Gln Met Arg Leu
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Leu Val His Tyr Asp Ile Pro Trp Ser Leu Ile Arg Ile Gln Gln Arg
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Asn Gly Arg Ile Asp Arg Tyr Gly Gln Thr His Asn Pro Ser Ile Val
165 170 175

Thr Phe Leu Leu Asp Pro Ala Glu Asp Ser Lys Val Gly Glu Val His
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Gly Asp Ala Ala Ser Leu Met Gly Lys His Ser Glu Arg Leu Glu Glu
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Glu Thr Ile Arg Glu Val Leu Arg Gly Ala Gln Asn Phe Asn Asp Ala
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Pro Gln Ala Leu Leu Ile Asp Ile Ala Glu Thr Met Ser Arg Tyr Gly
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Arg Val Arg Leu His Arg His Pro Ala His Gly Leu Ile Leu Glu Ser

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Gly	Glu	Tyr	Ser	Gly	Glu	Arg	Lys	Glu	Ile	Arg	Pro	Val	Thr	Ile	Ala
			260					265					270		
Thr	Tyr	Gln	Val	Val	Thr	Arg	Arg	Thr	Lys	Gly	Glu	Tyr	Lys	Ala	Leu
		275					280						285		
Glu	Leu	Phe	Asp	Ser	Arg	Asp	Trp	Gly	Leu	Ile	Ile	Tyr	Asp	Glu	Val
		290					295					300			
His	Leu	Leu	Pro	Ala	Pro	Val	Phe	Arg	Met	Thr	Ser	Asp	Leu	Gln	Ser
				305			310					315			320
Arg	Arg	Arg	Leu	Gly	Leu	Thr	Ala	Thr	Leu	Val	Arg	Glu	Asp	Gly	Arg
				325					330					335	
Glu	Gly	Asp	Val	Phe	Ser	Leu	Ile	Gly	Pro	Lys	Arg	Tyr	Asp	Ala	Pro
			340					345					350		
Trp	Lys	Asp	Leu	Glu	Ser	Gln	Gly	Phe	Ile	Ala	Thr	Ala	Asp	Cys	Val
		355					360					365			
Glu	Ile	Arg	Ser	Thr	Met	Thr	Asp	Ala	Glu	Arg	Met	Val	Tyr	Ala	Thr
		370					375					380			
Ala	Glu	Ser	Ala	Asp	Arg	Tyr	Arg	Leu	Ala	Ala	Thr	Ala	His	Thr	Lys
				385			390					395			400
Val	Ala	Val	Val	Arg	Lys	Leu	Leu	Glu	Glu	His	Ala	Gly	Lys	Pro	Thr
				405				410					415		
Leu	Ile	Ile	Gly	Ala	Tyr	Leu	Asp	Gln	Leu	Glu	Glu	Leu	Gly	Ala	Glu
			420					425					430		

Phe Asn Ala Pro Val Ile Asp Gly Lys Thr Pro Asn Lys Lys Arg Glu
435 440 445

Ala Leu Phe Asp Gln Phe Arg Ser Gly Ser Leu Ser Val Leu Val Val
450 455 460

Ser Lys Val Ala Asn Phe Ser Ile Asp Leu Pro Glu Ala Ser Val Ala
465 470 475 480

Ile Gln Val Ser Gly Thr Phe Gly Ser Arg Gln Glu Glu Ala Gln Arg
485 490 495

Leu Gly Arg Leu Leu Arg Pro Lys His Asp Gly Ser Glu Ala His Phe
500 505 510

Tyr Ser Ile Val Ser Arg Asp Thr Leu Asp Thr Glu Tyr Ala Ala His
515 520 525

Arg Gln Arg Phe Leu Ala Glu Gln Gly Tyr Ala Tyr Arg Ile Leu Asp
530 535 540

Ala Asp Asp Ile Leu Phe Pro Leu Pro Lys Lys Glu Leu
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<210> 253

<211> 849

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(826)

<223> RXN01066

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tttgaaccgc ctgggcttct agctttaagg ggggtgagttc atg cgt agg gac agt 115
Met Arg Arg Asp Ser
1 5

ttt cgg gac cgc gcg cta gta gtc aaa act tat gat ttt ggc gaa gcc 163
Phe Arg Asp Arg Ala Leu Val Val Lys Thr Tyr Asp Phe Gly Glu Ala
10 15 20

gac cgc att att gtg ctg ctc acc cga gac cac ggc atc gtg cgc gga 211
Asp Arg Ile Ile Val Leu Leu Thr Arg Asp His Gly Ile Val Arg Gly
25 30 35

gtt gcc aaa gga gta cgc cga tcc aaa tcc cgg ttt ggg tca agg ctg 259
Val Ala Lys Gly Val Arg Arg Ser Lys Ser Arg Phe Gly Ser Arg Leu
40 45 50

cag ctt ttt gtg gaa ctc gac gtg cag ctc tac cca ggt aga aaa ctg 307
Gln Leu Phe Val Glu Leu Asp Val Gln Leu Tyr Pro Gly Arg Lys Leu
55 60 65

tcc acc atc tct ggc gcg gac acc gtc ggc tac tac gca tca ggc atc 355
Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr Tyr Ala Ser Gly Ile

70	75	80	85	
atc gag gac ttc act cgg tat tcc tgt gcg tcc gcc atc ctg gaa atc				403
Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser Ala Ile Leu Glu Ile				
	90	95	100	
gcc acc cac atc gca gga ctg gaa aac gat ccg cac ctg ttt gaa gaa				451
Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro His Leu Phe Glu Glu				
	105	110	115	
acc acc cgg gcg ttg aaa aac att cag gac tcc cca gaa ccc atc ctc				499
Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser Pro Glu Pro Ile Leu				
	120	125	130	
aac cta gac gag ttc atg ctc cgc gcc atg aac cac gcc ggc tgg gca				547
Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn His Ala Gly Trp Ala				
	135	140	145	
cca agc ctt ttc gac tgc gca gcc tgc ggc cga cca gga cct cac aac				595
Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg Pro Gly Pro His Asn				
	150	155	160	165
gca ttc cac cca ggc gtc ggc ggg gca gtg tgc ctg tac tgc cga ccg				643
Ala Phe His Pro Gly Val Gly Gly Ala Val Cys Leu Tyr Cys Arg Pro				
	170	175	180	
ccg gga agc gcc gaa gtc cca cca gaa gca cta cac atg atg tgg ttg				691
Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu His Met Met Trp Leu				
	185	190	195	
gtc gcc aac ggc caa gca gcc cgc att ccc cgg gaa cac cca gag cag				739
Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg Glu His Pro Glu Gln				
	200	205	210	
caa acc acc att cac caa ctg aca acc gcg cat ctg cag tgg cat att				787
Gln Thr Thr Ile His Gln Leu Thr Thr Ala His Leu Gln Trp His Ile				
	215	220	225	
gaa aga aag ctg ccc acg ctg gcg gtg ctg gat cag gcc tagtgcttag				836
Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp Gln Ala				
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gcttaggcgt ccg				849

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<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

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Asp	Phe	Gly	Glu	Ala	Asp	Arg	Ile	Ile	Val	Leu	Leu	Thr	Arg	Asp	His
			20					25					30		

Gly	Ile	Val	Arg	Gly	Val	Ala	Lys	Gly	Val	Arg	Arg	Ser	Lys	Ser	Arg
		35					40					45			

Phe	Gly	Ser	Arg	Leu	Gln	Leu	Phe	Val	Glu	Leu	Asp	Val	Gln	Leu	Tyr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50		55		60
Pro Gly Arg Lys Leu Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr				
65		70		75
Tyr Ala Ser Gly Ile Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser				
	85		90	95
Ala Ile Leu Glu Ile Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro				
	100		105	110
His Leu Phe Glu Glu Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser				
	115		120	125
Pro Glu Pro Ile Leu Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn				
	130		135	140
His Ala Gly Trp Ala Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg				
	145		150	155
Pro Gly Pro His Asn Ala Phe His Pro Gly Val Gly Gly Ala Val Cys				
	165		170	175
Leu Tyr Cys Arg Pro Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu				
	180		185	190
His Met Met Trp Leu Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg				
	195		200	205
Glu His Pro Glu Gln Gln Thr Thr Ile His Gln Leu Thr Thr Ala His				
	210		215	220
Leu Gln Trp His Ile Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp				
	225		230	235
				240
Gln Ala				

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 <211> 707
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(684)
 <223> RXN01389

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ggt aaa att ttg cct cag aaa gat atg cca ttc ctt cca gac ggc act	96
Gly Lys Ile Leu Pro Gln Lys Asp Met Pro Phe Leu Pro Asp Gly Thr	
20 25 30	
cct gtt gac atc atc ttg aac acc cac ggt gtt cca cgt cgt atg aac	144
Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg Arg Met Asn	
35 40 45	

att ggt cag gtt ctt gag acc cac ctt ggc tgg ctg gca tct gct ggt 192
 Ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala Ser Ala Gly
 50 55 60

tgg tcc gtg gat cct gaa gat cct gag aac gct gag ctc gtc aag act 240
 Trp Ser Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr
 65 70 75 80

ctg cct gca gac ctc ctc gag gtt cct gct ggt tcc ttg act gca act 288
 Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr
 85 90 95

cct gtg ttc gac ggt gcg tca aac gaa gag ctc gca ggc ctg ctc gct 336
 Pro Val Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly Leu Leu Ala
 100 105 110

aat tca cgt cca aac cgc gac ggc gac gtc atg gtt aac gcg gat ggt 384
 Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly
 115 120 125

aaa gca acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg 432
 Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro
 130 135 140

gtt tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac 480
 Val Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp
 145 150 155 160

gag aag atc cac gca cgt tcc act ggt cct tac tcc atg att acc cag 528
 Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr Gln
 165 170 175

cag cca ctg ggt ggt aaa gca cag ttc ggt gga cag cgt ttc ggc gaa 576
 Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe Gly Glu
 180 185 190

atg gag gtg tgg gca atg cag gca tac ggc gct gcc tac aca ctt cag 624
 Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr Thr Leu Gln
 195 200 205

gag ctg ctg mcc ann nnn nnn nnn nnn nnn nnn nnn nnn nnt nnn 672
 Glu Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 210 215 220

nnn nnn nnn nnn naannnnnnn tgcacccccg atc 707
 Xaa Xaa Xaa Xaa
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<210> 256

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 256

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<223> RXN02070
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gaa tcc gct gtc cgc agc gcg cta tcc cgc gta gag gat cca gag atc 163
Glu Ser Ala Val Arg Ser Ala Leu Ser Arg Val Glu Asp Pro Glu Ile
10 15 20

ggt aag ccc atc aca gag ctc ggc atg gtc aaa tca gtg tcc atc gac	211
Gly Lys Pro Ile Thr Glu Leu Gly Met Val Lys Ser Val Ser Ile Asp	
25 30 35	
ggc tct gat gtc cag gtg gag gtc tac ctg acg atc gcg gct tgc ccg	259
Gly Ser Asp Val Gln Val Glu Val Tyr Leu Thr Ile Ala Ala Cys Pro	
40 45 50	
atg aaa acc acc att gtc acc aac act gaa gca gct ctc aaa gac atc	307
Met Lys Thr Thr Ile Val Thr Asn Thr Glu Ala Ala Leu Lys Asp Ile	
55 60 65	
gac ggg gtt ggc caa gtt cat gtc acc acc gat gtc atg agt gat gaa	355
Asp Gly Val Gly Gln Val His Val Thr Thr Asp Val Met Ser Asp Glu	
70 75 80 85	
cag cgc cgt gcg ctc cgc gtc tcc ctg cgc ggt gaa act tct gag cca	403
Gln Arg Arg Ala Leu Arg Val Ser Leu Arg Gly Glu Thr Ser Glu Pro	
90 95 100	
gtg att cca ttc gct cag cct ggt tcc act acc cgc gtt tac gct gtt	451
Val Ile Pro Phe Ala Gln Pro Gly Ser Thr Thr Arg Val Tyr Ala Val	
105 110 115	
gct tcc ggc aaa ggt ggc gta gga aaa tcc tcc atg acg gtg aac ttg	499
Ala Ser Gly Lys Gly Gly Val Gly Lys Ser Ser Met Thr Val Asn Leu	
120 125 130	
gct gca gcc cta gcc aag cgc ggg ctg tct gtg gga att ttg gat gcc	547
Ala Ala Ala Leu Ala Lys Arg Gly Leu Ser Val Gly Ile Leu Asp Ala	
135 140 145	
gat att tac gga cac tca gtg ccc gga atg ctc ggc tcg gac caa cgc	595
Asp Ile Tyr Gly His Ser Val Pro Gly Met Leu Gly Ser Asp Gln Arg	
150 155 160 165	
cca cac cag gtc gat gac atg atc atg cct ccc cag gcg cac ggc gtg	643
Pro His Gln Val Asp Asp Met Ile Met Pro Pro Gln Ala His Gly Val	
170 175 180	
aag atg ata tcc att gct cac ttc acc gaa gga aat gct cct gtg gtg	691
Lys Met Ile Ser Ile Ala His Phe Thr Glu Gly Asn Ala Pro Val Val	
185 190 195	
tgg cgt gga cca atg ctg cac cgt gcc atc cag caa ttc ctc act gac	739
Trp Arg Gly Pro Met Leu His Arg Ala Ile Gln Gln Phe Leu Thr Asp	
200 205 210	
gtg ttc tgg ggc gac ctg gat att ttg ctg ctg gat ctt cct cca gga	787
Val Phe Trp Gly Asp Leu Asp Ile Leu Leu Leu Asp Leu Pro Pro Gly	
215 220 225	
act ggt gac atc gcc atc acc gtt gcc caa ttg atc ccg aat gct gag	835
Thr Gly Asp Ile Ala Ile Thr Val Ala Gln Leu Ile Pro Asn Ala Glu	
230 235 240 245	
ttg ctc att gtg acc act cct cag gct gcc gca gct gag gtt gcc gag	883
Leu Leu Ile Val Thr Thr Pro Gln Ala Ala Ala Ala Glu Val Ala Glu	
250 255 260	

cga gca gga acg atc tct gtg cag acc aac cag aag gtt gct ggc gtg 931
 Arg Ala Gly Thr Ile Ser Val Gln Thr Asn Gln Lys Val Ala Gly Val
 265 270 275

att gaa aac atg tct gcc atg gtg ctt cct gat ggc acc acc atg gat 979
 Ile Glu Asn Met Ser Ala Met Val Leu Pro Asp Gly Thr Thr Met Asp
 280 285 290

gtt ttc ggc acc ggc ggc ggt caa aag att gct gat cgt ctt acc gct 1027
 Val Phe Gly Thr Gly Gly Gly Gln Lys Ile Ala Asp Arg Leu Thr Ala
 295 300 305

gtg aca ggt gaa gag gtc aag gtt atc gga tct gtt cca ttg gat ccg 1075
 Val Thr Gly Glu Glu Val Lys Val Ile Gly Ser Val Pro Leu Asp Pro
 310 315 320 325

aac ctg cgt atc ggt ggc gat gtg gga aat cct att gcg att tct gaa 1123
 Asn Leu Arg Ile Gly Gly Asp Val Gly Asn Pro Ile Ala Ile Ser Glu
 330 335 340

cca cac tcc cca acc gct gca gcg atc aat gag atc gct gaa cac cta 1171
 Pro His Ser Pro Thr Ala Ala Ala Ile Asn Glu Ile Ala Glu His Leu
 345 350 355

gct cac cgc aag gta tcg ctg gtg ggt aaa acg ctt ggg ctt ggc gtt 1219
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 360 365 370

aaa taaaagctaa ataatatcgg tcc 1245
 Lys

<210> 258
 <211> 374
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 258
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Ser Val Ser Ile Asp Gly Ser Asp Val Gln Val Glu Val Tyr Leu Thr
 35 40 45

Ile Ala Ala Cys Pro Met Lys Thr Thr Ile Val Thr Asn Thr Glu Ala
 50 55 60

Ala Leu Lys Asp Ile Asp Gly Val Gly Gln Val His Val Thr Thr Asp
 65 70 75 80

Val Met Ser Asp Glu Gln Arg Arg Ala Leu Arg Val Ser Leu Arg Gly
 85 90 95

Glu Thr Ser Glu Pro Val Ile Pro Phe Ala Gln Pro Gly Ser Thr Thr
 100 105 110

Arg Val Tyr Ala Val Ala Ser Gly Lys Gly Gly Val Gly Lys Ser Ser

115					120					125						
Met	Thr	Val	Asn	Leu	Ala	Ala	Ala	Leu	Ala	Lys	Arg	Gly	Leu	Ser	Val	
130					135					140						
Gly	Ile	Leu	Asp	Ala	Asp	Ile	Tyr	Gly	His	Ser	Val	Pro	Gly	Met	Leu	
145					150					155					160	
Gly	Ser	Asp	Gln	Arg	Pro	His	Gln	Val	Asp	Asp	Met	Ile	Met	Pro	Pro	
165					170					175						
Gln	Ala	His	Gly	Val	Lys	Met	Ile	Ser	Ile	Ala	His	Phe	Thr	Glu	Gly	
180					185					190						
Asn	Ala	Pro	Val	Val	Trp	Arg	Gly	Pro	Met	Leu	His	Arg	Ala	Ile	Gln	
195					200					205						
Gln	Phe	Leu	Thr	Asp	Val	Phe	Trp	Gly	Asp	Leu	Asp	Ile	Leu	Leu	Leu	
210					215					220						
Asp	Leu	Pro	Pro	Gly	Thr	Gly	Asp	Ile	Ala	Ile	Thr	Val	Ala	Gln	Leu	
225					230					235					240	
Ile	Pro	Asn	Ala	Glu	Leu	Leu	Ile	Val	Thr	Thr	Pro	Gln	Ala	Ala	Ala	
245					250					255						
Ala	Glu	Val	Ala	Glu	Arg	Ala	Gly	Thr	Ile	Ser	Val	Gln	Thr	Asn	Gln	
260					265					270						
Lys	Val	Ala	Gly	Val	Ile	Glu	Asn	Met	Ser	Ala	Met	Val	Leu	Pro	Asp	
275					280					285						
Gly	Thr	Thr	Met	Asp	Val	Phe	Gly	Thr	Gly	Gly	Gly	Gln	Lys	Ile	Ala	
290					295					300						
Asp	Arg	Leu	Thr	Ala	Val	Thr	Gly	Glu	Glu	Val	Lys	Val	Ile	Gly	Ser	
305					310					315					320	
Val	Pro	Leu	Asp	Pro	Asn	Leu	Arg	Ile	Gly	Gly	Asp	Val	Gly	Asn	Pro	
325					330					335						
Ile	Ala	Ile	Ser	Glu	Pro	His	Ser	Pro	Thr	Ala	Ala	Ala	Ile	Asn	Glu	
340					345					350						
Ile	Ala	Glu	His	Leu	Ala	His	Arg	Lys	Val	Ser	Leu	Val	Gly	Lys	Thr	
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Leu	Gly	Leu	Gly	Val	Lys											
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(3010)
 <223> RXN02082

<400> 259

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                                   Met Tyr Leu Lys Ser
                                   1 5

ttg acg ctc aag ggg ttt aag tct ttc gcg tct gcg acg acc ctg aaa 163
Leu Thr Leu Lys Gly Phe Lys Ser Phe Ala Ser Ala Thr Thr Leu Lys
                                   10 15 20

ttt gag cca ggc att tgt gcc gtg gtg ggt ccg aat ggt tca ggc aaa 211
Phe Glu Pro Gly Ile Cys Ala Val Val Gly Pro Asn Gly Ser Gly Lys
                                   25 30 35

tcc aat gtg gtt gat gcg ctg gcc tgg gtg atg ggt gaa ggt tct gcg 259
Ser Asn Val Val Asp Ala Leu Ala Trp Val Met Gly Glu Gly Ser Ala
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aag acc ttg cgt ggc ggc aaa atg gaa gat gtc att ttt gct ggc gcg 307
Lys Thr Leu Arg Gly Gly Lys Met Glu Asp Val Ile Phe Ala Gly Ala
                                   55 60 65

ggc gat cgt aaa ccg ttg ggt cgc gca gaa gtc acg ctg acc att gat 355
Gly Asp Arg Lys Pro Leu Gly Arg Ala Glu Val Thr Leu Thr Ile Asp
                                   70 75 80 85

aac tct gat ggc gca ctg ccc att gag tac acc gaa gtg tcg gtg acc 403
Asn Ser Asp Gly Ala Leu Pro Ile Glu Tyr Thr Glu Val Ser Val Thr
                                   90 95 100

aga cgg atg ttc cgt gat ggt gca agt gaa tat gag atc aat ggg gcg 451
Arg Arg Met Phe Arg Asp Gly Ala Ser Glu Tyr Glu Ile Asn Gly Ala
                                   105 110 115

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Lys Ala Arg Leu Met Asp Ile Gln Glu Leu Leu Ser Asp Thr Gly Ile
                                   120 125 130

ggc cgt gaa atg cac atc atg gtg ggg cag gga aag ctc gca gag att 547
Gly Arg Glu Met His Ile Met Val Gly Gln Gly Lys Leu Ala Glu Ile
                                   135 140 145

ttg gag tcc cgc ccc gaa gag cgc cga gcg tat atc gaa gaa gct gcg 595
Leu Glu Ser Arg Pro Glu Glu Arg Arg Ala Tyr Ile Glu Glu Ala Ala
                                   150 155 160 165

ggt gtg ctc aag cac cgg cgc agg aaa gaa aag gcg cag cgc aaa ctt 643
Gly Val Leu Lys His Arg Arg Arg Lys Glu Lys Ala Gln Arg Lys Leu
                                   170 175 180

cag ggc atg cag gtc aat ctt gat cgt ttg cag gat ctg acc cat gag 691
Gln Gly Met Gln Val Asn Leu Asp Arg Leu Leu Gln Asp Leu Thr His Glu
                                   185 190 195

ttg gcc aag cag ctc aag ccg ttg gct agg cag gcg gaa gca gcg cag 739
Leu Ala Lys Gln Leu Lys Pro Leu Ala Arg Gln Ala Glu Ala Ala Gln
                                   200 205 210

cgt gcg gcg acg gtg cag gct gat ttg cgt gat gcg cgt ttc cag att 787
Arg Ala Ala Thr Val Gln Ala Asp Leu Arg Asp Ala Arg Phe Gln Ile

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Ala Gly Phe Glu Ile Val Lys Leu Ser Glu Lys Leu Glu Thr Ser Thr			
230	235	240	245
gag cgc gag aaa atg att cgt gag cag gcg gaa gca gca caa gag cag			883
Glu Arg Glu Lys Met Ile Arg Glu Gln Ala Glu Ala Ala Gln Glu Gln			
	250	255	260
ctg gaa gaa gcc acc aca act cag atg gaa gtg gag atg gag ttg gcg			931
Leu Glu Glu Ala Thr Thr Thr Gln Met Glu Val Glu Met Glu Leu Ala			
	265	270	275
gag atc act ccg cag gct gaa gct gcg caa cag ttg tgg ttt gat ttg			979
Glu Ile Thr Pro Gln Ala Glu Ala Ala Gln Gln Leu Trp Phe Asp Leu			
	280	285	290
tct tcg ctg gct gag cgg gtg tcg gca acg atg cgt att gct gca gac			1027
Ser Ser Leu Ala Glu Arg Val Ser Ala Thr Met Arg Ile Ala Ala Asp			
	295	300	305
cgt gcg agt tca ggt gcc gcg gat gtg ccg tat gcg ggc cag gat cct			1075
Arg Ala Ser Ser Gly Ala Ala Asp Val Pro Tyr Ala Gly Gln Asp Pro			
	310	315	320
gat gag ttg ctt ggt cgg gcc gaa act gct gac aaa gaa tta gaa gaa			1123
Asp Glu Leu Leu Gly Arg Ala Glu Thr Ala Asp Lys Glu Leu Glu Glu			
	330	335	340
ctc gag atg gcc gtg gaa atg acc acc gag cgt ttg acc tcc att caa			1171
Leu Glu Met Ala Val Glu Met Thr Thr Glu Arg Leu Thr Ser Ile Gln			
	345	350	355
gag gaa gcc gag gat aag gcc gcg cag gct cgt gag gct gag cgt gaa			1219
Glu Glu Ala Glu Asp Lys Ala Ala Gln Ala Arg Glu Ala Glu Arg Glu			
	360	365	370
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His Leu Ala Gln Val Arg Ala Ile Ser Asp Arg Arg Glu Gly Val Val			
	375	380	385
cgc ctg ctt gca tct gag gaa tct ttg cgc acc cag cac acg tca gca			1315
Arg Leu Leu Ala Ser Glu Glu Ser Leu Arg Thr Gln His Thr Ser Ala			
	390	395	400
gag gag gaa gct gag cga ctc agt gag cag ctt gag gag ttc atc ggc			1363
Glu Glu Glu Ala Glu Arg Leu Ser Glu Gln Leu Glu Glu Phe Ile Gly			
	410	415	420
cgc att ttg gat gtg gaa cgt gaa cgt cgc ctc acc gat gag cgt aaa			1411
Arg Ile Leu Asp Val Glu Arg Glu Arg Arg Leu Thr Asp Glu Arg Lys			
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cag ggc gtt gac acg gat cgt gcg ccc ttg gaa gaa gcc ctc aaa cag			1459
Gln Gly Val Asp Thr Asp Arg Ala Pro Leu Glu Glu Ala Leu Lys Gln			
	440	445	450
gca aaa cat gaa gcc gaa gca gca gag act cgt ctt gag gag ctt cgt			1507
Ala Lys His Glu Ala Glu Ala Ala Glu Thr Arg Leu Glu Glu Leu Arg			
	455	460	465

act	aag	cgc	agc	gat	ctg	gaa	aaa	gaa	gta	tcc	agg	ttg	cag	tcg	cgc	1555
Thr	Lys	Arg	Ser	Asp	Leu	Glu	Lys	Glu	Val	Ser	Arg	Leu	Gln	Ser	Arg	
470					475					480					485	
att	gag	acg	ctt	aac	caa	aat	agg	cca	cgt	tcc	gat	gct	gct	gat	gtg	1603
Ile	Glu	Thr	Leu	Asn	Gln	Asn	Arg	Pro	Arg	Ser	Asp	Ala	Ala	Asp	Val	
				490					495						500	
gtg	gat	tac	ccg	cag	ctg	gcc	acg	ttg	att	cga	ccg	caa	cga	aac	gtc	1651
Val	Asp	Tyr	Pro	Gln	Leu	Ala	Thr	Leu	Ile	Arg	Pro	Gln	Arg	Asn	Val	
			505					510					515			
gat	aag	gct	ctc	gct	gcc	gcc	ctg	ggg	gcg	cat	gcc	gag	gcg	ctg	gct	1699
Asp	Lys	Ala	Leu	Ala	Ala	Ala	Leu	Gly	Ala	His	Ala	Glu	Ala	Leu	Ala	
		520					525					530				
ggc	gag	gct	gcg	gaa	ggg	ctc	gtc	gag	aag	ctt	atc	gac	gcc	ggc	gtt	1747
Gly	Glu	Ala	Ala	Glu	Gly	Leu	Val	Glu	Lys	Leu	Ile	Asp	Ala	Gly	Val	
	535					540					545					
gca	cgc	acc	atc	atc	gtt	gat	ggc	acg	cag	gct	ggc	ggc	gca	tgg	cgc	1795
Ala	Arg	Thr	Ile	Ile	Val	Asp	Gly	Thr	Gln	Ala	Gly	Gly	Ala	Trp	Arg	
550					555				560						565	
ctg	gac	gcg	aac	att	ccg	gcc	ggg	gcg	agc	tgg	ctg	ctc	gac	cat	gtt	1843
Leu	Asp	Ala	Asn	Ile	Pro	Ala	Gly	Ala	Ser	Trp	Leu	Leu	Asp	His	Val	
				570					575					580		
gat	ctg	gat	ccg	gcg	att	gcc	ggc	ccg	gta	aac	cgg	ctg	ctt	gcc	gac	1891
Asp	Leu	Asp	Pro	Ala	Ile	Ala	Gly	Pro	Val	Asn	Arg	Leu	Leu	Ala	Asp	
			585					590					595			
gtt	gtg	ctt	gtc	gac	gac	ccc	tcc	ctc	ggc	cgc	caa	gca	atc	gag	gat	1939
Val	Val	Leu	Val	Asp	Asp	Pro	Ser	Leu	Gly	Arg	Gln	Ala	Ile	Glu	Asp	
		600					605					610				
gat	ccc	cgt	ctg	cgt	gcc	gtt	gac	cgc	aat	ggg	gtg	ctc	atc	ggc	gct	1987
Asp	Pro	Arg	Leu	Arg	Ala	Val	Asp	Arg	Asn	Gly	Val	Leu	Ile	Gly	Ala	
	615					620					625					
ggg	tgg	att	cag	gtc	ggc	acc	gaa	acc	tcg	act	gtg	gaa	atc	aca	gct	2035
Gly	Trp	Ile	Gln	Val	Gly	Thr	Glu	Thr	Ser	Thr	Val	Glu	Ile	Thr	Ala	
630					635				640						645	
cat	att	gag	gaa	gca	gaa	gct	caa	ctt	gct	gcg	gcc	tct	gcc	gcc	ttg	2083
His	Ile	Glu	Glu	Ala	Glu	Ala	Gln	Leu	Ala	Ala	Ala	Ser	Ala	Ala	Leu	
				650				655						660		
gac	gac	att	gcc	ggc	act	ttt	gat	ggc	gcc	ctc	cac	gct	gcc	gac	aac	2131
Asp	Asp	Ile	Ala	Gly	Thr	Phe	Asp	Gly	Ala	Leu	His	Ala	Ala	Asp	Asn	
			665					670					675			
act	cgc	gtc	gag	gtg	gct	gcc	cgc	acc	gca	gcc	ctg	cgc	gaa	ctc	gac	2179
Thr	Arg	Val	Glu	Val	Ala	Ala	Arg	Thr	Ala	Ala	Leu	Arg	Glu	Leu	Asp	
		680				685						690				
atg	acc	agg	gat	tcc	atc	acc	cgc	gat	ctc	gcg	cgc	ttg	gac	aaa	caa	2227
Met	Thr	Arg	Asp	Ser	Ile	Thr	Arg	Asp	Leu	Ala	Arg	Leu	Asp	Lys	Gln	
	695					700					705					

cat gag gcc gcc gaa tcc gag cgc gtc cgc cat gtt gga cgc ctg cat	2275
His Glu Ala Ala Glu Ser Glu Arg Val Arg His Val Gly Arg Leu His	
710 715 720 725	
gct gcg gaa aca cgc cgt gaa gag ctg cgc gaa cag tta gaa gac atc	2323
Ala Ala Glu Thr Arg Arg Glu Glu Leu Arg Glu Gln Leu Glu Asp Ile	
730 735 740	
gtc gat cga ctc tcc cgc gtg gaa gac gaa gaa gac gct gac gaa ccc	2371
Val Asp Arg Leu Ser Arg Val Glu Asp Glu Glu Asp Ala Asp Glu Pro	
745 750 755	
tca acc acc gcc cgc gac caa gca aat gcc gag ctg caa caa atc cgc	2419
Ser Thr Thr Ala Arg Asp Gln Ala Asn Ala Glu Leu Gln Gln Ile Arg	
760 765 770	
gcc atg gaa atg gaa gca cgc ctt gcc caa cgc acc gcc gaa gag cgc	2467
Ala Met Glu Met Glu Ala Arg Leu Ala Gln Arg Thr Ala Glu Glu Arg	
775 780 785	
gcc ggg cag cag cgg ggc aag ggc gat agt ctg cga cgc cag gcc gag	2515
Ala Gly Gln Gln Arg Gly Lys Gly Asp Ser Leu Arg Arg Gln Ala Glu	
790 795 800 805	
cat gag cgc caa gcc aaa atc cgg cat gaa caa gcc atg gaa gcc cgt	2563
His Glu Arg Gln Ala Lys Ile Arg His Glu Gln Ala Met Glu Ala Arg	
810 815 820	
cgc agg cgc acc caa ttg gct gca gcc gtg cat aat ggc gca cgc gat	2611
Arg Arg Arg Thr Gln Leu Ala Ala Ala Val His Asn Gly Ala Arg Asp	
825 830 835	
gtg gcc gag cgt gtc tca agt gtc ctt gcc caa gca gcc atc gaa aga	2659
Val Ala Glu Arg Val Ser Ser Val Leu Ala Gln Ala Ala Ile Glu Arg	
840 845 850	
gat cag cac aac cgc gac aaa gcg ctg ctg acc tca cac tta gcg cgc	2707
Asp Gln His Asn Arg Asp Lys Ala Leu Leu Thr Ser His Leu Ala Arg	
855 860 865	
gcc aaa gat gct gtg agt gct gca cgc cag cac ctc aat cga ctc agc	2755
Ala Lys Asp Ala Val Ser Ala Ala Arg Gln His Leu Asn Arg Leu Ser	
870 875 880 885	
gac aac gcc cac tcc atg gaa ctt gcg cgc agc caa gct caa gtg cgc	2803
Asp Asn Ala His Ser Met Glu Leu Ala Arg Ser Gln Ala Gln Val Arg	
890 895 900	
atg gag gaa gcc gtt gcc aaa atc acc gag caa ctt ggc att ccg gtc	2851
Met Glu Glu Ala Val Ala Lys Ile Thr Glu Gln Leu Gly Ile Pro Val	
905 910 915	
gca gaa ttg ctg cgc gat tac acc cca gat gaa aac ttt gat gaa aag	2899
Ala Glu Leu Leu Arg Asp Tyr Thr Pro Asp Glu Asn Phe Asp Glu Lys	
920 925 930	
ttc caa cgg gca cgc ctc aaa caa gcc gaa aaa gac ctc gcc gca cta	2947
Phe Gln Arg Ala Arg Leu Lys Gln Ala Glu Lys Asp Leu Ala Ala Leu	
935 940 945	
ggc aaa gtc aac ccc ctg gcc ttg gaa gaa ttc aaa gcc ctt gga aga	2995

Gly Lys Val Asn Pro Leu Ala Leu Glu Glu Phe Lys Ala Leu Gly Arg
 950 955 960 965

gcg cta cga gtt cct
 Ala Leu Arg Val Pro
 970

3010

<210> 260
 <211> 970
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 260
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 Ala Thr Thr Leu Lys Phe Glu Pro Gly Ile Cys Ala Val Val Gly Pro
 20 25 30
 Asn Gly Ser Gly Lys Ser Asn Val Val Asp Ala Leu Ala Trp Val Met
 35 40 45
 Gly Glu Gly Ser Ala Lys Thr Leu Arg Gly Gly Lys Met Glu Asp Val
 50 55 60
 Ile Phe Ala Gly Ala Gly Asp Arg Lys Pro Leu Gly Arg Ala Glu Val
 65 70 75 80
 Thr Leu Thr Ile Asp Asn Ser Asp Gly Ala Leu Pro Ile Glu Tyr Thr
 85 90 95
 Glu Val Ser Val Thr Arg Arg Met Phe Arg Asp Gly Ala Ser Glu Tyr
 100 105 110
 Glu Ile Asn Gly Ala Lys Ala Arg Leu Met Asp Ile Gln Glu Leu Leu
 115 120 125
 Ser Asp Thr Gly Ile Gly Arg Glu Met His Ile Met Val Gly Gln Gly
 130 135 140
 Lys Leu Ala Glu Ile Leu Glu Ser Arg Pro Glu Glu Arg Arg Ala Tyr
 145 150 155 160
 Ile Glu Glu Ala Ala Gly Val Leu Lys His Arg Arg Arg Lys Glu Lys
 165 170 175
 Ala Gln Arg Lys Leu Gln Gly Met Gln Val Asn Leu Asp Arg Leu Gln
 180 185 190
 Asp Leu Thr His Glu Leu Ala Lys Gln Leu Lys Pro Leu Ala Arg Gln
 195 200 205
 Ala Glu Ala Ala Gln Arg Ala Ala Thr Val Gln Ala Asp Leu Arg Asp
 210 215 220
 Ala Arg Phe Gln Ile Ala Gly Phe Glu Ile Val Lys Leu Ser Glu Lys
 225 230 235 240
 Leu Glu Thr Ser Thr Glu Arg Glu Lys Met Ile Arg Glu Gln Ala Glu
 245 250 255

Ala Ala Gln Glu Gln Leu Glu Glu Ala Thr Thr Thr Gln Met Glu Val
 260 265 270
 Glu Met Glu Leu Ala Glu Ile Thr Pro Gln Ala Glu Ala Ala Gln Gln
 275 280 285
 Leu Trp Phe Asp Leu Ser Ser Leu Ala Glu Arg Val Ser Ala Thr Met
 290 295 300
 Arg Ile Ala Ala Asp Arg Ala Ser Ser Gly Ala Ala Asp Val Pro Tyr
 305 310 315 320
 Ala Gly Gln Asp Pro Asp Glu Leu Leu Gly Arg Ala Glu Thr Ala Asp
 325 330 335
 Lys Glu Leu Glu Glu Leu Glu Met Ala Val Glu Met Thr Thr Glu Arg
 340 345 350
 Leu Thr Ser Ile Gln Glu Glu Ala Glu Asp Lys Ala Ala Gln Ala Arg
 355 360 365
 Glu Ala Glu Arg Glu His Leu Ala Gln Val Arg Ala Ile Ser Asp Arg
 370 375 380
 Arg Glu Gly Val Val Arg Leu Leu Ala Ser Glu Glu Ser Leu Arg Thr
 385 390 395 400
 Gln His Thr Ser Ala Glu Glu Glu Ala Glu Arg Leu Ser Glu Gln Leu
 405 410 415
 Glu Glu Phe Ile Gly Arg Ile Leu Asp Val Glu Arg Glu Arg Arg Leu
 420 425 430
 Thr Asp Glu Arg Lys Gln Gly Val Asp Thr Asp Arg Ala Pro Leu Glu
 435 440 445
 Glu Ala Leu Lys Gln Ala Lys His Glu Ala Glu Ala Ala Glu Thr Arg
 450 455 460
 Leu Glu Glu Leu Arg Thr Lys Arg Ser Asp Leu Glu Lys Glu Val Ser
 465 470 475 480
 Arg Leu Gln Ser Arg Ile Glu Thr Leu Asn Gln Asn Arg Pro Arg Ser
 485 490 495
 Asp Ala Ala Asp Val Val Asp Tyr Pro Gln Leu Ala Thr Leu Ile Arg
 500 505 510
 Pro Gln Arg Asn Val Asp Lys Ala Leu Ala Ala Ala Leu Gly Ala His
 515 520 525
 Ala Glu Ala Leu Ala Gly Glu Ala Ala Glu Gly Leu Val Glu Lys Leu
 530 535 540
 Ile Asp Ala Gly Val Ala Arg Thr Ile Ile Val Asp Gly Thr Gln Ala
 545 550 555 560
 Gly Gly Ala Trp Arg Leu Asp Ala Asn Ile Pro Ala Gly Ala Ser Trp
 565 570 575

Leu Leu Asp His Val Asp Leu Asp Pro Ala Ile Ala Gly Pro Val Asn
 580 585 590
 Arg Leu Leu Ala Asp Val Val Leu Val Asp Asp Pro Ser Leu Gly Arg
 595 600 605
 Gln Ala Ile Glu Asp Asp Pro Arg Leu Arg Ala Val Asp Arg Asn Gly
 610 615 620
 Val Leu Ile Gly Ala Gly Trp Ile Gln Val Gly Thr Glu Thr Ser Thr
 625 630 635 640
 Val Glu Ile Thr Ala His Ile Glu Glu Ala Glu Ala Gln Leu Ala Ala
 645 650 655
 Ala Ser Ala Ala Leu Asp Asp Ile Ala Gly Thr Phe Asp Gly Ala Leu
 660 665 670
 His Ala Ala Asp Asn Thr Arg Val Glu Val Ala Ala Arg Thr Ala Ala
 675 680 685
 Leu Arg Glu Leu Asp Met Thr Arg Asp Ser Ile Thr Arg Asp Leu Ala
 690 695 700
 Arg Leu Asp Lys Gln His Glu Ala Ala Glu Ser Glu Arg Val Arg His
 705 710 715 720
 Val Gly Arg Leu His Ala Ala Glu Thr Arg Arg Glu Glu Leu Arg Glu
 725 730 735
 Gln Leu Glu Asp Ile Val Asp Arg Leu Ser Arg Val Glu Asp Glu Glu
 740 745 750
 Asp Ala Asp Glu Pro Ser Thr Thr Ala Arg Asp Gln Ala Asn Ala Glu
 755 760 765
 Leu Gln Gln Ile Arg Ala Met Glu Met Glu Ala Arg Leu Ala Gln Arg
 770 775 780
 Thr Ala Glu Glu Arg Ala Gly Gln Gln Arg Gly Lys Gly Asp Ser Leu
 785 790 795 800
 Arg Arg Gln Ala Glu His Glu Arg Gln Ala Lys Ile Arg His Glu Gln
 805 810 815
 Ala Met Glu Ala Arg Arg Arg Arg Thr Gln Leu Ala Ala Val His
 820 825 830
 Asn Gly Ala Arg Asp Val Ala Glu Arg Val Ser Ser Val Leu Ala Gln
 835 840 845
 Ala Ala Ile Glu Arg Asp Gln His Asn Arg Asp Lys Ala Leu Leu Thr
 850 855 860
 Ser His Leu Ala Arg Ala Lys Asp Ala Val Ser Ala Ala Arg Gln His
 865 870 875 880
 Leu Asn Arg Leu Ser Asp Asn Ala His Ser Met Glu Leu Ala Arg Ser
 885 890 895
 Gln Ala Gln Val Arg Met Glu Glu Ala Val Ala Lys Ile Thr Glu Gln

900	905	910
Leu Gly Ile Pro Val Ala Glu Leu Leu Arg Asp Tyr Thr Pro Asp Glu		
915	920	925
Asn Phe Asp Glu Lys Phe Gln Arg Ala Arg Leu Lys Gln Ala Glu Lys		
930	935	940
Asp Leu Ala Ala Leu Gly Lys Val Asn Pro Leu Ala Leu Glu Glu Phe		
945	950	955
Lys Ala Leu Gly Arg Ala Leu Arg Val Pro		
965	970	

<210> 261
 <211> 570
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(547)
 <223> RXA01495

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 agaattatatt cgactctgtg aagatgagga gtgggtccacc atg gct gac aac gcc 115
 Met Ala Asp Asn Ala
 1 5
 cgc gcg gct cgt atg gca aag cgc att caa act atc gtg gcc agc gcc 163
 Arg Ala Ala Arg Met Ala Lys Arg Ile Gln Thr Ile Val Ala Ser Ala
 10 15 20
 att gaa cgc gat atc aag gac cgc cga ctt gag ttc gtc aca att act 211
 Ile Glu Arg Asp Ile Lys Asp Arg Arg Leu Glu Phe Val Thr Ile Thr
 25 30 35
 gat gtg acc atg acc ggt gac ctg cac gat gca aag gtg ttt tac acc 259
 Asp Val Thr Met Thr Gly Asp Leu His Asp Ala Lys Val Phe Tyr Thr
 40 45 50
 gtt cgt gga gct tcc att gaa gaa gaa cca gat ctt gag gca gca gca 307
 Val Arg Gly Ala Ser Ile Glu Glu Glu Pro Asp Leu Glu Ala Ala Ala
 55 60 65
 gag gct ctt cac cga gca cgc ggc cag ctg agg aag atc gtt ggc cag 355
 Glu Ala Leu His Arg Ala Arg Gly Gln Leu Arg Lys Ile Val Gly Gln
 70 75 80 85
 cag ctg ggt gtt cgg ttt acc ccg acc ctg act tac agc atc gat acc 403
 Gln Leu Gly Val Arg Phe Thr Pro Thr Leu Thr Tyr Ser Ile Asp Thr
 90 95 100
 gtc cca gag gca tcc gca cac atg gaa gct ttg ttg gat cgt gct cgc 451
 Val Pro Glu Ala Ser Ala His Met Glu Ala Leu Leu Asp Arg Ala Arg
 105 110 115
 aag cgc gat gag gag ctg gct aaa ttg cgc gaa ggt gca gcg cct gca 499

Lys Arg Asp Glu Glu Leu Ala Lys Leu Arg Glu Gly Ala Ala Pro Ala
 120 125 130

ggt gat gca gat cct tac aag act tca tcc aag tct gaa tct gag gaa 547
 Gly Asp Ala Asp Pro Tyr Lys Thr Ser Ser Lys Ser Glu Ser Glu Glu
 135 140 145

taacaccagt gacggataat agt 570

<210> 262

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Met Ala Asp Asn Ala Arg Ala Ala Arg Met Ala Lys Arg Ile Gln Thr
 1 5 10 15

Ile Val Ala Ser Ala Ile Glu Arg Asp Ile Lys Asp Arg Arg Leu Glu
 20 25 30

Phe Val Thr Ile Thr Asp Val Thr Met Thr Gly Asp Leu His Asp Ala
 35 40 45

Lys Val Phe Tyr Thr Val Arg Gly Ala Ser Ile Glu Glu Glu Pro Asp
 50 55 60

Leu Glu Ala Ala Ala Glu Ala Leu His Arg Ala Arg Gly Gln Leu Arg
 65 70 75 80

Lys Ile Val Gly Gln Gln Leu Gly Val Arg Phe Thr Pro Thr Leu Thr
 85 90 95

Tyr Ser Ile Asp Thr Val Pro Glu Ala Ser Ala His Met Glu Ala Leu
 100 105 110

Leu Asp Arg Ala Arg Lys Arg Asp Glu Glu Leu Ala Lys Leu Arg Glu
 115 120 125

Gly Ala Ala Pro Ala Gly Asp Ala Asp Pro Tyr Lys Thr Ser Ser Lys
 130 135 140

Ser Glu Ser Glu Glu
 145

<210> 263

<211> 678

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(655)

<223> RXA01893

<400> 263

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atcagaatcc acgctgtag aaaaacacag gaggtaataa atg att gat gaa att 115

	Met	Ile	Asp	Glu	Ile	
	1				5	
ctg ttc gaa gcg gaa gag cgc atg acc gca acg gtc gag cac acc cgc						163
Leu Phe Glu Ala Glu Glu Arg Met Thr Ala Thr Val Glu His Thr Arg						
				10	15	20
gaa gac ttg acc acc att cgt acc ggt cgc gca aac ccg gct atg ttc						211
Glu Asp Leu Thr Thr Ile Arg Thr Gly Arg Ala Asn Pro Ala Met Phe						
				25	30	35
aac ggt gtc atg gct gaa tac tac ggc gtg cct act cct att act cag						259
Asn Gly Val Met Ala Glu Tyr Tyr Gly Val Pro Thr Pro Ile Thr Gln						
				40	45	50
atg tca ggc atc act gtt cca gag cct cgc atg ctg ctg atc aag cct						307
Met Ser Gly Ile Thr Val Pro Glu Pro Arg Met Leu Leu Ile Lys Pro						
				55	60	65
tat gag atg tct tcc atg cag gtc att gag aat gct atc cgt aac tct						355
Tyr Glu Met Ser Ser Met Gln Val Ile Glu Asn Ala Ile Arg Asn Ser						
				70	75	80
gac ctt ggt gtt aac ccc acc aac gat ggc cag gtg ctg cgt gtg acc						403
Asp Leu Gly Val Asn Pro Thr Asn Asp Gly Gln Val Leu Arg Val Thr						
				90	95	100
atc cca cag ctt act gaa gag cgt cgt aag gac atg gtc aag ctt gct						451
Ile Pro Gln Leu Thr Glu Glu Arg Arg Lys Asp Met Val Lys Leu Ala						
				105	110	115
aag ggt aag ggc gaa gac ggc aag att gcc att cgt aac atc cgc cgc						499
Lys Gly Lys Gly Glu Asp Gly Lys Ile Ala Ile Arg Asn Ile Arg Arg						
				120	125	130
aag ggc atg gac cag cta aag aag ctg caa aaa gat ggc gac gct ggc						547
Lys Gly Met Asp Gln Leu Lys Lys Leu Gln Lys Asp Gly Asp Ala Gly						
				135	140	145
gaa gat gaa gta cag gca gca gaa aaa gaa cta gat aaa gtc acc gct						595
Glu Asp Glu Val Gln Ala Ala Glu Lys Glu Leu Asp Lys Val Thr Ala						
				150	155	160
ggt ttt gtt gcg cag gtc gat gaa gtc gtt gct cgc aag gaa aag gaa						643
Gly Phe Val Ala Gln Val Asp Glu Val Val Ala Arg Lys Glu Lys Glu						
				170	175	180
ctg atg gag gtc tagaagacct ttatcgcaat ggc						678
Leu Met Glu Val						
				185		

<210> 264

<211> 185

<212> PRT

<213> Corynebacterium glutamicum

<400> 264

Met	Ile	Asp	Glu	Ile	Leu	Phe	Glu	Ala	Glu	Glu	Arg	Met	Thr	Ala	Thr
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Val Glu His Thr Arg Glu Asp Leu Thr Thr Ile Arg Thr Gly Arg Ala
 20 25 30
 Asn Pro Ala Met Phe Asn Gly Val Met Ala Glu Tyr Tyr Gly Val Pro
 35 40 45
 Thr Pro Ile Thr Gln Met Ser Gly Ile Thr Val Pro Glu Pro Arg Met
 50 55 60
 Leu Leu Ile Lys Pro Tyr Glu Met Ser Ser Met Gln Val Ile Glu Asn
 65 70 75 80
 Ala Ile Arg Asn Ser Asp Leu Gly Val Asn Pro Thr Asn Asp Gly Gln
 85 90 95
 Val Leu Arg Val Thr Ile Pro Gln Leu Thr Glu Glu Arg Arg Lys Asp
 100 105 110
 Met Val Lys Leu Ala Lys Gly Lys Gly Glu Asp Gly Lys Ile Ala Ile
 115 120 125
 Arg Asn Ile Arg Arg Lys Gly Met Asp Gln Leu Lys Lys Leu Gln Lys
 130 135 140
 Asp Gly Asp Ala Gly Glu Asp Glu Val Gln Ala Ala Glu Lys Glu Leu
 145 150 155 160
 Asp Lys Val Thr Ala Gly Phe Val Ala Gln Val Asp Glu Val Val Ala
 165 170 175
 Arg Lys Glu Lys Glu Leu Met Glu Val
 180 185

<210> 265

<211> 458

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(435)

<223> RXA01568

<400> 265

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 Trp Asp Asn Ile Thr Tyr Leu Met Arg Ala Ala Arg Lys Gly Thr Val
 1 5 10 15

gtt ccc atg gtc atc gag ttg gat ggc cgg ttc gtg ggg cag ttg act 96
 Val Pro Met Val Ile Glu Leu Asp Gly Arg Phe Val Gly Gln Leu Thr
 20 25 30

atc ggc aac atc cag cac ggc ggc atc tcc gat gcc tgg att ggc tat 144
 Ile Gly Asn Ile Gln His Gly Gly Ile Ser Asp Ala Trp Ile Gly Tyr
 35 40 45

tgg gtt tcc agc gcg gtg acg ggg cgc ggt atc gct acg gcc gcc tgc 192
 Trp Val Ser Ser Ala Val Thr Gly Arg Gly Ile Ala Thr Ala Ala Cys
 50 55 60

gcg ctc ggc gtg gat cat gct ttt cga cgc ata ggt ctg cat cgc ctc 240
 Ala Leu Gly Val Asp His Ala Phe Arg Arg Ile Gly Leu His Arg Leu
 65 70 75 80

acc gcc acc tat cta ccc agc aac cca gca tcc ggg aag gtg ctc gga 288
 Thr Ala Thr Tyr Leu Pro Ser Asn Pro Ala Ser Gly Lys Val Leu Gly
 85 90 95

cac agc ggt ttc cgc cca gaa ggc tat ctc att aga aat ctg cat att 336
 His Ser Gly Phe Arg Pro Glu Gly Tyr Leu Ile Arg Asn Leu His Ile
 100 105 110

gat gga caa tgg atg gat cac cat ttt gtg gca ttg ctg gcg gat gag 384
 Asp Gly Gln Trp Met Asp His His Phe Val Ala Leu Leu Ala Asp Glu
 115 120 125

tat tca ata acc gcg gtg gaa cgt ctc act aga gag gga cga ttg cgc 432
 Tyr Ser Ile Thr Ala Val Glu Arg Leu Thr Arg Glu Gly Arg Leu Arg
 130 135 140

cga tgattactaa tgcgaagaaa ttt 458
 Arg
 145

<210> 266

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 266

Trp Asp Asn Ile Thr Tyr Leu Met Arg Ala Ala Arg Lys Gly Thr Val
 1 5 10 15

Val Pro Met Val Ile Glu Leu Asp Gly Arg Phe Val Gly Gln Leu Thr
 20 25 30

Ile Gly Asn Ile Gln His Gly Gly Ile Ser Asp Ala Trp Ile Gly Tyr
 35 40 45

Trp Val Ser Ser Ala Val Thr Gly Arg Gly Ile Ala Thr Ala Ala Cys
 50 55 60

Ala Leu Gly Val Asp His Ala Phe Arg Arg Ile Gly Leu His Arg Leu
 65 70 75 80

Thr Ala Thr Tyr Leu Pro Ser Asn Pro Ala Ser Gly Lys Val Leu Gly
 85 90 95

His Ser Gly Phe Arg Pro Glu Gly Tyr Leu Ile Arg Asn Leu His Ile
 100 105 110

Asp Gly Gln Trp Met Asp His His Phe Val Ala Leu Leu Ala Asp Glu
 115 120 125

Tyr Ser Ile Thr Ala Val Glu Arg Leu Thr Arg Glu Gly Arg Leu Arg
 130 135 140

Arg
 145

<210> 267
 <211> 789
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(766)
 <223> RXA01661

<400> 267
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 gaaggccttc cttaccgcag cttgctggga ctttctgata ttg gac tca act aac 115
 Leu Asp Ser Thr Asn
 1 5
 acc ccc ggc ccc acg gag tgg ggc gag tcc cgc gtg ggc aaa ggt cca 163
 Thr Pro Gly Pro Thr Glu Trp Gly Glu Ser Arg Val Gly Lys Gly Pro
 10 15 20
 tgg gaa gag gaa aac ccc ggc gta cct cgg cct aca agc ccg ctt ttc 211
 Trp Glu Glu Glu Asn Pro Gly Val Pro Arg Pro Thr Ser Pro Leu Phe
 25 30 35
 gac gtc acc ctc ctc aac gag ggc gat cgc cgc aac gtt gtt gac gcc 259
 Asp Val Thr Leu Leu Asn Glu Gly Asp Arg Arg Asn Val Val Asp Ala
 40 45 50
 tat cgt tat tgg acc cgt gag gcg att gtt gaa gat atc gac acc cgc 307
 Tyr Arg Tyr Trp Thr Arg Glu Ala Ile Val Glu Asp Ile Asp Thr Arg
 55 60 65
 cgc cac agc ctc cac gta gcg atc gaa aac ttt gaa aac gac gcc aac 355
 Arg His Ser Leu His Val Ala Ile Glu Asn Phe Glu Asn Asp Ala Asn
 70 75 80 85
 atc ggc acc gtc gtg cgc acc gcc aac gcc ttt gcc gtg aac aca gtc 403
 Ile Gly Thr Val Val Arg Thr Ala Asn Ala Phe Ala Val Asn Thr Val
 90 95 100
 cac att gtg ggc agg cgt cgg tgg aac cgc agg gga gcc atg gtg act 451
 His Ile Val Gly Arg Arg Arg Trp Asn Arg Arg Gly Ala Met Val Thr
 105 110 115
 gac cgt tac cag cac ctc atg cac cac gaa gac gtt gat tcg ctg ctt 499
 Asp Arg Tyr Gln His Leu Met His His Glu Asp Val Asp Ser Leu Leu
 120 125 130
 gcg tgg gca atc gcg gag cgg ctt acc atc gtc gcg atc gat aac acc 547
 Ala Trp Ala Ile Ala Glu Arg Leu Thr Ile Val Ala Ile Asp Asn Thr
 135 140 145
 cca ggt tcc gtg cct ttg gaa acc gct gag ttg ccg aag aac tgc ctg 595
 Pro Gly Ser Val Pro Leu Glu Thr Ala Glu Leu Pro Lys Asn Cys Leu
 150 155 160 165
 ttg ctg ttt ggt cag gaa ggc cca ggt gtc acc gaa gct gcg cgt gca 643
 Leu Leu Phe Gly Gln Glu Gly Pro Gly Val Thr Glu Ala Ala Arg Ala
 170 175 180

tta 789

<213> *Corynebacterium glutamicum*

Gly Ser Thr Arg Ser Ile Asn Ala Gly Val Ala Ala Gly Ile Ala Met
195 200 205

His Ala Trp Ile Arg Gln His Ala Asp Leu Ser Gln Ala Trp
 210 215 220

<210> 269

<211> 936

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(913)

<223> RXA01581

<400> 269

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agcaaagtgt accgcacggt taactgttag tgttatgagc atg gca ttg gac ttt 115
 Met Ala Leu Asp Phe
 1 5

aat gag gcg ttt acc gaa cgc acc ccg cgc atc gtc aac gca gct aaa 163
 Asn Glu Ala Phe Thr Glu Arg Thr Pro Arg Ile Val Asn Ala Ala Lys
 10 15 20

ctg cat cgc gcc gcg cag cgc aaa aaa gat aag cgt ttt cta gtt gaa 211
 Leu His Arg Ala Ala Gln Arg Lys Lys Asp Lys Arg Phe Leu Val Glu
 25 30 35

ggc gaa aat tcc gtt gaa gca gct gtc gct acc ggc gca gca act gac 259
 Gly Glu Asn Ser Val Glu Ala Ala Val Ala Thr Gly Ala Ala Thr Asp
 40 45 50

ctc ttt gtc act gaa tcc gct gcg gag cgc ttc gag gaa atc gtc cgc 307
 Leu Phe Val Thr Glu Ser Ala Ala Glu Arg Phe Glu Glu Ile Val Arg
 55 60 65

acc gcc ggt tac atg aat gtc tac acc cac gcg atc acg gac aag gcc 355
 Thr Ala Gly Tyr Met Asn Val Tyr Thr His Ala Ile Thr Asp Lys Ala
 70 75 80 85

gcg aag cat ctt agc gac acc gtc acc acc acg ggc att ttt gcg ctt 403
 Ala Lys His Leu Ser Asp Thr Val Thr Thr Thr Gly Ile Phe Ala Leu
 90 95 100

tgc gac gac gtc ctg tgg tca gtc ggc aag gcg atc acc ggc cag cca 451
 Cys Asp Asp Val Leu Trp Ser Val Gly Lys Ala Ile Thr Gly Gln Pro
 105 110 115

cgt cta gtg agc gtg ccg gtt gag acc cgc gag ccc ggt aat gcc gga 499
 Arg Leu Val Ser Val Pro Val Glu Thr Arg Glu Pro Gly Asn Ala Gly
 120 125 130

acc ttg att cgc gta tcc gac gcg gtc ggc gcc gac gcc gtc gtc ttc 547
 Thr Leu Ile Arg Val Ser Asp Ala Val Gly Ala Asp Ala Val Val Phe
 135 140 145

gct ggt gaa tca gta gat cca ctt ggc gca aaa gct gtg cgc tcc tca 595
 Ala Gly Glu Ser Val Asp Pro Leu Gly Ala Lys Ala Val Arg Ser Ser
 150 155 160 165

gcg gga tcg ctg ttt cac att cca gtg gca cgc aac aac aac atc gca 643
 Ala Gly Ser Leu Phe His Ile Pro Val Ala Arg Asn Asn Asn Ile Ala
 170 175 180

gat gtc ttg ggg cag ctt cgt tcc aag ggt ctg cag atc ctt gcg acc 691
 Asp Val Leu Gly Gln Leu Arg Ser Lys Gly Leu Gln Ile Leu Ala Thr
 185 190 195

tca gcc gat ggg gaa gta gac ctc gat gac gcc gat gag ctg cta gcc 739
 Ser Ala Asp Gly Glu Val Asp Leu Asp Asp Ala Asp Glu Leu Leu Ala
 200 205 210

aag cca acc gca tgg ctt ttt ggt aat gaa gct cac gga ctt gat gag 787
 Lys Pro Thr Ala Trp Leu Phe Gly Asn Glu Ala His Gly Leu Asp Glu
 215 220 225

agc ctg ctt gct cag gct gat cac cgc gtg cgt att ccg atc cgc ggc 835
 Ser Leu Leu Ala Gln Ala Asp His Arg Val Arg Ile Pro Ile Arg Gly
 230 235 240 245

cgc gca gaa tca ctc aat ttg gcc aca gca gcg tca att tgt ctg tac 883
 Arg Ala Glu Ser Leu Asn Leu Ala Thr Ala Ala Ser Ile Cys Leu Tyr
 250 255 260

gaa tcc tcc aag gca cta ttc gcc ggt gag taaaccccaa ttcattgccca 933
 Glu Ser Ser Lys Ala Leu Phe Ala Gly Glu
 265 270

gcg 936

<210> 270

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 270

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 20 25 30

Arg Phe Leu Val Glu Gly Glu Asn Ser Val Glu Ala Ala Val Ala Thr
 35 40 45

Gly Ala Ala Thr Asp Leu Phe Val Thr Glu Ser Ala Ala Glu Arg Phe
 50 55 60

Glu Glu Ile Val Arg Thr Ala Gly Tyr Met Asn Val Tyr Thr His Ala
 65 70 75 80

Ile Thr Asp Lys Ala Ala Lys His Leu Ser Asp Thr Val Thr Thr Thr
 85 90 95

Gly Ile Phe Ala Leu Cys Asp Asp Val Leu Trp Ser Val Gly Lys Ala
 100 105 110

Ile Thr Gly Gln Pro Arg Leu Val Ser Val Pro Val Glu Thr Arg Glu
 115 120 125

Pro Gly Asn Ala Gly Thr Leu Ile Arg Val Ser Asp Ala Val Gly Ala
 130 135 140

Asp Ala Val Val Phe Ala Gly Glu Ser Val Asp Pro Leu Gly Ala Lys
 145 150 155 160

Ala Val Arg Ser Ser Ala Gly Ser Leu Phe His Ile Pro Val Ala Arg
 165 170 175

Asn Asn Asn Ile Ala Asp Val Leu Gly Gln Leu Arg Ser Lys Gly Leu
 180 185 190

Gln Ile Leu Ala Thr Ser Ala Asp Gly Glu Val Asp Leu Asp Asp Ala
 195 200 205

Asp Glu Leu Leu Ala Lys Pro Thr Ala Trp Leu Phe Gly Asn Glu Ala
 210 215 220

His Gly Leu Asp Glu Ser Leu Leu Ala Gln Ala Asp His Arg Val Arg
 225 230 235 240

Ile Pro Ile Arg Gly Arg Ala Glu Ser Leu Asn Leu Ala Thr Ala Ala
 245 250 255

Ser Ile Cys Leu Tyr Glu Ser Ser Lys Ala Leu Phe Ala Gly Glu
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<210> 271

<211> 1062

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1039)

<223> RXA00313

<400> 271

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ttgcagtaat tacagacact ttttaaggaga taatttaaac atg gca gga aat gac 115
 Met Ala Gly Asn Asp
 1 5

agt cgt cga ggc ggc tta cgc aag acc aat aaa aaa ggt gca acc aag 163
 Ser Arg Arg Gly Gly Leu Arg Lys Thr Asn Lys Lys Gly Ala Thr Lys
 10 15 20

ggc agt ggc gga cag gtt cgt cgc ggt ctg aaa ggt aag ggg cct acc 211
 Gly Ser Gly Gly Gln Val Arg Arg Gly Leu Lys Gly Lys Gly Pro Thr
 25 30 35

cct aaa gct gag gat cgc acc tat cac gca gct cac aag cgc aag gtg 259
 Pro Lys Ala Glu Asp Arg Thr Tyr His Ala Ala His Lys Arg Lys Val
 40 45 50

gag cgt gat cgt cgt gat cgt gga cgc cac cag cgt gaa atg cca gag 307
 Glu Arg Asp Arg Arg Asp Arg Gly Arg His Gln Arg Glu Met Pro Glu
 55 60 65

ttg gtt gtg ggc cgt aac cca gtg ctg gaa tgt ctg cat gca cgc gtt	355
Leu Val Val Gly Arg Asn Pro Val Leu Glu Cys Leu His Ala Arg Val	
70 75 80 85	
cca gcg act gct ttg tat gtt gca gag ggt gcg gcg aac gat gag cgt	403
Pro Ala Thr Ala Leu Tyr Val Ala Glu Gly Ala Ala Asn Asp Glu Arg	
90 95 100	
ctg agc gag gca gtg cac act gcg gct ggc cga aat ctt cca gtg ctg	451
Leu Ser Glu Ala Val His Thr Ala Ala Gly Arg Asn Leu Pro Val Leu	
105 110 115	
gag gtt aac aag ctg gag ctg gat cgt atg acc gcg aac gcg atg cac	499
Glu Val Asn Lys Leu Glu Leu Asp Arg Met Thr Gly Asn Gly Met His	
120 125 130	
cag ggc atc ggc ctg gcg atc cct cct tac gag tac gca gat gtt cat	547
Gln Gly Ile Gly Leu Ala Ile Pro Pro Tyr Glu Tyr Ala Asp Val His	
135 140 145	
gat ctg atc gcc aat gct gcg gct tct aag aag cca gcg atg ttc gtg	595
Asp Leu Ile Ala Asn Ala Ala Ser Lys Lys Pro Gly Met Phe Val	
150 155 160 165	
att ctg gat aac atc acc gac cca cgt aac ttg ggt gct gtg att cgt	643
Ile Leu Asp Asn Ile Thr Asp Pro Arg Asn Leu Gly Ala Val Ile Arg	
170 175 180	
tcc gtc ggt gct ttc ggc ggc aac ggt gtc atc att ccg gag cgt cgt	691
Ser Val Gly Ala Phe Gly Gly Asn Gly Val Ile Ile Pro Glu Arg Arg	
185 190 195	
tca gca tct gtg acc gct gtt gca tgg cgt act tct gct ggt acc gca	739
Ser Ala Ser Val Thr Ala Val Ala Trp Arg Thr Ser Ala Gly Thr Ala	
200 205 210	
gcg cgt gtg cca gtg gcg aag gaa acc aac atg act cgt gtc gtg aag	787
Ala Arg Val Pro Val Ala Lys Glu Thr Asn Met Thr Arg Val Val Lys	
215 220 225	
gaa ttc cag caa aac ggt tac cag gtc gtc ggc ctt gac gct ggc ggc	835
Glu Phe Gln Gln Asn Gly Tyr Gln Val Val Gly Leu Asp Ala Gly Gly	
230 235 240 245	
gac cac act ttg gac acc tac gac ggc acc gac aac gtt gtc atc gtc	883
Asp His Thr Leu Asp Thr Tyr, Asp Gly Thr Asp Asn Val Val Ile Val	
250 255 260	
gtc ggt tct gag ggc aag gga att tcc cgt ctc gtt cgc gaa aac tgc	931
Val Gly Ser Glu Gly Lys Gly Ile Ser Arg Leu Val Arg Glu Asn Cys	
265 270 275	
gac acc atc atg tcc ata ccc acc gag ggc tgg gtt gaa tcg ctg aac	979
Asp Thr Ile Met Ser Ile Pro Thr Glu Gly Trp Val Glu Ser Leu Asn	
280 285 290	
gct tcg gtt gct gcc ggc gtc gtg ctg tcg gag ttc tcg cgc cag cgt	1027
Ala Ser Val Ala Ala Gly Val Val Leu Ser Glu Phe Ser Arg Gln Arg	
295 300 305	
cgc att aag ggt taagccggag gttggcgctcg aaa	1062

<400> 272															
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Lys	Gly	Ala	Thr 20	Lys	Gly	Ser	Gly	Gly 25	Gln	Val	Arg	Arg	Gly 30	Leu	Lys
Gly	Lys	Gly 35	Pro	Thr	Pro	Lys	Ala 40	Glu	Asp	Arg	Thr	Tyr 45	His	Ala	Ala
His	Lys 50	Arg	Lys	Val	Glu	Arg 55	Asp	Arg	Arg	Asp	Arg 60	Gly	Arg	His	Gln
Arg 65	Glu	Met	Pro	Glu	Leu 70	Val	Val	Gly	Arg	Asn 75	Pro	Val	Leu	Glu	Cys 80
Leu	His	Ala	Arg 85	Val	Pro	Ala	Thr	Ala 90	Leu	Tyr	Val	Ala	Glu	Gly 95	Ala
Ala	Asn	Asp	Glu 100	Arg	Leu	Ser	Glu	Ala 105	Val	His	Thr	Ala	Ala 110	Gly	Arg
Asn	Leu	Pro 115	Val	Leu	Glu	Val	Asn 120	Lys	Leu	Glu	Leu	Asp 125	Arg	Met	Thr
Gly 130	Asn	Gly	Met	His	Gln	Gly 135	Ile	Gly	Leu	Ala	Ile 140	Pro	Pro	Tyr	Glu
Tyr 145	Ala	Asp	Val	His	Asp 150	Leu	Ile	Ala	Asn	Ala 155	Ala	Ala	Ser	Lys	Lys 160
Pro	Gly	Met	Phe 165	Val	Ile	Leu	Asp	Asn 170	Ile	Thr	Asp	Pro	Arg	Asn 175	Leu
Gly	Ala	Val	Ile 180	Arg	Ser	Val	Gly	Ala 185	Phe	Gly	Gly	Asn	Gly 190	Val	Ile
Ile	Pro	Glu 195	Arg	Arg	Ser	Ala	Ser 200	Val	Thr	Ala	Val	Ala 205	Trp	Arg	Thr
Ser 210	Ala	Gly	Thr	Ala	Ala 215	Arg	Val	Pro	Val	Ala	Lys 220	Glu	Thr	Asn	Met
Thr 225	Arg	Val	Val	Lys	Glu 230	Phe	Gln	Gln	Asn	Gly 235	Tyr	Gln	Val	Val	Gly 240
Leu	Asp	Ala	Gly	Gly 245	Asp	His	Thr	Leu	Asp 250	Thr	Tyr	Asp	Gly	Thr 255	Asp
Asn	Val	Val	Ile 260	Val	Val	Gly	Ser	Glu 265	Gly	Lys	Gly	Ile	Ser 270	Arg	Leu

Val Arg Glu Asn Cys Asp Thr Ile Met Ser Ile Pro Thr Glu Gly Trp
 275 280 285

Val Glu Ser Leu Asn Ala Ser Val Ala Ala Gly Val Val Leu Ser Glu
 290 295 300

Phe Ser Arg Gln Arg Arg Ile Lys Gly
 305 310

<210> 273

<211> 594

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(571)

<223> RXN00460

<400> 273

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ctattattcc acccttttcc aaggccttac aatcaaacac atg ccg gaa cac cca 115
 Met Pro Glu His Pro
 1 5

ctt cac gtt atc ttc gac aat cct gtc atc cct ccc aac acc gga aac 163
 Leu His Val Ile Phe Asp Asn Pro Val Ile Pro Pro Asn Thr Gly Asn
 10 15 20

gcc atc cga atg tgt gca gga aca ggc gct cac ctg cac ctt gtt gaa 211
 Ala Ile Arg Met Cys Ala Gly Thr Gly Ala His Leu His Leu Val Glu
 25 30 35

cct tta ggc ttt gag ctg aca gaa aag cac ctt cgc cga gca ggc ctt 259
 Pro Leu Gly Phe Glu Leu Thr Glu Lys His Leu Arg Arg Ala Gly Leu
 40 45 50

gac tac cac gac tta gcc gat gtc aca gtg cat gca acc ttc gat gaa 307
 Asp Tyr His Asp Leu Ala Asp Val Thr Val His Ala Thr Phe Asp Glu
 55 60 65

gcc atg gct gca gtc cct ggt cgc gta ttt gcc ttc acc aca acg gcc 355
 Ala Met Ala Ala Val Pro Gly Arg Val Phe Ala Phe Thr Thr Thr Ala
 70 75 80 85

aat acc cgc ttc acc gat atc gct ttt gaa cct ggc gat gca ctc ctt 403
 Asn Thr Arg Phe Thr Asp Ile Ala Phe Glu Pro Gly Asp Ala Leu Leu
 90 95 100

ttt gga act gaa cca aca gga ctc cct caa gaa cat gtt gag cat tcc 451
 Phe Gly Thr Glu Pro Thr Gly Leu Pro Gln Glu His Val Glu His Ser
 105 110 115

cga atc acc agt gag ctt cgg atc ccc atg ctt ccc ggt agg cgt tcc 499
 Arg Ile Thr Ser Glu Leu Arg Ile Pro Met Leu Pro Gly Arg Arg Ser
 120 125 130

atg aac ctt tca aat tcc gcg gcg gta gcg acc tat gaa gca tgg cgt 547
 Met Asn Leu Ser Asn Ser Ala Ala Val Ala Thr Tyr Glu Ala Trp Arg

135

140

145

caa ctc gga ttt gtg ggt ggg gtt tagttttttg ctgggcttct ggg
 Gln Leu Gly Phe Val Gly Gly Val
 150 155

594

<210> 274

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

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Pro Asn Thr Gly Asn Ala Ile Arg Met Cys Ala Gly Thr Gly Ala His
 20 25 30

Leu His Leu Val Glu Pro Leu Gly Phe Glu Leu Thr Glu Lys His Leu
 35 40 45

Arg Arg Ala Gly Leu Asp Tyr His Asp Leu Ala Asp Val Thr Val His
 50 55 60

Ala Thr Phe Asp Glu Ala Met Ala Ala Val Pro Gly Arg Val Phe Ala
 65 70 75 80

Phe Thr Thr Thr Ala Asn Thr Arg Phe Thr Asp Ile Ala Phe Glu Pro
 85 90 95

Gly Asp Ala Leu Leu Phe Gly Thr Glu Pro Thr Gly Leu Pro Gln Glu
 100 105 110

His Val Glu His Ser Arg Ile Thr Ser Glu Leu Arg Ile Pro Met Leu
 115 120 125

Pro Gly Arg Arg Ser Met Asn Leu Ser Asn Ser Ala Ala Val Ala Thr
 130 135 140

Tyr Glu Ala Trp Arg Gln Leu Gly Phe Val Gly Gly Val
 145 150 155

<210> 275

<211> 478

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(478)

<223> FRXA00460

<400> 275

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ctattattcc acccttttcc aaggccttac aatcaaacac atg ccg gaa cac cca 115
 Met Pro Glu His Pro
 1 5

ctt cac gtt atc ttc gac aat cct gtc atc cct ccc aac acc gga aac 163
 Leu His Val Ile Phe Asp Asn Pro Val Ile Pro Pro Asn Thr Gly Asn
 10 15 20

gcc atc cga atg tgt gca gga aca ggc gct cac ctg cac ctt gtt gaa 211
 Ala Ile Arg Met Cys Ala Gly Thr Gly Ala His Leu His Leu Val Glu
 25 30 35

cct tta ggc ttt gag ctg aca gaa aag cac ctt cgc cga gca ggc ctt 259
 Pro Leu Gly Phe Glu Leu Thr Glu Lys His Leu Arg Arg Ala Gly Leu
 40 45 50

gac tac cac gac tta gcc gat gtc aca gtg cat gca acc ttc gat gaa 307
 Asp Tyr His Asp Leu Ala Asp Val Thr Val His Ala Thr Phe Asp Glu
 55 60 65

gcc atg gct gca gtc cct ggt cgc gta ttt gcc ttc acc aca acg gcc 355
 Ala Met Ala Ala Val Pro Gly Arg Val Phe Ala Phe Thr Thr Thr Ala
 70 75 80 85

aat acc cgc ttc acc gat atc gct ttt gaa cct ggc gat gca ctc ctt 403
 Asn Thr Arg Phe Thr Asp Ile Ala Phe Glu Pro Gly Asp Ala Leu Leu
 90 95 100

ttt gga act gaa cca aca gga ctc cct caa gaa cat gtt gag cat tcc 451
 Phe Gly Thr Glu Pro Thr Gly Leu Pro Gln Glu His Val Glu His Ser
 105 110 115

cga atc acc agt gag ctt cgg atc cta 478
 Arg Ile Thr Ser Glu Leu Arg Ile Leu
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<210> 276

<211> 126

<212> PRT

<213> Corynebacterium glutamicum

<400> 276

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 20 25 30

Leu His Leu Val Glu Pro Leu Gly Phe Glu Leu Thr Glu Lys His Leu
 35 40 45

Arg Arg Ala Gly Leu Asp Tyr His Asp Leu Ala Asp Val Thr Val His
 50 55 60

Ala Thr Phe Asp Glu Ala Met Ala Ala Val Pro Gly Arg Val Phe Ala
 65 70 75 80

Phe Thr Thr Thr Ala Asn Thr Arg Phe Thr Asp Ile Ala Phe Glu Pro
 85 90 95

Gly Asp Ala Leu Leu Phe Gly Thr Glu Pro Thr Gly Leu Pro Gln Glu
 100 105 110

His Val Glu His Ser Arg Ile Thr Ser Glu Leu Arg Ile Leu

125

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<222> (101)..(928)  
<223> RXA02179
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1 5

aac cat tcc gat tcc cgg cca gac cta ccc ggt ggc aaa ggc ctt gtt 211
 Asn His Ser Asp Ser Arg Pro Asp Leu Pro Gly Gly Lys Gly Leu Val
 25 30 35

gtt gcc gaa ggt ccg ttg gtg gtt ggt cgg ctt ctg gaa tcg cgt tac 259
Val Ala Glu Gly Pro Leu Val Val Gly Arg Leu Leu Glu Ser Arg Tyr
40 45 50

cca gtg cgt gcg atc gtc ggg ttt aaa aac aag ctg gat tct ttc ctc 307
Pro Val Arg Ala Ile Val Gly Phe Lys Asn Lys Leu Asp Ser Phe Leu
55 60 65

gac agc atc gat gca tcc ctt gtt gaa ggc atc cca gtg tat gag gta 355
Asp Ser Ile Asp Ala Ser Leu Val Glu Gly Ile Pro Val Tyr Glu Val
70 75 80 85

tcc	cgc	gag	ctc	ctc	gca	gag	gtc	gca	ggg	ttt	gat	atg	cac	cgc	gga	403
Ser	Arg	Glu	Leu	Leu	Ala	Glu	Val	Ala	Gly	Phe	Asp	Met	His	Arg	Gly	
				90					95					100		

ctt ctg gcg aca gcc gat cgc acc gag gaa gca agt gtt gcg cag gtt 451
 Leu Leu Ala Thr Ala Asp Arg Thr Glu Glu Ala Ser Val Ala Gln Val
 105 110 115

cta gaa aac gcc cgc acc gtg gtg gtg ctg gaa ggc gta ggc gat cac 499
Leu Glu Asn Ala Arg Thr Val Val Val Leu Glu Gly Val Gly Asp His
120 125 130

gaa aac atc gga tcc atg ttc cgc aac gca gca ggc atg ggc gtt gac 547
Glu Asn Ile Gly Ser Met Phe Arg Asn Ala Ala Gly Met Gly Val Asp
135 140 145

gcc atc ttg ttc ggc aac ggt tgt gcc gat cct ttg tat cga cgt gtc 595
Ala Ile Leu Phe Gly Asn Gly Cys Ala Asp Pro Leu Tyr Arg Arg Val
150 155 160 165

gtt cga gtc tca atg ggc cac gtg ctc cgc ctg ccg ttc gca cac ttg 643

Val Arg Val Ser Met Gly His Val Leu Arg Leu Pro Phe Ala His Leu
 170 175 180

gaa ggc acc tac acc acg tgg cag cgc agc tta gag cag ctc aaa gaa 691
 Glu Gly Thr Tyr Thr Thr Trp Gln Arg Ser Leu Glu Gln Leu Lys Glu
 185 190 195

gcc gga ttc cac ctc gtt tca ctc acc cca gat cca gag gcg gaa cac 739
 Ala Gly Phe His Leu Val Ser Leu Thr Pro Asp Pro Glu Ala Glu His
 200 205 210

ctc gaa gat gcg ctc gca ggc aaa gac aaa gtg gct cta ctc gtg ggc 787
 Leu Glu Asp Ala Leu Ala Gly Lys Asp Lys Val Ala Leu Leu Val Gly
 215 220 225

gct gaa ggc cca ggc ctg acc gag cat gcg atg cgc gcc acc gat gtc 835
 Ala Glu Gly Pro Gly Leu Thr Glu His Ala Met Arg Ala Thr Asp Val
 230 235 240 245

cgc gcc cgc atc ccg atg gcg ccg ggt acc gat agc ttg aac ctg gct 883
 Arg Ala Arg Ile Pro Met Ala Pro Gly Thr Asp Ser Leu Asn Leu Ala
 250 255 260

acc tcg gcg gcg att gcg ttt tat gaa cgg gat cgc tca cag cgt 928
 Thr Ser Ala Ala Ile Ala Phe Tyr Glu Arg Asp Arg Ser Gln Arg
 265 270 275

taagtaacag cgctaagtag tag 951

<210> 278

<211> 276

<212> PRT

<213> Corynebacterium glutamicum

<400> 278

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 20 25 30

Gly Lys Gly Leu Val Val Ala Glu Gly Pro Leu Val Val Gly Arg Leu
 35 40 45

Leu Glu Ser Arg Tyr Pro Val Arg Ala Ile Val Gly Phe Lys Asn Lys
 50 55 60

Leu Asp Ser Phe Leu Asp Ser Ile Asp Ala Ser Leu Val Glu Gly Ile
 65 70 75 80

Pro Val Tyr Glu Val Ser Arg Glu Leu Leu Ala Glu Val Ala Gly Phe
 85 90 95

Asp Met His Arg Gly Leu Leu Ala Thr Ala Asp Arg Thr Glu Glu Ala
 100 105 110

Ser Val Ala Gln Val Leu Glu Asn Ala Arg Thr Val Val Val Leu Glu
 115 120 125

Gly Val Gly Asp His Glu Asn Ile Gly Ser Met Phe Arg Asn Ala Ala

130					135					140					
Gly	Met	Gly	Val	Asp	Ala	Ile	Leu	Phe	Gly	Asn	Gly	Cys	Ala	Asp	Pro
145					150					155					160
Leu	Tyr	Arg	Arg	Val	Val	Arg	Val	Ser	Met	Gly	His	Val	Leu	Arg	Leu
				165					170					175	
Pro	Phe	Ala	His	Leu	Glu	Gly	Thr	Tyr	Thr	Thr	Trp	Gln	Arg	Ser	Leu
			180					185					190		
Glu	Gln	Leu	Lys	Glu	Ala	Gly	Phe	His	Leu	Val	Ser	Leu	Thr	Pro	Asp
		195					200					205			
Pro	Glu	Ala	Glu	His	Leu	Glu	Asp	Ala	Leu	Ala	Gly	Lys	Asp	Lys	Val
	210					215					220				
Ala	Leu	Leu	Val	Gly	Ala	Glu	Gly	Pro	Gly	Leu	Thr	Glu	His	Ala	Met
225					230					235					240
Arg	Ala	Thr	Asp	Val	Arg	Ala	Arg	Ile	Pro	Met	Ala	Pro	Gly	Thr	Asp
				245					250					255	
Ser	Leu	Asn	Leu	Ala	Thr	Ser	Ala	Ala	Ile	Ala	Phe	Tyr	Glu	Arg	Asp
			260					265					270		
Arg	Ser	Gln	Arg												
			275												

<210> 279

<211> 666

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(643)

<223> RXA02522

<400> 279

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				Met	Trp	Ala	Arg	Asp		
				1				5		

ata	aac	ttt	cta	tac	atg	agt	aca	gag	cag	gaa	ctg	caa	atc	gga	aaa	163
Ile	Asn	Phe	Leu	Tyr	Met	Ser	Thr	Glu	Gln	Glu	Leu	Gln	Ile	Gly	Lys	
			10						15					20		

gtt	gta	aaa	tcc	cac	ggc	att	cgg	ggt	gaa	gtc	gtg	gtg	gaa	ttg	agc	211
Val	Val	Lys	Ser	His	Gly	Ile	Arg	Gly	Glu	Val	Val	Val	Glu	Leu	Ser	
			25					30					35			

acc	gat	gat	cca	gac	att	cgc	ttc	gcc	att	ggg	gaa	gtt	ctc	aac	ggc	259
Thr	Asp	Asp	Pro	Asp	Ile	Arg	Phe	Ala	Ile	Gly	Glu	Val	Leu	Asn	Gly	
			40					45					50			

aag	cag	gca	ggc	aag	gag	cat	tca	ctg	acc	atc	gat	gca	gcg	cgc	atg	307
Lys	Gln	Ala	Gly	Lys	Glu	His	Ser	Leu	Thr	Ile	Asp	Ala	Ala	Arg	Met	

55	60	65	
cac caa ggt cga ctc ttg gtg aag ttc gca gag gtc cca gat cgt acc			355
His Gln Gly Arg Leu Leu Val Lys Phe Ala Glu Val Pro Asp Arg Thr			
70	75	80	85
gct gct gat tct ttg cgt gga act cga ttc ttt gcg gca cct ctt gag			403
Ala Ala Asp Ser Leu Arg Gly Thr Arg Phe Phe Ala Ala Pro Leu Glu			
90	95		100
gat gaa gac gat gag gat ggc ttc tac gac cat gag ttg gaa ggt ctg			451
Asp Glu Asp Asp Glu Asp Gly Phe Tyr Asp His Glu Leu Glu Gly Leu			
105	110		115
cgc gtc att cac gag ggc gag gat atc ggt gaa gtc acc ggc gtg atg			499
Arg Val Ile His Glu Gly Glu Asp Ile Gly Glu Val Thr Gly Val Met			
120	125		130
cat ggc cca gcc ggt gag atc ctg gaa gtc cgc ctg acc tca ggc aag			547
His Gly Pro Ala Gly Glu Ile Leu Glu Val Arg Leu Thr Ser Gly Lys			
135	140		145
gaa aca ctg att cct ttt gtg cac gcc att gtt cct gag gtg gat ctg			595
Glu Thr Leu Ile Pro Phe Val His Ala Ile Val Pro Glu Val Asp Leu			
150	155	160	165
gaa gaa gga acc gca acg atc acc cct cca gag ggc ttg tta gat ctt			643
Glu Glu Gly Thr Ala Thr Ile Thr Pro Pro Glu Gly Leu Leu Asp Leu			
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Leu Gln Ile Gly Lys Val Val Lys Ser His Gly Ile Arg Gly Glu Val			
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Val Val Glu Leu Ser Thr Asp Asp Pro Asp Ile Arg Phe Ala Ile Gly			
35	40		45
Glu Val Leu Asn Gly Lys Gln Ala Gly Lys Glu His Ser Leu Thr Ile			
50	55	60	
Asp Ala Ala Arg Met His Gln Gly Arg Leu Leu Val Lys Phe Ala Glu			
65	70	75	80
Val Pro Asp Arg Thr Ala Ala Asp Ser Leu Arg Gly Thr Arg Phe Phe			
85	90		95
Ala Ala Pro Leu Glu Asp Glu Asp Asp Glu Asp Gly Phe Tyr Asp His			
100	105		110
Glu Leu Glu Gly Leu Arg Val Ile His Glu Gly Glu Asp Ile Gly Glu			

115		120		125
Val Thr Gly Val Met His Gly Pro Ala Gly Glu Ile Leu Glu Val Arg				
130		135		140
Leu Thr Ser Gly Lys Glu Thr Leu Ile Pro Phe Val His Ala Ile Val				
145		150		155
				160
Pro Glu Val Asp Leu Glu Glu Gly Thr Ala Thr Ile Thr Pro Pro Glu				
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Gly Leu Leu Asp Leu				
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<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1060)

<223> RXA00717

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	Val Thr Pro Pro Ala	
	1 5	

cgc cga gat ggc aca ccg gac aag aag cag agc aat cgc tct ggc gga	163
Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser Asn Arg Ser Gly Gly	
10 15 20	

tac cgg tct tca gtt cgt ggc tac aag cca gga tca tcc cgc cca aac	211
Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly Ser Ser Arg Pro Asn	
25 30 35	

aca cgc cag cag cct cag aag aag gat gag att ctt ctc tcc aac gct	259
Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile Leu Leu Ser Asn Ala	
40 45 50	

aag cct gcc aag aag caa aac gta aaa tcc gac gac gat tgg tgg atg	307
Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp Asp Asp Trp Ser Met	
55 60 65	

ggg ttc tta aac cgc aat gac tct gac gga gtt cgc ctg cag aag gtc	355
Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val Arg Leu Gln Lys Val	
70 75 80 85	

ctt gcc caa gca ggt gtg gca tca cgt cga cac gca gaa atc ctg att	403
Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His Ala Glu Ile Leu Ile	
90 95 100	

gat cag ggc cgt gtg gag gtc aac gat cgt atc gtg acc acc cag ggc	451
Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile Val Thr Thr Gln Gly	
105 110 115	

gtg cgc gtg. gat cca aac aac gat gtc atc cgt gtt gac ggc gtc cgc	499
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Val	Arg	Val	Asp	Pro	Asn	Asn	Asp	Val	Ile	Arg	Val	Asp	Gly	Val	Arg		
		120					125					130					
atc	cac	atc	aac	gag	gac	ctc	gag	tac	ttc	gtg	ctc	aac	aag	cct	cgt	547	
Ile	His	Ile	Asn	Glu	Asp	Leu	Glu	Tyr	Phe	Val	Leu	Asn	Lys	Pro	Arg		
	135					140					145						
ggc	atg	cac	tcc	acc	atg	agc	gat	gaa	ctt	ggc	cgc	cca	tgc	gtg	ggc	595	
Gly	Met	His	Ser	Thr	Met	Ser	Asp	Glu	Leu	Gly	Arg	Pro	Cys	Val	Gly		
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gat	ctg	gtc	agt	gag	aag	act	gca	tct	gga	cag	cgt	ctg	ttc	cac	gtc	643	
Asp	Leu	Val	Ser	Glu	Lys	Thr	Ala	Ser	Gly	Gln	Arg	Leu	Phe	His	Val		
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ggc	cgc	ctc	gac	gag	gac	acc	gaa	ggc	ttg	ctg	ctg	ctc	acc	aac	gat	691	
Gly	Arg	Leu	Asp	Ala	Asp	Thr	Glu	Gly	Leu	Leu	Leu	Leu	Leu	Thr	Asn	Asp	
		185					190						195				
ggc	gag	ttg	gct	aac	cgc	ctc	atg	cac	cct	aag	tac	gaa	gtg	tcc	aag	739	
Gly	Glu	Leu	Ala	Asn	Arg	Leu	Met	His	Pro	Lys	Tyr	Glu	Val	Ser	Lys		
	200					205						210					
act	tac	ctt	gct	acc	gtt	cgc	ggc	gaa	gca	acc	aac	aag	cta	gtc	agc	787	
Thr	Tyr	Leu	Ala	Thr	Val	Arg	Gly	Glu	Ala	Thr	Asn	Lys	Leu	Val	Ser		
	215					220					225						
gct	ctt	cgt	gat	ggc	gtg	gag	ttg	gaa	gat	ggc	cct	gcc	aag	gct	gac	835	
Ala	Leu	Arg	Asp	Gly	Val	Glu	Leu	Glu	Asp	Gly	Pro	Ala	Lys	Ala	Asp		
230					235					240				245			
ttt	gag	cag	att	atc	gac	gta	ttc	cag	ggc	aag	tcc	ttg	ttg	cgc	atc	883	
Phe	Ala	Gln	Ile	Ile	Asp	Val	Phe	Gln	Gly	Lys	Ser	Leu	Leu	Arg	Ile		
				250				255						260			
gaa	atc	cac	gaa	ggc	cgc	aag	cac	att	gtg	cga	cgc	ctc	ttc	gat	gag	931	
Glu	Ile	His	Glu	Gly	Arg	Lys	His	Ile	Val	Arg	Arg	Leu	Phe	Asp	Glu		
		265						270					275				
ctc	ggc	ttc	cca	gtc	gag	cgc	ctc	gtg	cgc	acc	aag	ctg	cac	acc	gtt	979	
Leu	Gly	Phe	Pro	Val	Glu	Arg	Leu	Val	Arg	Thr	Lys	Leu	His	Thr	Val		
		280				285						290					
cag	ctt	ggc	gat	cag	aag	cca	ggc	tcc	ctt	cgt	gca	ctg	aac	tcc	tct	1027	
Gln	Leu	Gly	Asp	Gln	Lys	Pro	Gly	Ser	Leu	Arg	Ala	Leu	Asn	Ser	Ser		
	295					300					305						
gag	ctg	acc	agc	tta	tac	aag	gtg	gtc	caa	ctg	tgacg	gaaat	ttcca	acatg	1080		
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cct																1083	

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<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

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Ser Ser Arg Pro 35	Asn Thr Arg Gln 40	Gln Pro Gln Lys 45	Lys Asp Glu Ile
Leu Leu Ser Asn 50	Ala Lys Pro Ala 55	Lys Lys Gln Asn 60	Val Lys Ser Asp
Asp Asp Trp Ser 65	Met Gly Phe Leu 70	Asn Arg Asn Asp 75	Ser Asp Gly Val 80
Arg Leu Gln Lys 85	Val Leu Ala Gln 90	Ala Gly Val Ala 95	Ser Arg Arg His
Ala Glu Ile Leu 100	Ile Asp Gln Gly 105	Arg Val Glu Val 110	Asn Asp Arg Ile
Val Thr Thr Gln 115	Gly Val Arg Val 120	Asp Pro Asn Asn 125	Asp Val Ile Arg
Val Asp Gly Val 130	Arg Ile His Ile 135	Asn Glu Asp Leu 140	Glu Tyr Phe Val
Leu Asn Lys Pro 145	Arg Gly Met His 150	Ser Thr Met Ser 155	Asp Glu Leu Gly 160
Arg Pro Cys Val 165	Gly Asp Leu Val 170	Ser Glu Lys Thr 175	Ala Ser Gly Gln
Arg Leu Phe His 180	Val Gly Arg Leu 185	Ala Asp Thr Glu 190	Gly Leu Leu
Leu Leu Thr Asn 195	Asp Gly Glu Leu 200	Ala Asn Arg Leu 205	Met His Pro Lys
Tyr Glu Val Ser 210	Lys Thr Tyr Leu 215	Ala Thr Val Arg 220	Gly Glu Ala Thr
Asn Lys Leu Val 225	Ser Ala Leu Arg 230	Asp Gly Val Glu 235	Leu Glu Asp Gly 240
Pro Ala Lys Ala 245	Asp Phe Ala Gln 250	Ile Ile Asp Val 255	Phe Gln Gly Lys
Ser Leu Leu Arg 260	Ile Glu Ile His 265	Glu Gly Arg Lys 270	His Ile Val Arg
Arg Leu Phe Asp 275	Glu Leu Gly Phe 280	Pro Val Glu Arg 285	Leu Val Arg Thr
Lys Leu His Thr 290	Val Gln Leu Gly 295	Asp Gln Lys Pro 300	Gly Ser Leu Arg
Ala Leu Asn Ser 305	Ser Glu Leu Thr 310	Ser Leu Tyr Lys 315	Val Val Gln Leu 320

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 <222> (101)..(736)
 <223> RXA02615

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 Met Gln Phe Ala Gln
 1 5
 aac ccg cgt ctg acg aac gac gcg gtg atc tta gaa cca ctg tca cat 163
 Asn Pro Arg Leu Thr Asn Asp Ala Val Ile Leu Glu Pro Leu Ser His
 10 15 20
 cag tgg act cag gat ctc cag gaa gct gtc gcc tca caa gaa ttg tgg 211
 Gln Trp Thr Gln Asp Leu Gln Glu Ala Val Ala Ser Gln Glu Leu Trp
 25 30 35
 cgc cat tgg ttc gtc gct cta ccc acc cca gag ggc atg gcg gag gaa 259
 Arg His Trp Phe Val Ala Leu Pro Thr Pro Glu Gly Met Ala Glu Glu
 40 45 50
 att gac cgc cgc cta gcc gaa cat gca gac gga ctg tgt gcg cct tgg 307
 Ile Asp Arg Arg Leu Ala Glu His Ala Asp Gly Leu Cys Ala Pro Trp
 55 60 65
 gca atc att tcc gct gca aca ggc cgt gcc gtt ggc atg acc tca ttt 355
 Ala Ile Ile Ser Ala Ala Thr Gly Arg Ala Val Gly Met Thr Ser Phe
 70 75 80 85
 cat acc ctt gac cac gcg aat aaa cgg ctg gaa att gga cgc aca tgg 403
 His Thr Leu Asp His Ala Asn Lys Arg Leu Glu Ile Gly Arg Thr Trp
 90 95 100
 atg gct gcc cat gtc caa gga acc ggc atc aac ccc tcg gtg aaa ttc 451
 Met Ala Ala His Val Gln Gly Thr Gly Ile Asn Pro Ser Val Lys Phe
 105 110 115
 ctg cag ttg cag cgc gct ttt gaa gac ctc ggt gtc aat gcc gtg gaa 499
 Leu Gln Leu Gln Arg Ala Phe Glu Asp Leu Gly Val Asn Ala Val Glu
 120 125 130
 ttc cga acg aac tgg cac aac cac cgc tcc cgc gcc gca atc gaa cga 547
 Phe Arg Thr Asn Trp His Asn His Arg Ser Arg Ala Ala Ile Glu Arg
 135 140 145
 ctc gga gca aaa caa gac ggc gta cta cgc aaa cat cgc atc cac cct 595
 Leu Gly Ala Lys Gln Asp Gly Val Leu Arg Lys His Arg Ile His Pro
 150 155 160 165
 gac ggc acc gtc cgc gac acc gtc atc tat tcc atc acc aac gat gaa 643
 Asp Gly Thr Val Arg Asp Thr Val Ile Tyr Ser Ile Thr Asn Asp Glu

170	175	180	
tgg cct gcc gtc aaa ctg acg ctc atg gag cga ctg tac cgt cac atg			691
Trp Pro Ala Val Lys Leu Thr Leu Met Glu Arg Leu Tyr Arg His Met			
185	190	195	
cag gtt ccc atc att ccc aac gag gca tcg ctt ttc gac gcc agc			736
Gln Val Pro Ile Ile Pro Asn Glu Ala Ser Leu Phe Asp Ala Ser			
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<211> 212

<212> PRT

<213> Corynebacterium glutamicum

<400> 284

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Glu Pro Leu Ser His Gln Trp Thr Gln Asp Leu Gln Glu Ala Val Ala		
20	25	30
Ser Gln Glu Leu Trp Arg His Trp Phe Val Ala Leu Pro Thr Pro Glu		
35	40	45
Gly Met Ala Glu Glu Ile Asp Arg Arg Leu Ala Glu His Ala Asp Gly		
50	55	60
Leu Cys Ala Pro Trp Ala Ile Ile Ser Ala Ala Thr Gly Arg Ala Val		
65	70	75 80
Gly Met Thr Ser Phe His Thr Leu Asp His Ala Asn Lys Arg Leu Glu		
85	90	95
Ile Gly Arg Thr Trp Met Ala Ala His Val Gln Gly Thr Gly Ile Asn		
100	105	110
Pro Ser Val Lys Phe Leu Gln Leu Gln Arg Ala Phe Glu Asp Leu Gly		
115	120	125
Val Asn Ala Val Glu Phe Arg Thr Asn Trp His Asn His Arg Ser Arg		
130	135	140
Ala Ala Ile Glu Arg Leu Gly Ala Lys Gln Asp Gly Val Leu Arg Lys		
145	150	155 160
His Arg Ile His Pro Asp Gly Thr Val Arg Asp Thr Val Ile Tyr Ser		
165	170	175
Ile Thr Asn Asp Glu Trp Pro Ala Val Lys Leu Thr Leu Met Glu Arg		
180	185	190
Leu Tyr Arg His Met Gln Val Pro Ile Ile Pro Asn Glu Ala Ser Leu		
195	200	205
Phe Asp Ala Ser		
210		

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<222> (101) .. (808)
<223> RXN01343
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				Met	Ser	Lys	Asn	Ser									5
				1													
aag	gcg	tac	cgc	gag	gcc	gct	gag	aag	atc	gac	gct	ggc	cgc	atc	tac		163
Lys	Ala	Tyr	Arg	Glu	Ala	Ala	Glu	Lys	Ile	Asp	Ala	Gly	Arg	Ile	Tyr		
				10					15					20			
tcc	cca	ctc	gag	gct	gca	aac	ctg	gtc	aag	gag	acc	tcc	tcc	aag	aac		211
Ser	Pro	Leu	Glu	Ala	Ala	Asn	Leu	Val	Lys	Glu	Thr	Ser	Ser	Lys	Asn		
			25					30					35				
tac	gac	gct	tcc	atc	gac	gta	gct	atc	cgc	ctg	ggc	gtt	gac	cca	cgt		259
Tyr	Asp	Ala	Ser	Ile	Asp	Val	Ala	Ile	Arg	Leu	Gly	Val	Asp	Pro	Arg		
		40					45					50					
aag	gct	gat	cag	ctt	gtt	cgt	ggc	acc	gtc	tcc	ctg	cct	aac	ggc	acc		307
Lys	Ala	Asp	Gln	Leu	Val	Arg	Gly	Thr	Val	Ser	Leu	Pro	Asn	Gly	Thr		
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ggc	aag	acc	gtt	cgc	gtt	gct	gtg	ttc	gca	cag	ggc	gag	aag	gct	act		355
Gly	Lys	Thr	Val	Arg	Val	Ala	Val	Phe	Ala	Gln	Gly	Glu	Lys	Ala	Thr		
70					75					80					85		
gag	gct	gag	gct	gct	ggc	gct	gac	ttc	gtt	ggc	acc	gac	gag	ctc	gtt		403
Glu	Ala	Glu	Ala	Ala	Gly	Ala	Asp	Phe	Val	Gly	Thr	Asp	Glu	Leu	Val		
			90					95						100			
gag	aag	atc	cag	ggc	ggc	tgg	acc	gac	ttc	gac	gtt	gct	att	gca	acc		451
Glu	Lys	Ile	Gln	Gly	Gly	Trp	Thr	Asp	Phe	Asp	Val	Ala	Ile	Ala	Thr		
			105					110					115				
cct	gat	cag	atg	gct	aag	atc	ggc	cgt	atc	gct	cgt	gtc	ttg	ggc	cca		499
Pro	Asp	Gln	Met	Ala	Lys	Ile	Gly	Arg	Ile	Ala	Arg	Val	Leu	Gly	Pro		
		120					125					130					
cgt	ggc	ctg	atg	cct	aac	cct	aag	acc	ggc	acc	gtc	acc	aac	gat	gtc		547
Arg	Gly	Leu	Met	Pro	Asn	Pro	Lys	Thr	Gly	Thr	Val	Thr	Asn	Asp	Val		
	135					140					145						
gct	aag	gct	atc	gaa	gag	gtc	aag	ggc	ggc	aag	att	tcc	ttc	cgc	gtt		595
Ala	Lys	Ala	Ile	Glu	Glu	Val	Lys	Gly	Gly	Lys	Ile	Ser	Phe	Arg	Val		

gcg aag aag ctg gct gag aac tac ggc gct ctc ctc gac gag atc atc 691
 Ala Lys Lys Leu Ala Glu Asn Tyr Gly Ala Leu Leu Asp Glu Ile Ile
 185 190 195

cgt atc aag cct tct tcc gct aag ggc atc tac gtc aag cgc gtg acc 739
 Arg Ile Lys Pro Ser Ser Ala Lys Gly Ile Tyr Val Lys Arg Val Thr
 200 205 210

ctg tct tcc acc acc ggt cct ggt gtt gag gtt gac act cac gtc acc 787
 Leu Ser Ser Thr Thr Gly Pro Gly Val Glu Val Asp Thr His Val Thr
 215 220 225

aag aac tac gca gaa gag gca taagccttcc cagcgtaac tct 831
 Lys Asn Tyr Ala Glu Glu Ala
 230 235

<210> 286

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 286

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 20 25 30

Thr Ser Ser Lys Asn Tyr Asp Ala Ser Ile Asp Val Ala Ile Arg Leu
 35 40 45

Gly Val Asp Pro Arg Lys Ala Asp Gln Leu Val Arg Gly Thr Val Ser
 50 55 60

Leu Pro Asn Gly Thr Gly Lys Thr Val Arg Val Ala Val Phe Ala Gln
 65 70 75 80

Gly Glu Lys Ala Thr Glu Ala Glu Ala Ala Gly Ala Asp Phe Val Gly
 85 90 95

Thr Asp Glu Leu Val Glu Lys Ile Gln Gly Gly Trp Thr Asp Phe Asp
 100 105 110

Val Ala Ile Ala Thr Pro Asp Gln Met Ala Lys Ile Gly Arg Ile Ala
 115 120 125

Arg Val Leu Gly Pro Arg Gly Leu Met Pro Asn Pro Lys Thr Gly Thr
 130 135 140

Val Thr Asn Asp Val Ala Lys Ala Ile Glu Glu Val Lys Gly Gly Lys
 145 150 155 160

Ile Ser Phe Arg Val Asp Lys Ala Ser Asn Leu His Ala Ala Ile Gly
 165 170 175

Lys Ala Ser Phe Asp Ala Lys Lys Leu Ala Glu Asn Tyr Gly Ala Leu
 180 185 190

Leu Asp Glu Ile Ile Arg Ile Lys Pro Ser Ser Ala Lys Gly Ile Tyr

195					200					205						
Val	Lys	Arg	Val	Thr	Leu	Ser	Ser	Thr	Thr	Gly	Pro	Gly	Val	Glu	Val	
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Asp	Thr	His	Val	Thr	Lys	Asn	Tyr	Ala	Glu	Glu	Ala					
225					230					235						
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Ile	Tyr	Ser	Pro	Leu	Glu	Ala	Ala	Asn	Leu	Val	Lys	Glu	Thr	Ser	Ser	
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Lys	Asn	Tyr	Asp	Ala	Ser	Ile	Asp	Val	Ala	Ile	Arg	Leu	Gly	Val	Asp	
			20				25					30				
cca	cgt	aag	gct	gat	cag	ctt	gtt	cgt	ggc	acc	gtc	tcc	ctg	cct	aac	144
Pro	Arg	Lys	Ala	Asp	Gln	Leu	Val	Arg	Gly	Thr	Val	Ser	Leu	Pro	Asn	
		35				40						45				
ggc	acc	ggt	aag	acc	gtt	cgc	gtt	gct	gtg	ttc	gca	cag	ggc	gag	aag	192
Gly	Thr	Gly	Lys	Thr	Val	Arg	Val	Ala	Val	Phe	Ala	Gln	Gly	Glu	Lys	
	50					55					60					
gct	act	gag	gct	gag	gct	gct	ggc	gct	gac	ttc	gtt	ggc	acc	gac	gag	240
Ala	Thr	Glu	Ala	Glu	Ala	Ala	Gly	Ala	Asp	Phe	Val	Gly	Thr	Asp	Glu	
65				70					75						80	
ctc	gtt	gag	aag	atc	cag	ggt	ggc	tgg	acc	gac	ttc	gac	gtt	gct	att	288
Leu	Val	Glu	Lys	Ile	Gln	Gly	Gly	Trp	Thr	Asp	Phe	Asp	Val	Ala	Ile	
			85					90					95			
gca	acc	cct	gat	cag	atg	gct	aag	atc	ggc	cgt	atc	gct	cgt	gtc	ttg	336
Ala	Thr	Pro	Asp	Gln	Met	Ala	Lys	Ile	Gly	Arg	Ile	Ala	Arg	Val	Leu	
			100					105					110			
ggc	cca	cgt	ggt	ctg	atg	cct	aac	cct	aag	acc	ggc	acc	gtc	acc	aac	384
Gly	Pro	Arg	Gly	Leu	Met	Pro	Asn	Pro	Lys	Thr	Gly	Thr	Val	Thr	Asn	
		115					120					125				
gat	gtc	gct	aag	gct	atc	gaa	gag	gtc	aag	ggc	ggc	aag	att	tcc	ttc	432
Asp	Val	Ala	Lys	Ala	Ile	Glu	Glu	Val	Lys	Gly	Gly	Lys	Ile	Ser	Phe	
	130			135							140					
cgc	gtt	gac	aag	gct	tcc	aac	ctg	cac	gct	gca	att	ggt	aag	gct	tcc	480
Arg	Val	Asp	Lys	Ala	Ser	Asn	Leu	His	Ala	Ala	Ile	Gly	Lys	Ala	Ser	
145				150					155						160	
ttc	gat	gcg	aag	aag	ctg	gct	gag	aac	tac	ggc	gct	ctc	ctc	gac	gag	528

Phe Asp Ala Lys Lys Leu Ala Glu Asn Tyr Gly Ala Leu Leu Asp Glu
 165 170 175
 atc atc cgt atc aag cct tct tcc gct aag ggc atc tac gtc aag cgc 576
 Ile Ile Arg Ile Lys Pro Ser Ser Ala Lys Gly Ile Tyr Val Lys Arg
 180 185 190
 gtg acc ctg tct tcc acc acc ggt cct ggt gtt gag gtt gac act cac 624
 Val Thr Leu Ser Ser Thr Thr Gly Pro Gly Val Glu Val Asp Thr His
 195 200 205
 gtc acc aag aac tac gca gaa gag gca taagccttcc cacgcgtaac 671
 Val Thr Lys Asn Tyr Ala Glu Glu Ala
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 tct 674

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<213> Corynebacterium glutamicum

<400> 288

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Lys Asn Tyr Asp Ala Ser Ile Asp Val Ala Ile Arg Leu Gly Val Asp
 20 25 30

Pro Arg Lys Ala Asp Gln Leu Val Arg Gly Thr Val Ser Leu Pro Asn
 35 40 45

Gly Thr Gly Lys Thr Val Arg Val Ala Val Phe Ala Gln Gly Glu Lys
 50 55 60

Ala Thr Glu Ala Glu Ala Ala Gly Ala Asp Phe Val Gly Thr Asp Glu
 65 70 75 80

Leu Val Glu Lys Ile Gln Gly Gly Trp Thr Asp Phe Asp Val Ala Ile
 85 90 95

Ala Thr Pro Asp Gln Met Ala Lys Ile Gly Arg Ile Ala Arg Val Leu
 100 105 110

Gly Pro Arg Gly Leu Met Pro Asn Pro Lys Thr Gly Thr Val Thr Asn
 115 120 125

Asp Val Ala Lys Ala Ile Glu Glu Val Lys Gly Gly Lys Ile Ser Phe
 130 135 140

Arg Val Asp Lys Ala Ser Asn Leu His Ala Ala Ile Gly Lys Ala Ser
 145 150 155 160

Phe Asp Ala Lys Lys Leu Ala Glu Asn Tyr Gly Ala Leu Leu Asp Glu
 165 170 175

Ile Ile Arg Ile Lys Pro Ser Ser Ala Lys Gly Ile Tyr Val Lys Arg
 180 185 190

Val Thr Leu Ser Ser Thr Thr Gly Pro Gly Val Glu Val Asp Thr His

195

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205

Val Thr Lys Asn Tyr Ala Glu Glu Ala
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<223> RXA01951

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cacatcgagt acgacccaaa ccgtaccgct aacattgcac ttg ctt cac tac ttc 115
Leu Leu His Tyr Phe
1 5

gat ggc gag aag cgt tac atc ctc gca ccg aag ggc ctg acc cag ggc 163
Asp Gly Glu Lys Arg Tyr Ile Leu Ala Pro Lys Gly Leu Thr Gln Gly
10 15 20

acc gtt atc gag tcc ggc gct gca gcc gac atc aag gtt ggt aac aac 211
Thr Val Ile Glu Ser Gly Ala Ala Ala Asp Ile Lys Val Gly Asn Asn
25 30 35

ctg cca ctg cgt aac atc ccg act ggt acc acc atc cac aac gtg gag 259
Leu Pro Leu Arg Asn Ile Pro Thr Gly Thr Thr Ile His Asn Val Glu
40 45 50

ttg aag cca ggc gca ggt gca aag ctg gca cgt tcc gct gga gct tcc 307
Leu Lys Pro Gly Ala Gly Ala Lys Leu Ala Arg Ser Ala Gly Ala Ser
55 60 65

atc cag ctt ctt ggt aag gaa ggc tcc tac gca gtt ctg cgt atg cca 355
Ile Gln Leu Leu Gly Lys Glu Gly Ser Tyr Ala Val Leu Arg Met Pro
70 75 80 85

tcc tcc gag atc cga cgc gta aac atc cgc tgc cgc gcg act gtt ggt 403
Ser Ser Glu Ile Arg Arg Val Asn Ile Arg Cys Arg Ala Thr Val Gly
90 95 100

gag gtc ggc aac gcc gag cag atc aac att cgt tgg ggt aaa gct ggt 451
Glu Val Gly Asn Ala Glu Gln Ile Asn Ile Arg Trp Gly Lys Ala Gly
105 110 115

cgt atg cgt tgg aag ggc tgg cgc cca acc gtc cgt ggt gtc gtt atg 499
Arg Met Arg Trp Lys Gly Trp Arg Pro Thr Val Arg Gly Val Val Met
120 125 130

aac ccg gtc gac cac cca cac ggt ggt ggt gaa ggt aag act tct ggt 547
Asn Pro Val Asp His Pro His Gly Gly Gly Glu Gly Lys Thr Ser Gly
135 140 145

ggt cgc cac cca gtc tcc cca tgg gga cag aag gaa ggc cgc acc cgc 595
Gly Arg His Pro Val Ser Pro Trp Gly Gln Lys Glu Gly Arg Thr Arg

aac aag aac aag aag cgt taagaggagg taacggtgaa tgt 684
Asn Lys Asn Lys Lys Arg
185

<400> 290															
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Lys	Val	Gly 35	Asn	Asn	Leu	Pro	Leu 40	Arg	Asn	Ile	Pro	Thr 45	Gly	Thr	Thr
Ile	His 50	Asn	Val	Glu	Leu	Lys 55	Pro	Gly	Ala	Gly	Ala 60	Lys	Leu	Ala	Arg
Ser 65	Ala	Gly	Ala	Ser	Ile 70	Gln	Leu	Leu	Gly	Lys 75	Glu	Gly	Ser	Tyr	Ala 80
Val	Leu	Arg	Met	Pro 85	Ser	Ser	Glu	Ile	Arg 90	Arg	Val	Asn	Ile	Arg 95	Cys
Arg	Ala	Thr	Val 100	Gly	Glu	Val	Gly	Asn 105	Ala	Glu	Gln	Ile	Asn 110	Ile	Arg
Trp	Gly	Lys 115	Ala	Gly	Arg	Met	Arg 120	Trp	Lys	Gly	Trp	Arg 125	Pro	Thr	Val
Arg 130	Gly	Val	Val	Met	Asn 135	Pro	Val	Asp	His	Pro	His 140	Gly	Gly	Gly	Glu
Gly 145	Lys	Thr	Ser	Gly	Gly 150	Arg	His	Pro	Val	Ser 155	Pro	Trp	Gly	Gln	Lys 160
Glu	Gly	Arg	Thr	Arg 165	Lys	Pro	Lys	Arg	Tyr 170	Ser	Asp	Asp	Met	Ile 175	Val
Arg	Arg	Arg	Arg 180	Ala	Asn	Lys	Asn 185	Lys	Lys	Arg					

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cggctccgtc gcttaagacg tcgatagaaa aggacacatt atg gct att cgt aag 115
 Met Ala Ile Arg Lys
 1 5

tac aag ccg aca acc ccg ggt cgc cgc gca agc tcc gtt tcc atg ttc 163
 Tyr Lys Pro Thr Thr Pro Gly Arg Arg Ala Ser Ser Val Ser Met Phe
 10 15 20

acg gag atc acc cgt tcg acc cct gag aag tca ctt ctc cgc cca ctg 211
 Thr Glu Ile Thr Arg Ser Thr Pro Glu Lys Ser Leu Leu Arg Pro Leu
 25 30 35

agc aag acc ggc gga cgt aac tct cac ggc cac atc acc acc cgt cac 259
 Ser Lys Thr Gly Gly Arg Asn Ser His Gly His Ile Thr Thr Arg His
 40 45 50

cgc ggt ggt gga cac aag cgc cgc tac cgc gtc atc gac ttc cgt cgt 307
 Arg Gly Gly Gly His Lys Arg Arg Tyr Arg Val Ile Asp Phe Arg Arg
 55 60 65

aac gac aag gat ggc gta ttg gca aag gtc gct cac atc gag tac gac 355
 Asn Asp Lys Asp Gly Val Leu Ala Lys Val Ala His Ile Glu Tyr Asp
 70 75 80 85

cca aac cgt acc gct aac att gca ctt gct tca cta ctt cga tgg cga 403
 Pro Asn Arg Thr Ala Asn Ile Ala Leu Ala Ser Leu Leu Arg Trp Arg
 90 95 100

gaa gcg tta cat cct cgc acc gaa ggg cct gac cca ggg cac cgt tat 451
 Glu Ala Leu His Pro Arg Thr Glu Gly Pro Asp Pro Gly His Arg Tyr
 105 110 115

cga gtc cgg cgc tgc agc cga cat caa ggt tgg taacaacctg ccaactgcgta 504
 Arg Val Arg Arg Cys Ser Arg His Gln Gly Trp
 120 125

aca 507

<210> 292

<211> 128

<212> PRT

<213> Corynebacterium glutamicum

<400> 292

Met Ala Ile Arg Lys Tyr Lys Pro Thr Thr Pro Gly Arg Arg Ala Ser
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Ser Val Ser Met Phe Thr Glu Ile Thr Arg Ser Thr Pro Glu Lys Ser
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Leu Leu Arg Pro Leu Ser Lys Thr Gly Gly Arg Asn Ser His Gly His
 35 40 45

Ile Thr Thr Arg His Arg Gly Gly Gly His Lys Arg Arg Tyr Arg Val

50	55	60
Ile Asp Phe Arg Arg Asn Asp Lys Asp Gly Val Leu Ala Lys Val Ala		
65	70	75 80
His Ile Glu Tyr Asp Pro Asn Arg Thr Ala Asn Ile Ala Leu Ala Ser		
	85	90 95
Leu Leu Arg Trp Arg Glu Ala Leu His Pro Arg Thr Glu Gly Pro Asp		
	100	105 110
Pro Gly His Arg Tyr Arg Val Arg Arg Cys Ser Arg His Gln Gly Trp		
	115	120 125

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<211> 777

<212> DNA

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ttcagtgatc gacggaattt ttggcagcgg agaataaata atg agt gaa aac gag	115
Met Ser Glu Asn Glu	
1 5	

atc aag ggc att ctg ggc acc aag ctc ggc atg act cag atc ttc gac	163
Ile Lys Gly Ile Leu Gly Thr Lys Leu Gly Met Thr Gln Ile Phe Asp	
10 15 20	

gag gag aac cgc gtt att ccg gtt acc gtc gtt gaa gcg ggt cca tgc	211
Glu Glu Asn Arg Val Ile Pro Val Thr Val Val Glu Ala Gly Pro Cys	
25 30 35	

gta gtt tcc cag att cgc acc gtt gag acc gat ggc tac aac gcc atc	259
Val Val Ser Gln Ile Arg Thr Val Glu Thr Asp Gly Tyr Asn Ala Ile	
40 45 50	

cag atc gcc tac ggc gaa atc gac cca cgc aag gtg aac cag cca ttg	307
Gln Ile Ala Tyr Gly Glu Ile Asp Pro Arg Lys Val Asn Gln Pro Leu	
55 60 65	

act ggt cac ttc aag aaa gca ggc gtt acc ccc cgc cgc cac gtc acc	355
Thr Gly His Phe Lys Lys Ala Gly Val Thr Pro Arg Arg His Val Thr	
70 75 80 85	

gag att cgt atg gac gat gtc tcc ggt tac gag gtt gga cag gac gtt	403
Glu Ile Arg Met Asp Asp Val Ser Gly Tyr Glu Val Gly Gln Asp Val	
90 95 100	

acc gtt gaa atc ttc aac gac atc aag ttc gtt gac gtc acc ggt acc	451
Thr Val Glu Ile Phe Asn Asp Ile Lys Phe Val Asp Val Thr Gly Thr	

105	110	115	
acc aag ggt aag ggc tac gcc ggc gct atg aag cgc cat ggc ttc gct			499
Thr Lys Gly Lys Gly Tyr Ala Gly Ala Met Lys Arg His Gly Phe Ala			
120	125	130	
ggc cag ggt gcc ggc cac ggt aac cag gct gca cac cgc cgc gta ggt			547
Gly Gln Gly Ala Gly His Gly Asn Gln Ala Ala His Arg Arg Val Gly			
135	140	145	
ggc att ggt gca gct gct acc cca ggt cgc atc ttc aag ggc aag cgt			595
Gly Ile Gly Ala Ala Ala Thr Pro Gly Arg Ile Phe Lys Gly Lys Arg			
150	155	160	165
atg gct ggc cgc atg ggt aat gac cgc gtc acc acc cag aac ctc aag			643
Met Ala Gly Arg Met Gly Asn Asp Arg Val Thr Thr Gln Asn Leu Lys			
170	175	180	
gtt cag aag att gac gcc gat gcc aac atc atc ctt atc aag ggc gca			691
Val Gln Lys Ile Asp Ala Asp Ala Asn Ile Ile Leu Ile Lys Gly Ala			
185	190	195	
atc cct ggt aac cgt ggt ggc atc gtt acc gtt aag acc gca gtg aag			739
Ile Pro Gly Asn Arg Gly Gly Ile Val Thr Val Lys Thr Ala Val Lys			
200	205	210	
ggc ggt gca cac gca tgacgaatct gaagctgtat gtt			777
Gly Gly Ala His Ala			
215			
<210> 294			
<211> 218			
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Thr Gln Ile Phe Asp Glu Glu Asn Arg Val Ile Pro Val Thr Val Val			
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Glu Ala Gly Pro Cys Val Val Ser Gln Ile Arg Thr Val Glu Thr Asp			
35	40	45	
Gly Tyr Asn Ala Ile Gln Ile Ala Tyr Gly Glu Ile Asp Pro Arg Lys			
50	55	60	
Val Asn Gln Pro Leu Thr Gly His Phe Lys Lys Ala Gly Val Thr Pro			
65	70	75	80
Arg Arg His Val Thr Glu Ile Arg Met Asp Asp Val Ser Gly Tyr Glu			
85	90	95	
Val Gly Gln Asp Val Thr Val Glu Ile Phe Asn Asp Ile Lys Phe Val			
100	105	110	
Asp Val Thr Gly Thr Thr Lys Gly Lys Gly Tyr Ala Gly Ala Met Lys			
115	120	125	

Arg His Gly Phe Ala Gly Gln Gly Ala Gly His Gly Asn Gln Ala Ala
 130 135 140

His Arg Arg Val Gly Gly Ile Gly Ala Ala Ala Thr Pro Gly Arg Ile
 145 150 155 160

Phe Lys Gly Lys Arg Met Ala Gly Arg Met Gly Asn Asp Arg Val Thr
 165 170 175

Thr Gln Asn Leu Lys Val Gln Lys Ile Asp Ala Asp Ala Asn Ile Ile
 180 185 190

Leu Ile Lys Gly Ala Ile Pro Gly Asn Arg Gly Gly Ile Val Thr Val
 195 200 205

Lys Thr Ala Val Lys Gly Gly Ala His Ala
 210 215

<210> 295

<211> 626

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(603)

<223> RXA01948

<400> 295

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 1 5 10 15

ctg ctg cac cag gtt gtc aac gca cag ctt gca gca gct cga cag ggc 96
 Leu Leu His Gln Val Val Asn Ala Gln Leu Ala Ala Ala Arg Gln Gly
 20 25 30

acc cac tcc acc aag acc cgt ggc gaa gta cgt ggc ggt ggc cgt aag 144
 Thr His Ser Thr Lys Thr Arg Gly Glu Val Arg Gly Gly Gly Arg Lys
 35 40 45

cca ttc cgt cag aag gga acc ggt cgc gct cgt cag ggc tcg atc cgc 192
 Pro Phe Arg Gln Lys Gly Thr Gly Arg Ala Arg Gln Gly Ser Ile Arg
 50 55 60

gca cct cac ttc acc ggt ggt ggc atc tcc cac ggc cct aag cca cgc 240
 Ala Pro His Phe Thr Gly Gly Gly Ile Ser His Gly Pro Lys Pro Arg
 65 70 75 80

gac tac tct cag cgc acc cct aag aag atg atc aag gct gca ctt tac 288
 Asp Tyr Ser Gln Arg Thr Pro Lys Lys Met Ile Lys Ala Ala Leu Tyr
 85 90 95

ggt gca ctg tct gat cgt gca cgc aat gca cgt atc cac gtc gtc tcc 336
 Gly Ala Leu Ser Asp Arg Ala Arg Asn Ala Arg Ile His Val Val Ser
 100 105 110

gaa ttg gtg cct ggc cag acc cct tcg acc aag tct gca aag gct ttc 384
 Glu Leu Val Pro Gly Gln Thr Pro Ser Thr Lys Ser Ala Lys Ala Phe
 115 120 125

atc gag cgt ctg acc gag cgt aag tcc gtg ctg ctc gta gtg agc cgt 432
 Ile Glu Arg Leu Thr Glu Arg Lys Ser Val Leu Leu Val Val Ser Arg
 130 135 140

gag gat atc aac gcc cag aag agt gct aac aac ctg cct ggc gtc cac 480
 Glu Asp Ile Asn Ala Gln Lys Ser Ala Asn Asn Leu Pro Gly Val His
 145 150 155 160

atc ctg gcc gct gat cag ctg aac acc tac gac gtt ctc aag tct gac 528
 Ile Leu Ala Ala Asp Gln Leu Asn Thr Tyr Asp Val Leu Lys Ser Asp
 165 170 175

gac gtt gtg ttc tcc gtt gag gct ctc cac acc ttc atc aac cgc gct 576
 Asp Val Val Phe Ser Val Glu Ala Leu His Thr Phe Ile Asn Arg Ala
 180 185 190

tcc ggt gcg gca cag gag gag cag aac taatggctac tatcgccaac 623
 Ser Gly Ala Ala Gln Glu Glu Gln Asn
 195 200

cca 626

<210> 296

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 296

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 20 25 30

Thr His Ser Thr Lys Thr Arg Gly Glu Val Arg Gly Gly Arg Lys
 35 40 45

Pro Phe Arg Gln Lys Gly Thr Gly Arg Ala Arg Gln Gly Ser Ile Arg
 50 55 60

Ala Pro His Phe Thr Gly Gly Gly Ile Ser His Gly Pro Lys Pro Arg
 65 70 75 80

Asp Tyr Ser Gln Arg Thr Pro Lys Lys Met Ile Lys Ala Ala Leu Tyr
 85 90 95

Gly Ala Leu Ser Asp Arg Ala Arg Asn Ala Arg Ile His Val Val Ser
 100 105 110

Glu Leu Val Pro Gly Gln Thr Pro Ser Thr Lys Ser Ala Lys Ala Phe
 115 120 125

Ile Glu Arg Leu Thr Glu Arg Lys Ser Val Leu Leu Val Val Ser Arg
 130 135 140

Glu Asp Ile Asn Ala Gln Lys Ser Ala Asn Asn Leu Pro Gly Val His
 145 150 155 160

Ile Leu Ala Ala Asp Gln Leu Asn Thr Tyr Asp Val Leu Lys Ser Asp

aag atc gac cgt cct cgt ggt atg gac atc acc gtt gtt acc acc gct 595
Lys Ile Asp Arg Pro Arg Gly Met Asp Ile Thr Val Val Thr Thr Ala
150 155 160 165

gta acc gac gat gaa ggt cgc tcc ctg ctc cgc gag ctc ggc ttc cca 643
Val Thr Asp Asp Glu Gly Arg Ser Leu Arg Glu Leu Gly Phe Pro
170 175 180

ttc aag ggt gaa gac ggc aac cgc cag cag taaactgcat agttaaaagc 693
Phe Lys Gly Glu Asp Gly Asn Arg Gln Gln
185 190

act 696

<210> 298

<211> 191

<212> PRT

<213> Corynebacterium glutamicum

<400> 298

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20 25 30

Ile Pro Gly Val Thr Lys Ile Val Val Asn Met Gly Val Gly Asp Ala
35 40 45

Ala Arg Asp Ser Lys Leu Ile Asn Gly Ala Ile Glu Asp Leu Thr Ala
50 55 60

Ile Thr Gly Gln Lys Pro Gln Leu Arg Arg Ala Lys Lys Ser Ile Ala
65 70 75 80

Asn Phe Lys Leu Arg Glu Gly Met Pro Ile Gly Ala Lys Val Thr Leu
85 90 95

Arg Gly Asp Arg Met Trp Glu Phe Leu Asp Arg Leu Leu Thr Val Ala
100 105 110

Leu Pro Arg Ile Arg Asp Phe Arg Gly Leu Ser Asp Gln Gln Phe Asp
115 120 125

Gly His Gly Asn Tyr Thr Phe Gly Leu Thr Glu Gln Thr Met Phe Tyr
130 135 140

Glu Ile Asp Val Asp Lys Ile Asp Arg Pro Arg Gly Met Asp Ile Thr
145 150 155 160

Val Val Thr Thr Ala Val Thr Asp Asp Glu Gly Arg Ser Leu Leu Arg
165 170 175

Glu Leu Gly Phe Pro Phe Lys Gly Glu Asp Gly Asn Arg Gln Gln
180 185 190

<210> 299

<211> 256

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(256)

<223> FRXA00711

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agaaggtccg	cgtttctcgt	cgcaatggga	aggatatcta	atg	act	gag	aat	tac	115
				Met	Thr	Glu	Asn	Tyr	
				1				5	

atc	cct	cgt	ctg	aag	acc	cgt	tac	cag	gac	gaa	atc	cgc	acc	aag	ctt	163
Ile	Pro	Arg	Leu	Lys	Thr	Arg	Tyr	Gln	Asp	Glu	Ile	Arg	Thr	Lys	Leu	
			10					15						20		

cag	ggc	gag	ttc	gag	ttc	gaa	aac	gtc	atg	cag	atc	cca	ggc	gtc	acc	211
Gln	Gly	Glu	Phe	Glu	Phe	Glu	Asn	Val	Met	Gln	Ile	Pro	Gly	Val	Thr	
			25					30					35			

aag	att	gtc	gtc	aac	atg	ggc	gtc	ggc	gac	gca	gct	cgt	gac	tcc	256
Lys	Ile	Val	Val	Asn	Met	Gly	Val	Gly	Asp	Ala	Ala	Arg	Asp	Ser	
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<212> PRT

<213> Corynebacterium glutamicum

<400> 300

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			20					25					30		

Ile	Pro	Gly	Val	Thr	Lys	Ile	Val	Val	Asn	Met	Gly	Val	Gly	Asp	Ala
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Ala	Arg	Asp	Ser
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<212> DNA

<213> Corynebacterium glutamicum

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<222> (1)..(267)

<223> FRXA00706

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Glu	Phe	Leu	Asp	Arg	Leu	Leu	Thr	Val	Ala	Leu	Pro	Arg	Ile	Arg	Asp	
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Phe Arg Gly Leu Ser Asp Gln Gln Phe Asp Gly His Gly Asn Tyr Thr
          20             25             30
Phe Gly Leu Thr Glu Gln Thr Met Phe Tyr Glu Ile Asp Val Asp Lys
          35             40             45
Ile Asp Arg Pro Arg Gly Met Asp Ile Thr Val Val Thr Thr Ala Val
      50             55             60
Thr Asp Asp Glu Gly Arg Ser Leu Leu Arg Glu Leu Gly Phe Pro Phe
 65             70             75             80
Lys Gly Glu Asp Gly Asn Arg Gln Gln
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<223> RXA00695
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 Met Ser Arg Ile Gly 5
 1

aaa gaa ccg atc acc atc cca tcc ggt gtc gaa acc aag att gac gga 163
 Lys Glu Pro Ile Thr Ile Pro Ser Gly Val Glu Thr Lys Ile Asp Gly 20
 10 15

cag ctc gtt gag gtt aag ggt cct aag ggc acc ctg aac gtt aac gtt 211
 Gln Leu Val Glu Val Lys Gly Pro Lys Gly Thr Leu Asn Val Asn Val 35
 25 30

cca gag cca atc tcc gtt gca gtg gaa gac ggc aag att gtc gtc acc 259
 Pro Glu Pro Ile Ser Val Ala Val Glu Asp Gly Lys Ile Val Val Thr 50
 40 45

cgc ccg gat gat cac cgc act aac cgt tcc ctc cac ggt ctc tcc cgc 307
 Arg Pro Asp Asp His Arg Thr Asn Arg Ser Leu His Gly Leu Ser Arg 65
 55 60

tcc ctg gtt aac aac ctg gtt gtc ggc gtc acc gag ggc tac acc atc 355
 Ser Leu Val Asn Asn Leu Val Val Gly Val Thr Glu Gly Tyr Thr Ile 85
 70 75 80

aag atg gaa atc ttc ggt gtc ggt tac cgt gtc gcg ctg aag ggc aag 403
 Lys Met Glu Ile Phe Gly Val Gly Tyr Arg Val Ala Leu Lys Gly Lys 100
 90 95

gac ctt gag ttc tcc ctc ggc tac tca cac cca gtt ctg att gaa gct 451
 Asp Leu Glu Phe Ser Leu Gly Tyr Ser His Pro Val Leu Ile Glu Ala 115
 105 110

tct gaa ggc atc act ttc gca gtt gat ggc aac acc aag ctt tca gtt 499
 Ser Glu Gly Ile Thr Phe Ala Val Asp Gly Asn Thr Lys Leu Ser Val 130
 120 125

tct ggc atc gac aag cag aag gtt gga cag gtc gca gca gtg atc cgc 547
 Ser Gly Ile Asp Lys Gln Lys Val Gly Gln Val Ala Ala Val Ile Arg 145
 135 140

cgc ctg cgt aag gac gat cct tac aag ggt aag ggc atc cgc tac gag 595
 Arg Leu Arg Lys Asp Asp Pro Tyr Lys Gly Lys Gly Ile Arg Tyr Glu 165
 150 155 160

ggt gag cag atc cgc cgc aag gtc gga aag acg ggt aag taagcaatga 644
 Gly Glu Gln Ile Arg Arg Lys Val Gly Lys Thr Gly Lys 175
 170

gcaacactga aaa 657

<210> 304

<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 304

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Thr Lys Ile Asp Gly Gln Leu Val Glu Val Lys Gly Pro Lys Gly Thr
 20 25 30
 Leu Asn Val Asn Val Pro Glu Pro Ile Ser Val Ala Val Glu Asp Gly
 35 40 45
 Lys Ile Val Val Thr Arg Pro Asp Asp His Arg Thr Asn Arg Ser Leu
 50 55 60
 His Gly Leu Ser Arg Ser Leu Val Asn Asn Leu Val Val Gly Val Thr
 65 70 75 80
 Glu Gly Tyr Thr Ile Lys Met Glu Ile Phe Gly Val Gly Tyr Arg Val
 85 90 95
 Ala Leu Lys Gly Lys Asp Leu Glu Phe Ser Leu Gly Tyr Ser His Pro
 100 105 110
 Val Leu Ile Glu Ala Ser Glu Gly Ile Thr Phe Ala Val Asp Gly Asn
 115 120 125
 Thr Lys Leu Ser Val Ser Gly Ile Asp Lys Gln Lys Val Gly Gln Val
 130 135 140
 Ala Ala Val Ile Arg Arg Leu Arg Lys Asp Asp Pro Tyr Lys Gly Lys
 145 150 155 160
 Gly Ile Arg Tyr Glu Gly Glu Gln Ile Arg Arg Lys Val Gly Lys Thr
 165 170 175
 Gly Lys

<210> 305
 <211> 549
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(526)
 <223> RXA00543

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 aacattcaca aacactcaaa aaccacgaaa ggcagggatc atg aag ctg atc ctc 115
 Met Lys Leu Ile Leu
 1 5
 acc gcc gcc gtt gaa aac ctt ggt gtc gct ggc gac atc gta gag gtt 163
 Thr Ala Ala Val Glu Asn Leu Gly Val Ala Gly Asp Ile Val Glu Val
 10 15 20
 aag aac ggc tac gga cgt aac ctg ctg ctc ccc cgt ggc ctg gca atc 211
 Lys Asn Gly Tyr Gly Arg Asn Leu Leu Leu Pro Arg Gly Leu Ala Ile
 25 30 35
 gta gcc acc ccg ggt gct gag aag cag atc gag ggc atc aag cgt gcc 259
 Val Ala Thr Pro Gly Ala Glu Lys Gln Ile Glu Gly Ile Lys Arg Ala

40	45	50	
cag gag gct cgc gag att cgc gac ctc gac cac gct cgc gaa gtt aag			307
Gln Glu Ala Arg Glu Ile Arg Asp Leu Asp His Ala Arg Glu Val Lys			
55	60	65	
gta gca ctg gaa gca ctt gaa ggt gtt acc att gca gtc cgc acc tcc			355
Val Ala Leu Glu Ala Leu Glu Gly Val Thr Ile Ala Val Arg Thr Ser			
70	75	80	85
gag agc gga aaa ctg ttc ggc tcc gtt aag act gac gac atc gtc gac			403
Glu Ser Gly Lys Leu Phe Gly Ser Val Lys Thr Asp Asp Ile Val Asp			
90	95	100	
gca gtc aag gca gcc ggc ggc ccg aac ctg gac aag cgt gcc att gtt			451
Ala Val Lys Ala Ala Gly Gly Pro Asn Leu Asp Lys Arg Ala Ile Val			
105	110	115	
ctc ccg aag aac ctg gtt aag acc acc ggt aag tac cag gta gaa gca			499
Leu Pro Lys Asn Leu Val Lys Thr Thr Gly Lys Tyr Gln Val Glu Ala			
120	125	130	
aag ctc acc gac gga att gtt tcc gcg tgaagtttga ggctcgtcgca			546
Lys Leu Thr Asp Gly Ile Val Ser Ala			
135	140		
gcg			549
<210> 306			
<211> 142			
<212> PRT			
<213> Corynebacterium glutamicum			
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Asp Ile Val Glu Val Lys Asn Gly Tyr Gly Arg Asn Leu Leu Leu Pro			
20	25	30	
Arg Gly Leu Ala Ile Val Ala Thr Pro Gly Ala Glu Lys Gln Ile Glu			
35	40	45	
Gly Ile Lys Arg Ala Gln Glu Ala Arg Glu Ile Arg Asp Leu Asp His			
50	55	60	
Ala Arg Glu Val Lys Val Ala Leu Glu Ala Leu Glu Gly Val Thr Ile			
65	70	75	80
Ala Val Arg Thr Ser Glu Ser Gly Lys Leu Phe Gly Ser Val Lys Thr			
85	90	95	
Asp Asp Ile Val Asp Ala Val Lys Ala Ala Gly Gly Pro Asn Leu Asp			
100	105	110	
Lys Arg Ala Ile Val Leu Pro Lys Asn Leu Val Lys Thr Thr Gly Lys			
115	120	125	
Tyr Gln Val Glu Ala Lys Leu Thr Asp Gly Ile Val Ser Ala			
130	135	140	

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<223> RXA01335
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Met Ala Asn Pro Arg																5
1																
aac gaa gca gct ctg gca gag ctc aag gca cgt ttc gct gag acc gac																163
Asn Glu Ala Ala Leu Ala Glu Leu Lys Ala Arg Phe Ala Glu Thr Asp																20
10 15																
acc gtc gtt ctc acc gag tac cgt ggc ctg acc gtg gct cag acc acc																211
Thr Val Val Leu Thr Glu Tyr Arg Gly Leu Thr Val Ala Gln Thr Thr																35
25 30																
gaa ctg cgt aag gca ctg ggc ttc gat gtc cag tac tcc gtc gcc aag																259
Glu Leu Arg Lys Ala Leu Gly Phe Asp Val Gln Tyr Ser Val Ala Lys																50
40 45																
aac acc ctt gtt aag atc gcc gct aac gaa gct ggc gtc gag ggc ctt																307
Asn Thr Leu Val Lys Ile Ala Ala Asn Glu Ala Gly Val Glu Gly Leu																65
55 60																
gat gat ctc ctg acc ggt cca acc gct gtt gcc ttc atc aag ggc gaa																355
Asp Asp Leu Leu Thr Gly Pro Thr Ala Val Ala Phe Ile Lys Gly Glu																85
70 75 80																
gca gtt gac acc gct aag gtg ctg aag aaa ttc ggc gaa gaa aac aag																403
Ala Val Asp Thr Ala Lys Val Leu Lys Lys Phe Gly Glu Glu Asn Lys																100
90 95																
gca ttc gta gtc aag ggt ggc tac atg gat ggc aac gcg ctg acc gct																451
Ala Phe Val Val Lys Gly Gly Tyr Met Asp Gly Asn Ala Leu Thr Ala																115
105 110																
gaa cag gtc aac gca atc gcc gag ctg gac aac cgt gag acc act ctc																499
Glu Gln Val Asn Ala Ile Ala Glu Leu Asp Asn Arg Glu Thr Thr Leu																130
120 125 130																
gcg aag ctt gcc ggc gcc atg aag ggc agc ttg gca aag gcc gca ggc																547
Ala Lys Leu Ala Gly Ala Met Lys Gly Ser Leu Ala Lys Ala Ala Gly																145
135 140 145																
ctg ttc aac gct cct gct tcc cag gtc gca cgc ctc gcc gtt gcg ctc																595
Leu Phe Asn Ala Pro Ala Ser Gln Val Ala Arg Leu Ala Val Ala Leu																165
150 155 160 165																
cag gac aag aag gac gca taagtcgccca ccaggcgcac cag																636
Gln Asp Lys Lys Asp Ala																

170

<210> 308
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 308
 Met Ala Asn Pro Arg Asn Glu Ala Ala Leu Ala Glu Leu Lys Ala Arg
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 Phe Ala Glu Thr Asp Thr Val Val Leu Thr Glu Tyr Arg Gly Leu Thr
 20 25 30
 Val Ala Gln Thr Thr Glu Leu Arg Lys Ala Leu Gly Phe Asp Val Gln
 35 40 45
 Tyr Ser Val Ala Lys Asn Thr Leu Val Lys Ile Ala Ala Asn Glu Ala
 50 55 60
 Gly Val Glu Gly Leu Asp Asp Leu Leu Thr Gly Pro Thr Ala Val Ala
 65 70 75 80
 Phe Ile Lys Gly Glu Ala Val Asp Thr Ala Lys Val Leu Lys Lys Phe
 85 90 95
 Gly Glu Glu Asn Lys Ala Phe Val Val Lys Gly Gly Tyr Met Asp Gly
 100 105 110
 Asn Ala Leu Thr Ala Glu Gln Val Asn Ala Ile Ala Glu Leu Asp Asn
 115 120 125
 Arg Glu Thr Thr Leu Ala Lys Leu Ala Gly Ala Met Lys Gly Ser Leu
 130 135 140
 Ala Lys Ala Ala Gly Leu Phe Asn Ala Pro Ala Ser Gln Val Ala Arg
 145 150 155 160
 Leu Ala Val Ala Leu Gln Asp Lys Lys Asp Ala
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<210> 309
 <211> 558
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(535)
 <223> RXN02826

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 cgtcccagtt gtggccggta acaaggaagc aggtttaacg atg gct cct aag aag 115
 Met Ala Pro Lys Lys
 1 5
 aag aag aag gtc act ggc ctc atc aag ctc cag atc cag gca gga cag 163

Lys Lys Lys Val Thr Gly Leu Ile Lys Leu Gln Ile Gln Ala Gly Gln
 10 15 20
 gca aac cct gct cct cca gtt ggc cca gca ctt ggt gct cac ggc gtc 211
 Ala Asn Pro Ala Pro Pro Val Gly Pro Ala Leu Gly Ala His Gly Val
 25 30 35
 aac atc atg gaa ttc tgc aag gct tac aac gct gcg act gaa aac cag 259
 Asn Ile Met Glu Phe Cys Lys Ala Tyr Asn Ala Ala Thr Glu Asn Gln
 40 45 50
 cgc ggc aac gtt gtt cct gtt gag atc acc gtt tac gaa gac cgt tca 307
 Arg Gly Asn Val Val Pro Val Glu Ile Thr Val Tyr Glu Asp Arg Ser
 55 60 65
 ttc gac ttc aag ctg aag act cct cca gct gca aag ctt ctt ctg aag 355
 Phe Asp Phe Lys Leu Lys Thr Pro Pro Ala Ala Lys Leu Leu Leu Lys
 70 75 80 85
 gct gct ggc ctg cag aag ggc tcc ggc gtt cct cac acc cag aag gtc 403
 Ala Ala Gly Leu Gln Lys Gly Ser Gly Val Pro His Thr Gln Lys Val
 90 95 100
 ggc aag gtt tcc atg gct cag gtt cgt gag atc gct gag acc aag aag 451
 Gly Lys Val Ser Met Ala Gln Val Arg Glu Ile Ala Glu Thr Lys Lys
 105 110 115
 gaa gac ctg aac gct cgc gat atc gac gct gct gcg aag atc atc gct 499
 Glu Asp Leu Asn Ala Arg Asp Ile Asp Ala Ala Ala Lys Ile Ile Ala
 120 125 130
 ggt acc gct cgt tcc atg ggc atc acc gtc gaa ggc taaaagcttt 545
 Gly Thr Ala Arg Ser Met Gly Ile Thr Val Glu Gly
 135 140 145
 cacaccgggtt agt 558

<210> 310

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 310

Met Ala Pro Lys Lys Lys Lys Lys Val Thr Gly Leu Ile Lys Leu Gln
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 Ile Gln Ala Gly Gln Ala Asn Pro Ala Pro Pro Val Gly Pro Ala Leu
 20 25 30
 Gly Ala His Gly Val Asn Ile Met Glu Phe Cys Lys Ala Tyr Asn Ala
 35 40 45
 Ala Thr Glu Asn Gln Arg Gly Asn Val Val Pro Val Glu Ile Thr Val
 50 55 60
 Tyr Glu Asp Arg Ser Phe Asp Phe Lys Leu Lys Thr Pro Pro Ala Ala
 65 70 75 80
 Lys Leu Leu Leu Lys Ala Ala Gly Leu Gln Lys Gly Ser Gly Val Pro
 85 90 95

His Thr Gln Lys Val Gly Lys Val Ser Met Ala Gln Val Arg Glu Ile
 100 105 110

Ala Glu Thr Lys Lys Glu Asp Leu Asn Ala Arg Asp Ile Asp Ala Ala
 115 120 125

Ala Lys Ile Ile Ala Gly Thr Ala Arg Ser Met Gly Ile Thr Val Glu
 130 135 140

Gly
 145

<210> 311

<211> 465

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (67)..(465)

<223> FRXA02826

<400> 311

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ttaacgatg gct cct aag aag aag aag aag gtc act ggc ctc atc aag ctc 111
 Met Ala Pro Lys Lys Lys Lys Lys Val Thr Gly Leu Ile Lys Leu
 1 5 10 15

cag atc cag gca gga cag gca aac cct gct cct cca gtt ggc cca gaa 159
 Gln Ile Gln Ala Gly Gln Ala Asn Pro Ala Pro Pro Val Gly Pro Glu
 20 25 30

ctt ggt gct cac ggc gtc aac atc atg gaa ttc tgc aag gct tac aac 207
 Leu Gly Ala His Gly Val Asn Ile Met Glu Phe Cys Lys Ala Tyr Asn
 35 40 45

gct gcg act gaa aac cag cgc ggg aac gtt gtt cct gtt gag atc acc 255
 Ala Ala Thr Glu Asn Gln Arg Gly Asn Val Val Pro Val Glu Ile Thr
 50 55 60

gtt tac gaa gac cgt tca ttc gac ttc aag ctg aag act cct cca gct 303
 Val Tyr Glu Asp Arg Ser Phe Asp Phe Lys Leu Lys Thr Pro Pro Ala
 65 70 75

gca aag ctt ctt ctg aaa gct gct ggc ctg cag aag ggc tcc ggc gtt 351
 Ala Lys Leu Leu Leu Lys Ala Ala Gly Leu Gln Lys Gly Ser Gly Val
 80 85 90 95

cct cac acc cag aag gtc ggc aag gtt tcc atg gct cag gtt cgt gag 399
 Pro His Thr Gln Lys Val Gly Lys Val Ser Met Ala Gln Val Arg Glu
 100 105 110

atc cct gcg acc aag aac gaa gac ctg acg ctc gcg ata tcg acg ctg 447
 Ile Pro Ala Thr Lys Asn Glu Asp Leu Thr Leu Ala Ile Ser Thr Leu
 115 120 125

ctg cga aga tca tcg ctg 465
 Leu Arg Arg Ser Ser Leu

130

<210> 312

<211> 133

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 312

Met Ala Pro Lys Lys Lys Lys Lys Val Thr Gly Leu Ile Lys Leu Gln
 1 5 10 15

Ile Gln Ala Gly Gln Ala Asn Pro Ala Pro Pro Val Gly Pro Glu Leu
 20 25 30

Gly Ala His Gly Val Asn Ile Met Glu Phe Cys Lys Ala Tyr Asn Ala
 35 40 45

Ala Thr Glu Asn Gln Arg Gly Asn Val Val Pro Val Glu Ile Thr Val
 50 55 60

Tyr Glu Asp Arg Ser Phe Asp Phe Lys Leu Lys Thr Pro Pro Ala Ala
 65 70 75 80

Lys Leu Leu Leu Lys Ala Ala Gly Leu Gln Lys Gly Ser Gly Val Pro
 85 90 95

His Thr Gln Lys Val Gly Lys Val Ser Met Ala Gln Val Arg Glu Ile
 100 105 110

Pro Ala Thr Lys Asn Glu Asp Leu Thr Leu Ala Ile Ser Thr Leu Leu
 115 120 125

Arg Arg Ser Ser Leu
 130

<210> 313

<211> 507

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(484)

<223> RXA01334

<400> 313

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tcgagcgtgt taaacgctca acaacaggaa ggatgccacc atg gct aag ctc acc 115
 Met Ala Lys Leu Thr
 1 5

aaa gac gag ctc atc gag gct ttc aag gaa atg acc ctc atc gag ctc 163
 Lys Asp Glu Leu Ile Glu Ala Phe Lys Glu Met Thr Leu Ile Glu Leu
 10 15 20

tcc gag ttc gtt aag gaa ttc gaa gag gtc ttc gac gta acc gca gct 211
 Ser Glu Phe Val Lys Glu Phe Glu Glu Val Phe Asp Val Thr Ala Ala
 25 30 35

gct cca gtt gca gtt gct gct gca ggc gct gca ggc ggc gaa gct gct 259
 Ala Pro Val Ala Val Ala Ala Ala Gly Ala Ala Gly Gly Glu Ala Ala
 40 45 50

gct gca gaa gag aag gac gag ttc gac gtc gtt ctc gaa gac gca ggc 307
 Ala Ala Glu Glu Lys Asp Glu Phe Asp Val Val Leu Glu Asp Ala Gly
 55 60 65

gca aag aag atc ggc gtc atc aag gct gtc cgc gag ctc gtc tcc ggc 355
 Ala Lys Lys Ile Gly Val Ile Lys Ala Val Arg Glu Leu Val Ser Gly
 70 75 80 85

ctg ggc ctg aag gaa gca aag gag ctc gtt gag ggc gca cct aag gct 403
 Leu Gly Leu Lys Glu Ala Lys Glu Leu Val Glu Gly Ala Pro Lys Ala
 90 95 100

atc ctc gag ggc gca aac aag gac gac gct gag gct gca aag gct aag 451
 Ile Leu Glu Gly Ala Asn Lys Asp Asp Ala Glu Ala Ala Lys Ala Lys
 105 110 115

ctc gaa gag gct ggc gca aag gtc acc ctt aag taagaacttt cttacacctt 504
 Leu Glu Glu Ala Gly Ala Lys Val Thr Leu Lys
 120 125

ttc 507

<210> 314
 <211> 128
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 314
 Met Ala Lys Leu Thr Lys Asp Glu Leu Ile Glu Ala Phe Lys Glu Met
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Thr Leu Ile Glu Leu Ser Glu Phe Val Lys Glu Phe Glu Glu Val Phe
 20 25 30

Asp Val Thr Ala Ala Ala Pro Val Ala Val Ala Ala Ala Gly Ala Ala
 35 40 45

Gly Gly Glu Ala Ala Ala Ala Glu Glu Lys Asp Glu Phe Asp Val Val
 50 55 60

Leu Glu Asp Ala Gly Ala Lys Lys Ile Gly Val Ile Lys Ala Val Arg
 65 70 75 80

Glu Leu Val Ser Gly Leu Gly Leu Lys Glu Ala Lys Glu Leu Val Glu
 85 90 95

Gly Ala Pro Lys Ala Ile Leu Glu Gly Ala Asn Lys Asp Asp Ala Glu
 100 105 110

Ala Ala Lys Ala Lys Leu Glu Glu Ala Gly Ala Lys Val Thr Leu Lys
 115 120 125

<210> 315
 <211> 353
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(330)
 <223> RXA02037

<400> 315
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 Gly Lys Gly Lys Pro Leu Tyr Ala Pro Asn Val Asp Cys Gly Asp His
 1 5 10 15
 gta atc gtg atc aac gct gac aag gtt gca gtt acc tcc aac aag cgc 96
 Val Ile Val Ile Asn Ala Asp Lys Val Ala Val Thr Ser Asn Lys Arg
 20 25 30
 gag cgc gaa atg cgt tac cgc cac tcc ggt tac cct ggt ggc ctg aag 144
 Glu Arg Glu Met Arg Tyr Arg His Ser Gly Tyr Pro Gly Gly Leu Lys
 35 40 45
 tcc atg acc ctg ggt cgt tcc ctg gat ctg cac cca gag cgc acc atc 192
 Ser Met Thr Leu Gly Arg Ser Leu Asp Leu His Pro Glu Arg Thr Ile
 50 55 60
 gag gat tcc atc gtc ggc atg atg cca cac aac aag ctc act gct gct 240
 Glu Asp Ser Ile Val Gly Met Met Pro His Asn Lys Leu Thr Ala Ala
 65 70 75 80
 tcc gca aag aag ctg cac gtt ttc tcc ggc tcc gag cac cca tac gct 288
 Ser Ala Lys Lys Leu His Val Phe Ser Gly Ser Glu His Pro Tyr Ala
 85 90 95
 gct cag aag cct gag gcc tac gag atc aag aag gtg gcc cag 330
 Ala Gln Lys Pro Glu Ala Tyr Glu Ile Lys Lys Val Ala Gln
 100 105 110
 taatgtcaga gcctatccag aac 353

<210> 316
 <211> 110
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 316
 Gly Lys Gly Lys Pro Leu Tyr Ala Pro Asn Val Asp Cys Gly Asp His
 1 5 10 15
 Val Ile Val Ile Asn Ala Asp Lys Val Ala Val Thr Ser Asn Lys Arg
 20 25 30
 Glu Arg Glu Met Arg Tyr Arg His Ser Gly Tyr Pro Gly Gly Leu Lys
 35 40 45
 Ser Met Thr Leu Gly Arg Ser Leu Asp Leu His Pro Glu Arg Thr Ile
 50 55 60

Glu Asp Ser Ile Val Gly Met Met Pro His Asn Lys Leu Thr Ala Ala
65 70 75 80

Ser Ala Lys Lys Leu His Val Phe Ser Gly Ser Glu His Pro Tyr Ala
85 90 95

Ala Gln Lys Pro Glu Ala Tyr Glu Ile Lys Lys Val Ala Gln
100 105 110

<210> 317

<211> 567

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(544)

<223> RXA00699

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cctgatcgtc gtcgaagaag tggcggggga gtaggtaaca atg agc gaa cca att 115
Met Ser Glu Pro Ile
1 5

aag ctc cac gat ttg cgc cca gca gcg ggc tca aac aaa gct aag acc 163
Lys Leu His Asp Leu Arg Pro Ala Ala Gly Ser Asn Lys Ala Lys Thr
10 15 20

cgc gtt ggt cga ggc gaa gca tcc aag ggt aag act gca ggt cgc ggt 211
Arg Val Gly Arg Gly Glu Ala Ser Lys Gly Lys Thr Ala Gly Arg Gly
25 30 35

acc aag ggt acc aag gca cgc aag cag gtt tct gca gca ttc gaa ggt 259
Thr Lys Gly Thr Lys Ala Arg Lys Gln Val Ser Ala Ala Phe Glu Gly
40 45 50

ggc cag atg cca ctg cag atg cgt ctt cct aag ctg aag ggc ttc aag 307
Gly Gln Met Pro Leu Gln Met Arg Leu Pro Lys Leu Lys Gly Phe Lys
55 60 65

aac cct aac aag gtt gac tac cag gta gtt aac att gca gat ctc gca 355
Asn Pro Asn Lys Val Asp Tyr Gln Val Val Asn Ile Ala Asp Leu Ala
70 75 80 85

gag aag ttc cca cag ggc ggc gac gtc agc att gct gac atc gtt gca 403
Glu Lys Phe Pro Gln Gly Gly Asp Val Ser Ile Ala Asp Ile Val Ala
90 95 100

gca gga ctt gtc cgc aag aac gaa ctg gtt aag gtt ctt ggc aac ggc 451
Ala Gly Leu Val Arg Lys Asn Glu Leu Val Lys Val Leu Gly Asn Gly
105 110 115

gac atc agc gtc aag ctg aac gtc acc gct aac aag ttc tcc ggc tct 499
Asp Ile Ser Val Lys Leu Asn Val Thr Ala Asn Lys Phe Ser Gly Ser
120 125 130

gcc aag gaa aag atc gaa gcc gct ggc ggc tcc gca acc gtg gca 544
Ala Lys Glu Lys Ile Glu Ala Ala Gly Gly Ser Ala Thr Val Ala

135

140

145

taagttcacc agaactttaa aaa

567

<210> 318

<211> 148

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

Met Ser Glu Pro Ile Lys Leu His Asp Leu Arg Pro Ala Ala Gly Ser
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Asn Lys Ala Lys Thr Arg Val Gly Arg Gly Glu Ala Ser Lys Gly Lys
 20 25 30

Thr Ala Gly Arg Gly Thr Lys Gly Thr Lys Ala Arg Lys Gln Val Ser
 35 40 45

Ala Ala Phe Glu Gly Gly Gln Met Pro Leu Gln Met Arg Leu Pro Lys
 50 55 60

Leu Lys Gly Phe Lys Asn Pro Asn Lys Val Asp Tyr Gln Val Val Asn
 65 70 75 80

Ile Ala Asp Leu Ala Glu Lys Phe Pro Gln Gly Gly Asp Val Ser Ile
 85 90 95

Ala Asp Ile Val Ala Ala Gly Leu Val Arg Lys Asn Glu Leu Val Lys
 100 105 110

Val Leu Gly Asn Gly Asp Ile Ser Val Lys Leu Asn Val Thr Ala Asn
 115 120 125

Lys Phe Ser Gly Ser Ala Lys Glu Lys Ile Glu Ala Ala Gly Gly Ser
 130 135 140

Ala Thr Val Ala
 145

<210> 319

<211> 537

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(514)

<223> RXA02042

<400> 319

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agcgctcgtca gcgtgctgag cagaagcagg agggctaaac atg ctt att cct aag 115
 Met Leu Ile Pro Lys
 1 5

cgc gtt aag tac cgt cgc cag cac cgt cct acc cgt agt ggt atc tcc 163
 Arg Val Lys Tyr Arg Arg Gln His Arg Pro Thr Arg Ser Gly Ile Ser

	10	15	20	
aag ggc ggc aac cgc gtc act ttc ggt gag tac ggc atc cag gct ctc				211
Lys Gly Gly Asn Arg Val Thr Phe Gly Glu Tyr Gly Ile Gln Ala Leu				
	25	30	35	
gag cct gcc tac atc acc aac cgt cag att gaa tct gca cgt att gca				259
Glu Pro Ala Tyr Ile Thr Asn Arg Gln Ile Glu Ser Ala Arg Ile Ala				
	40	45	50	
atc aac cgc cac gtc agg cgt ggt ggc aag gtt tgg atc aac atc ttc				307
Ile Asn Arg His Val Arg Arg Gly Gly Lys Val Trp Ile Asn Ile Phe				
	55	60	65	
cca gac cgc cca ctg acc cag aag cca ctc ggc gtt cgt atg ggt tcc				355
Pro Asp Arg Pro Leu Thr Gln Lys Pro Leu Gly Val Arg Met Gly Ser				
	70	75	80	85
ggt aag ggc cct gtg gag aag tgg gtt gca aac atc aag ccg ggc cgt				403
Gly Lys Gly Pro Val Glu Lys Trp Val Ala Asn Ile Lys Pro Gly Arg				
	90	95	100	
atc ctc ttc gag atg agc tac ccg gac gaa gct act gct ctc gag gct				451
Ile Leu Phe Glu Met Ser Tyr Pro Asp Glu Ala Thr Ala Leu Glu Ala				
	105	110	115	
ctg cgc cgc gct ggc cag aag ctt cca tgc aag gtc cgt atc gtc aag				499
Leu Arg Arg Ala Gly Gln Lys Leu Pro Cys Lys Val Arg Ile Val Lys				
	120	125	130	
agg gag gat cag ctc taatggctat cggtacccca gca				537
Arg Glu Asp Gln Leu				
	135			

<210> 320

<211> 138

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

Met Leu Ile Pro Lys Arg Val Lys Tyr Arg Arg Gln His Arg Pro Thr			
1	5	10	15

Arg Ser Gly Ile Ser Lys Gly Gly Asn Arg Val Thr Phe Gly Glu Tyr			
20	25	30	

Gly Ile Gln Ala Leu Glu Pro Ala Tyr Ile Thr Asn Arg Gln Ile Glu			
35	40	45	

Ser Ala Arg Ile Ala Ile Asn Arg His Val Arg Arg Gly Gly Lys Val			
50	55	60	

Trp Ile Asn Ile Phe Pro Asp Arg Pro Leu Thr Gln Lys Pro Leu Gly			
65	70	75	80

Val Arg Met Gly Ser Gly Lys Gly Pro Val Glu Lys Trp Val Ala Asn			
85	90	95	

Ile Lys Pro Gly Arg Ile Leu Phe Glu Met Ser Tyr Pro Asp Glu Ala			
100	105	110	

Thr Ala Leu Glu Ala Leu Arg Arg Ala Gly Gln Lys Leu Pro Cys Lys
 115 120 125

Val Arg Ile Val Lys Arg Glu Asp Gln Leu
 130 135

<210> 321

<211> 612

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(589)

<223> RXA00670

<400> 321

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tcattggggccg cgctaaatca acgtacaagg agtacatcta atg cct acc cct aag 115
 Met Pro Thr Pro Lys
 1 5

aag ggc gcc cgc ctc ggc gga tcc gca agc cac cag aag aag atc ctc 163
 Lys Gly Ala Arg Leu Gly Gly Ser Ala Ser His Gln Lys Lys Ile Leu
 10 15 20

tct aac ctg gct gca tct ctg ttc gag cat ggc gca atc aag acc acc 211
 Ser Asn Leu Ala Ala Ser Leu Phe Glu His Gly Ala Ile Lys Thr Thr
 25 30 35

gat gct aag gca aag gct ctg cgt cca tac gct gag aag ctg atc acc 259
 Asp Ala Lys Ala Lys Ala Leu Arg Pro Tyr Ala Glu Lys Leu Ile Thr
 40 45 50

aag gct aag tcc ggt tcc gtt gca gat cgt cgt aac gtt ctc gca ctg 307
 Lys Ala Lys Ser Gly Ser Val Ala Asp Arg Arg Asn Val Leu Ala Leu
 55 60 65

gtt cct aac aag gaa atc gtg gct tac ctg ttc aac gaa ctt gct cct 355
 Val Pro Asn Lys Glu Ile Val Ala Tyr Leu Phe Asn Glu Leu Ala Pro
 70 75 80 85

aag ttc gag aac cgt cca ggt ggt tac acc cgc atc atc aag ctg gag 403
 Lys Phe Glu Asn Arg Pro Gly Gly Tyr Thr Arg Ile Ile Lys Leu Glu
 90 95 100

aac cgt aag ggc gac aac gct cct atg tcc cag atc tcc ctc gtt ctc 451
 Asn Arg Lys Gly Asp Asn Ala Pro Met Ser Gln Ile Ser Leu Val Leu
 105 110 115

gag gag acc gtc tcc gca gaa gca tcc cgc gca acc cgc gca tct gct 499
 Glu Glu Thr Val Ser Ala Glu Ala Ser Arg Ala Thr Arg Ala Ser Ala
 120 125 130

tcc aag aag gct gct gaa gag gct gag acc gaa gag gta gtc gag gct 547
 Ser Lys Lys Ala Ala Glu Glu Ala Glu Thr Glu Glu Val Val Glu Ala
 135 140 145

gctacatcga tgctgaggcg gaagattccg agtaagtcgc atgggtccaat 60

cca gct gag gag acc gca acc gaa gag gct gca gaa gag aag 589
 Pro Ala Glu Glu Thr Ala Thr Glu Glu Ala Ala Glu Glu Lys
 150 155 160

taaatttctc taactccgca tag 612

<210> 322

<211> 163

<212> PRT

<213> Corynebacterium glutamicum

<400> 322

Met Pro Thr Pro Lys Lys Gly Ala Arg Leu Gly Gly Ser Ala Ser His
 1 5 10 15

Gln Lys Lys Ile Leu Ser Asn Leu Ala Ala Ser Leu Phe Glu His Gly
 20 25 30

Ala Ile Lys Thr Thr Asp Ala Lys Ala Lys Ala Leu Arg Pro Tyr Ala
 35 40 45

Glu Lys Leu Ile Thr Lys Ala Lys Ser Gly Ser Val Ala Asp Arg Arg
 50 55 60

Asn Val Leu Ala Leu Val Pro Asn Lys Glu Ile Val Ala Tyr Leu Phe
 65 70 75 80

Asn Glu Leu Ala Pro Lys Phe Glu Asn Arg Pro Gly Gly Tyr Thr Arg
 85 90 95

Ile Ile Lys Leu Glu Asn Arg Lys Gly Asp Asn Ala Pro Met Ser Gln
 100 105 110

Ile Ser Leu Val Leu Glu Glu Thr Val Ser Ala Glu Ala Ser Arg Ala
 115 120 125

Thr Arg Ala Ser Ala Ser Lys Lys Ala Ala Glu Glu Ala Glu Thr Glu
 130 135 140

Glu Val Val Glu Ala Pro Ala Glu Glu Thr Ala Thr Glu Glu Ala Ala
 145 150 155 160

Glu Glu Lys

<210> 323

<211> 525

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(502)

<223> RXA00696

<400> 323

gatccgccgc ctgcgtaagg acgataccta caagggtaag ggcataccgct acgaggggtga 60

gcagatccgc cgcaagggtcg gaaagacggg taagtaagca atg agc aac act gaa 115

	Met	Ser	Asn	Thr	Glu	
	1				5	
aac aag cag aag cgc gtt tcc gtt ggc aag gac atc gcg act cgt cgt						163
Asn Lys Gln Lys Arg Val Ser Val Gly Lys Asp Ile Ala Thr Arg Arg						
			10		15	20
cgc gtt gcc cgt gca cgc cgc cac ttc cgc atc cgc aag aac ctg cgt						211
Arg Val Ala Arg Ala Arg Arg His Phe Arg Ile Arg Lys Asn Leu Arg			25		30	35
ggc acc cca gag gct cca cgt ttg gtt gtc cac cgc tct tct cgc cac						259
Gly Thr Pro Glu Ala Pro Arg Leu Val Val His Arg Ser Ser Arg His			40		45	50
atg cac gtt cag atc atc gat gac gtt gca ggc cac acc ctg gct gca						307
Met His Val Gln Ile Ile Asp Asp Val Ala Gly His Thr Leu Ala Ala			55		60	65
gct tct tcc atc gag gct gag gtt cgc gca act gag ggc gac aag aag						355
Ala Ser Ser Ile Glu Ala Glu Val Arg Ala Thr Glu Gly Asp Lys Lys			70		75	80
						85
gct aag ggc gca aag gtc ggt cag ctg atc gcc gag cgc gct aag gct						403
Ala Lys Gly Ala Lys Val Gly Gln Leu Ile Ala Glu Arg Ala Lys Ala			90		95	100
gct ggt atc gag cag gtc gtc ttc gac cgc gct ggt tac aag tac cac						451
Ala Gly Ile Glu Gln Val Val Phe Asp Arg Ala Gly Tyr Lys Tyr His			105		110	115
ggc cgc gtt gca gct ctc gct gac gcc gct cgt gaa ggt ggt ctg aaa						499
Gly Arg Val Ala Ala Leu Ala Asp Ala Ala Arg Glu Gly Gly Leu Lys			120		125	130
ttc taatgatgac catttctaag aac						525
Phe						

<210> 324

<211> 134

<212> PRT

<213> Corynebacterium glutamicum

<400> 324

Met	Ser	Asn	Thr	Glu	Asn	Lys	Gln	Lys	Arg	Val	Ser	Val	Gly	Lys	Asp
1				5					10					15	
Ile	Ala	Thr	Arg	Arg	Arg	Val	Ala	Arg	Ala	Arg	Arg	His	Phe	Arg	Ile
			20					25					30		
Arg	Lys	Asn	Leu	Arg	Gly	Thr	Pro	Glu	Ala	Pro	Arg	Leu	Val	Val	His
		35					40					45			
Arg	Ser	Ser	Arg	His	Met	His	Val	Gln	Ile	Ile	Asp	Asp	Val	Ala	Gly
	50					55					60				
His	Thr	Leu	Ala	Ala	Ala	Ser	Ser	Ile	Glu	Ala	Glu	Val	Arg	Ala	Thr
65					70					75					80

<400> 325																
cagcctcgaa	aattgaaacg	gaaacgaacc	ggccgagcac	cccaaacctg	gggaagtgcc	60										
gccagggtcc tctttcccta ctagtaaaag gattgtttat						atg	aac	att	ctg	gat	115					
						Met	Asn	Ile	Leu	Asp						
						1				5						
aag	atc	gac	gca	gca	tcc	ctg	cgc	gac	gac	ggt	cct	gca	ttc	cgc	gcc	163
Lys	Ile	Asp	Ala	Ala	Ser	Leu	Arg	Asp	Asp	Val	Pro	Ala	Phe	Arg	Ala	
				10					15					20		
ggc	gac	acc	ctc	gac	gta	cac	gtc	aag	gtc	atc	gaa	ggc	acc	acc	acc	211
Gly	Asp	Thr	Leu	Asp	Val	His	Val	Lys	Val	Ile	Glu	Gly	Thr	Thr	Thr	
				25					30					35		
cgt	acc	cag	ctg	ttc	aag	ggt	gtt	gtc	att	cgc	cgt	cag	ggc	ggc	gga	259
Arg	Thr	Gln	Leu	Phe	Lys	Gly	Val	Val	Ile	Arg	Arg	Gln	Gly	Gly	Gly	
				40					45					50		
atc	cgc	gag	acc	ttc	acc	gta	cgt	aag	gtt	tcc	ttc	ggc	atc	ggt	gtt	307
Ile	Arg	Glu	Thr	Phe	Thr	Val	Arg	Lys	Val	Ser	Phe	Gly	Ile	Gly	Val	
				55					60					65		
gag	cgt	acc	ttc	cca	gta	cac	tcc	cca	aac	atc	gag	aag	atc	gag	gtc	355
Glu	Arg	Thr	Phe	Pro	Val	His	Ser	Pro	Asn	Ile	Glu	Lys	Ile	Glu	Val	
				70					75					80	85	
att	cgt	cgt	ggt	gac	gtt	cgt	cgt	gcg	aag	ctg	tac	tac	ctg	cgc	gaa	403
Ile	Arg	Arg	Gly	Asp	Val	Arg	Arg	Ala	Lys	Leu	Tyr	Tyr	Leu	Arg	Glu	
				90					95					100		
ctg	cgc	ggc	aag	gct	gca	cgt	att	aag	gag	aag	cgc	taattatttta				449
Leu	Arg	Gly	Lys	Ala	Ala	Arg	Ile	Lys	Glu	Lys	Arg					
				105					110							
gcgtttggtta ggt															462	

<210> 326
 <211> 113
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 326
 Met Asn Ile Leu Asp Lys Ile Asp Ala Ala Ser Leu Arg Asp Asp Val
 1 5 10 15
 Pro Ala Phe Arg Ala Gly Asp Thr Leu Asp Val His Val Lys Val Ile
 20 25 30
 Glu Gly Thr Thr Thr Arg Thr Gln Leu Phe Lys Gly Val Val Ile Arg
 35 40 45
 Arg Gln Gly Gly Gly Ile Arg Glu Thr Phe Thr Val Arg Lys Val Ser
 50 55 60
 Phe Gly Ile Gly Val Glu Arg Thr Phe Pro Val His Ser Pro Asn Ile
 65 70 75 80
 Glu Lys Ile Glu Val Ile Arg Arg Gly Asp Val Arg Arg Ala Lys Leu
 85 90 95
 Tyr Tyr Leu Arg Glu Leu Arg Gly Lys Ala Ala Arg Ile Lys Glu Lys
 100 105 110
 Arg

<210> 327
 <211> 504
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(481)
 <223> RXA02420

<400> 327
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 ccctccacc tttcaagaca agatttaagg aagtaccacc gtg gca cgt gtc aag 115
 Val Ala Arg Val Lys
 1 5
 cgg tcc gtt aac gca aag aag aag cgt cgc gaa att ctg aag tcc gca 163
 Arg Ser Val Asn Ala Lys Lys Lys Arg Arg Glu Ile Leu Lys Ser Ala
 10 15 20
 aag ggc tac cgc ggc cag cgc tca cgc ctt tac cgt aag gct aag gag 211
 Lys Gly Tyr Arg Gly Gln Arg Ser Arg Leu Tyr Arg Lys Ala Lys Glu
 25 30 35
 cag tgg ctg cac tcc atg act tac tct tac cgc gat cgt cgc gcc cgt 259
 Gln Trp Leu His Ser Met Thr Tyr Ser Tyr Arg Asp Arg Arg Ala Arg
 40 45 50
 aag agc gag ttc cgt aag ctg tgg atc cag cgt atc aac gct gct gca 307

Lys Ser Glu Phe Arg Lys Leu Trp Ile Gln Arg Ile Asn Ala Ala Ala
 55 60 65
 cgt atg aac ggc atc acc tac aac cgt ctc atc cag ggc ctt cgc ctt 355
 Arg Met Asn Gly Ile Thr Tyr Asn Arg Leu Ile Gln Gly Leu Arg Leu
 70 75 80 85
 gct gag atc gag gtc gac cgc aag atc ctc gct gat ctc gca gtc aac 403
 Ala Glu Ile Glu Val Asp Arg Lys Ile Leu Ala Asp Leu Ala Val Asn
 90 95 100
 gac ttt gca acc ttc tcc gca atc tgc gag gct gca aag gct gca ctt 451
 Asp Phe Ala Thr Phe Ser Ala Ile Cys Glu Ala Ala Lys Ala Ala Leu
 105 110 115
 cct gag gac gtt aac gct cca aag gct gct taagcttaca aacgaattga 501
 Pro Glu Asp Val Asn Ala Pro Lys Ala Ala
 120 125
 cct 504

<210> 328
 <211> 127
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 328
 Val Ala Arg Val Lys Arg Ser Val Asn Ala Lys Lys Lys Arg Arg Glu
 1 5 10 15
 Ile Leu Lys Ser Ala Lys Gly Tyr Arg Gly Gln Arg Ser Arg Leu Tyr
 20 25 30
 Arg Lys Ala Lys Glu Gln Trp Leu His Ser Met Thr Tyr Ser Tyr Arg
 35 40 45
 Asp Arg Arg Ala Arg Lys Ser Glu Phe Arg Lys Leu Trp Ile Gln Arg
 50 55 60
 Ile Asn Ala Ala Ala Arg Met Asn Gly Ile Thr Tyr Asn Arg Leu Ile
 65 70 75 80
 Gln Gly Leu Arg Leu Ala Glu Ile Glu Val Asp Arg Lys Ile Leu Ala
 85 90 95
 Asp Leu Ala Val Asn Asp Phe Ala Thr Phe Ser Ala Ile Cys Glu Ala
 100 105 110
 Ala Lys Ala Ala Leu Pro Glu Asp Val Asn Ala Pro Lys Ala Ala
 115 120 125

<210> 329
 <211> 415
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(415)

<223> RXN02371

<400> 329

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cgagtacctg agccgagaat cagataaggg gtagccctct atg tac gcg atc gtc 115
                               Met Tyr Ala Ile Val
                               1 5
aag acc ggc gga aag cag tac aag gtt gcc gaa ggt gac ctc gtt aag 163
Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu Gly Asp Leu Val Lys
                               10 15 20
gtc gag aag atc gag ggt gag ccg ggt gca tcc gtg gct ctc acc ccg 211
Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser Val Ala Leu Thr Pro
                               25 30 35
gtt ctg ctc gtc gat ggc gcc gat gta acc acc gcc gct gac aag ctc 259
Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr Ala Ala Asp Lys Leu
                               40 45 50
gct tct gtg agc gtc aac acc gag atc gtc gag cac acc aag ggc ccg 307
Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu His Thr Lys Gly Pro
                               55 60 65
aag atc aag atc ctg aag tac aag aac aag acc gga tac aag aag cgc 355
Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr Gly Tyr Lys Lys Arg
                               70 75 80 85
cag gga cac cgt cag ccc ctg acc gtt ctg aag gta acc gga aat caa 403
Gln Gly His Arg Gln Pro Leu Thr Val Leu Lys Val Thr Gly Asn Gln
                               90 95 100
gta agc cct cgg 415
Val Ser Pro Arg
                               105

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<210> 330

<211> 105

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 330

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Met Tyr Ala Ile Val Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu
 1 5 10 15
Gly Asp Leu Val Lys Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser
 20 25 30
Val Ala Leu Thr Pro Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr
 35 40 45
Ala Ala Asp Lys Leu Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu
 50 55 60
His Thr Lys Gly Pro Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr
 65 70 75 80
Gly Tyr Lys Lys Arg Gln Gly His Arg Gln Pro Leu Thr Val Leu Lys
 85 90 95

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Val Thr Gly Asn Gln Val Ser Pro Arg
100 105

<210> 331
<211> 370
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(370)
<223> FRXA02371

<400> 331
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cgagtacctg agccgagaat cagataaggg gtagccctct atg tac gcg atc gtc 115
Met Tyr Ala Ile Val
1 5
aag acc ggc gga aag cag tac aag gtt gcc gaa ggt gac ctc gtt aag 163
Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu Gly Asp Leu Val Lys
10 15 20
gtc gag aag atc gag ggt gag ccg ggt gca tcc gtg gct ctc acc ccg 211
Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser Val Ala Leu Thr Pro
25 30 35
gtt ctg ctc gtc gat ggc gcc gat gta acc acc gcc gct gac aag ctc 259
Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr Ala Ala Asp Lys Leu
40 45 50
gct tct gtg agc gtc aac acc gag atc gtc gag cac acc aag ggc ccg 307
Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu His Thr Lys Gly Pro
55 60 65
aag atc aag atc ctg aag tac aag aac aag acc gga tac aag aag cgc 355
Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr Gly Tyr Lys Lys Arg
70 75 80 85
cag gga cac cgt cag 370
Gln Gly His Arg Gln
90

<210> 332
<211> 90
<212> PRT
<213> Corynebacterium glutamicum

<400> 332
Met Tyr Ala Ile Val Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu
1 5 10 15
Gly Asp Leu Val Lys Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser
20 25 30
Val Ala Leu Thr Pro Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr
35 40 45

Ala Ala Asp Lys Leu Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu
 50 55 60

His Thr Lys Gly Pro Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr
 65 70 75 80

Gly Tyr Lys Lys Arg Gln Gly His Arg Gln
 85 90

<210> 333

<211> 426

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(403)

<223> RXA01949

<400> 333

cctacgacgt tctcaagtct gacgacgttg tgttctccgt tgaggctctc cacaccttca 60

tcaaccgcgc ttccggtgcg gcacaggagg agcagaacta atg gct act atc gcc 115
 Met Ala Thr Ile Ala
 1 5

aac cca cgc gac atc atc atc gca ccg gtc gtt tct gag aag tcc tac 163
 Asn Pro Arg Asp Ile Ile Ile Ala Pro Val Val Ser Glu Lys Ser Tyr
 10 15 20

ggc ctc atg gag cag aac gtt tac acg ttc ttc gtc tcc act gac gct 211
 Gly Leu Met Glu Gln Asn Val Tyr Thr Phe Phe Val Ser Thr Asp Ala
 25 30 35

aac aag act cag atc aag att gcc atc gaa gag atc ttc ggc gtc aag 259
 Asn Lys Thr Gln Ile Lys Ile Ala Ile Glu Glu Ile Phe Gly Val Lys
 40 45 50

gtt gca tct gtg aac acc gtt aac cgt gca ggt aag cgc aag cgc tcc 307
 Val Ala Ser Val Asn Thr Val Asn Arg Ala Gly Lys Arg Lys Arg Ser
 55 60 65

cgc acc ggc ttc ggt act cgc aag gct acc aag cgc gct tat gtg act 355
 Arg Thr Gly Phe Gly Thr Arg Lys Ala Thr Lys Arg Ala Tyr Val Thr
 70 75 80 85

ctt cgc gaa ggc agc gac tcc atc gac atc ttc agc ggc tcc gtc gct 403
 Leu Arg Glu Gly Ser Asp Ser Ile Asp Ile Phe Ser Gly Ser Val Ala
 90 95 100

taagacgtcg atagaaaagg aca 426

<210> 334

<211> 101

<212> PRT

<213> Corynebacterium glutamicum

<400> 334

Met Ala Thr Ile Ala Asn Pro Arg Asp Ile Ile Ile Ala Pro Val Val
 1 5 10 15
 Ser Glu Lys Ser Tyr Gly Leu Met Glu Gln Asn Val Tyr Thr Phe Phe
 20 25 30
 Val Ser Thr Asp Ala Asn Lys Thr Gln Ile Lys Ile Ala Ile Glu Glu
 35 40 45
 Ile Phe Gly Val Lys Val Ala Ser Val Asn Thr Val Asn Arg Ala Gly
 50 55 60
 Lys Arg Lys Arg Ser Arg Thr Gly Phe Gly Thr Arg Lys Ala Thr Lys
 65 70 75 80
 Arg Ala Tyr Val Thr Leu Arg Glu Gly Ser Asp Ser Ile Asp Ile Phe
 85 90 95
 Ser Gly Ser Val Ala
 100

<210> 335
 <211> 489
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(466)
 <223> RXN00709

<400> 335
 ttgcccacat tcgtggagta tgtagacatc tgtagtataa agaccacgcg tgtttgggac 60
 ggaaatccag cacgcattaa tccaggtcag gagaccagta gtg att cag cag gaa 115
 Val Ile Gln Gln Glu
 1 5
 tcg cgt ctg aag gtc gcc gac aac act ggt gca cgt gaa att ctg tgc 163
 Ser Arg Leu Lys Val Ala Asp Asn Thr Gly Ala Arg Glu Ile Leu Cys
 10 15 20
 atc cgc gtt ctc ggt gga tcc acc cga cgt ttt gct ggc att ggt gac 211
 Ile Arg Val Leu Gly Gly Ser Thr Arg Arg Phe Ala Gly Ile Gly Asp
 25 30 35
 gtc atc gtc gcc act gtc aag gaa gca acc cca ggc ggc aac gta aag 259
 Val Ile Val Ala Thr Val Lys Glu Ala Thr Pro Gly Gly Asn Val Lys
 40 45 50
 tct ggc gaa atc gtc aag gct gtt atc gtt cgc acc aag aag gag acc 307
 Ser Gly Glu Ile Val Lys Ala Val Ile Val Arg Thr Lys Lys Glu Thr
 55 60 65
 cgt cgt gca gac ggt tct tac atc tcc ttc gat gag aac gct gcc gtc 355
 Arg Arg Ala Asp Gly Ser Tyr Ile Ser Phe Asp Glu Asn Ala Ala Val
 70 75 80 85
 atc atc aag aac gac aac gag cca cgt ggc acc cgt atc ttc gga cca 403
 Ile Ile Lys Asn Asp Asn Glu Pro Arg Gly Thr Arg Ile Phe Gly Pro

	90	95	100	
gtt gct cgt gaa ctt cgt gag aag aag ttc atg aag atc gtt tct ctc				451
Val Ala Arg Glu Leu Arg Glu Lys Lys Phe Met Lys Ile Val Ser Leu				
	105	110	115	

gca ccg gag gtg att taagaatgaa ggtccacaag ggc	489
Ala Pro Glu Val Ile	
120	

<210> 336

<211> 122

<212> PRT

<213> Corynebacterium glutamicum

<400> 336

Val Ile Gln Gln Glu Ser Arg Leu Lys Val Ala Asp Asn Thr Gly Ala	
1 5 10 15	

Arg Glu Ile Leu Cys Ile Arg Val Leu Gly Gly Ser Thr Arg Arg Phe	
20 25 30	

Ala Gly Ile Gly Asp Val Ile Val Ala Thr Val Lys Glu Ala Thr Pro	
35 40 45	

Gly Gly Asn Val Lys Ser Gly Glu Ile Val Lys Ala Val Ile Val Arg	
50 55 60	

Thr Lys Lys Glu Thr Arg Arg Ala Asp Gly Ser Tyr Ile Ser Phe Asp	
65 70 75 80	

Glu Asn Ala Ala Val Ile Ile Lys Asn Asp Asn Glu Pro Arg Gly Thr	
85 90 95	

Arg Ile Phe Gly Pro Val Ala Arg Glu Leu Arg Glu Lys Lys Phe Met	
100 105 110	

Lys Ile Val Ser Leu Ala Pro Glu Val Ile	
115 120	

<210> 337

<211> 362

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(339)

<223> FRXA00709

<400> 337

gtc gcc gac aac act ggt gca cgt gaa att ctg tgc atc cgc gtt ctc	48
Val Ala Asp Asn Thr Gly Ala Arg Glu Ile Leu Cys Ile Arg Val Leu	
1 5 10 15	

ggt gga tcc acc cga cgt ttt gct ggc att ggt gac gtc atc gtc gcc	96
Gly Gly Ser Thr Arg Arg Phe Ala Gly Ile Gly Asp Val Ile Val Ala	
20 25 30	

act gtc aag gaa gca acc cca ggc ggc aac gta aag tct ggc gaa atc 144
Thr Val Lys Glu Ala Thr Pro Gly Gly Asn Val Lys Ser Gly Glu Ile
35 40 45

gtc aag gct gtt atc gtt cgc acc aag aag gag acc cgt cgt gca gac 192
Val Lys Ala Val Ile Val Arg Thr Lys Lys Glu Thr Arg Arg Ala Asp
50 55 60

ggt tct tac atc tcc ttc gat gag aac gct gcc gtc atc atc aag aac 240
Gly Ser Tyr Ile Ser Phe Asp Glu Asn Ala Ala Val Ile Ile Lys Asn
65 70 75 80

gac aac gag cca cgt ggc acc cgt atc ttc gga cca gtt gct cgt gaa 288
Asp Asn Glu Pro Arg Gly Thr Arg Ile Phe Gly Pro Val Ala Arg Glu
85 90 95

ctt cgt gag aag aag ttc atg aag atc gtt tct ctc gca ccg gag gtg 336
Leu Arg Glu Lys Lys Phe Met Lys Ile Val Ser Leu Ala Pro Glu Val
100 105 110

att taagaatgaa ggtccacaag ggc 362
Ile

<210> 338

<211> 113

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

Val Ala Asp Asn Thr Gly Ala Arg Glu Ile Leu Cys Ile Arg Val Leu
1 5 10 15

Gly Gly Ser Thr Arg Arg Phe Ala Gly Ile Gly Asp Val Ile Val Ala
20 25 30

Thr Val Lys Glu Ala Thr Pro Gly Gly Asn Val Lys Ser Gly Glu Ile
35 40 45

Val Lys Ala Val Ile Val Arg Thr Lys Lys Glu Thr Arg Arg Ala Asp
50 55 60

Gly Ser Tyr Ile Ser Phe Asp Glu Asn Ala Ala Val Ile Ile Lys Asn
65 70 75 80

Asp Asn Glu Pro Arg Gly Thr Arg Ile Phe Gly Pro Val Ala Arg Glu
85 90 95

Leu Arg Glu Lys Lys Phe Met Lys Ile Val Ser Leu Ala Pro Glu Val
100 105 110

Ile

<210> 339

<211> 435

<212> DNA

<213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(412)
 <223> RXA00710

<400> 339

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tcatgaagat cgtttctctc gcaccggagg tgatttaaga atg aag gtc cac aag 115
              Met Lys Val His Lys
              1              5

ggc gat atg gtt ctg gtc atc tca ggt cca gac aag ggt gct aag gga 163
Gly Asp Met Val Leu Val Ile Ser Gly Pro Asp Lys Gly Ala Lys Gly
              10              15              20

cag gtc atc gcg gct ttc cct aag acc gaa aag gtt ctc gtc gaa ggc 211
Gln Val Ile Ala Ala Phe Pro Lys Thr Glu Lys Val Leu Val Glu Gly
              25              30              35

gtt aac cgc atc aag aag cac gta gct aac tcc gca cca gag cgt ggc 259
Val Asn Arg Ile Lys Lys His Val Ala Asn Ser Ala Pro Glu Arg Gly
              40              45              50

gca gag tcc ggc gga atc gtg acc cag gaa gct ccg atc cat gtc tct 307
Ala Glu Ser Gly Gly Ile Val Thr Gln Glu Ala Pro Ile His Val Ser
              55              60              65

aac gtc atg gtc atc gac tcc gac gga aac cca act cgc gtt ggc tac 355
Asn Val Met Val Ile Asp Ser Asp Gly Asn Pro Thr Arg Val Gly Tyr
              70              75              80              85

cgt ttc gat gaa aac ggc aag aag gtc cgc gtt tct cgt cgc aat ggg 403
Arg Phe Asp Glu Asn Gly Lys Lys Val Arg Val Ser Arg Arg Asn Gly
              90              95              100

aag gat atc taatgactga gaattacatc cct 435
Lys Asp Ile
  
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<210> 340
 <211> 104
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 340

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Met Lys Val His Lys Gly Asp Met Val Leu Val Ile Ser Gly Pro Asp
  1              5              10              15

Lys Gly Ala Lys Gly Gln Val Ile Ala Ala Phe Pro Lys Thr Glu Lys
              20              25              30

Val Leu Val Glu Gly Val Asn Arg Ile Lys Lys His Val Ala Asn Ser
              35              40              45

Ala Pro Glu Arg Gly Ala Glu Ser Gly Gly Ile Val Thr Gln Glu Ala
              50              55              60

Pro Ile His Val Ser Asn Val Met Val Ile Asp Ser Asp Gly Asn Pro
              65              70              75              80
  
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Val Gln Arg Arg Lys Phe Tyr Val Pro Ser Glu Gly Arg Thr Ile Thr

35

40

45

Leu Thr Val Ser Thr Lys Gly Leu Lys Val Ile Asp Arg Asp Gly Ile
 50 55 60

Glu Ala Val Val Ala Gln Ile Arg Ala Arg Gly Glu Lys Ile
 65 70 75

<210> 343

<211> 241

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(241)

<223> RXA02043

<400> 343

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catgcaaggt ccgtatcgtc aagagggagg atcagctcta atg gct atc ggt acc 115
 Met Ala Ile Gly Thr
 1 5

cca gca cac gag ttc cgt gag ctc aac gag gaa gaa ctg gtt acc cgc 163
 Pro Ala His Glu Phe Arg Glu Leu Asn Glu Glu Glu Leu Val Thr Arg
 10 15 20

ctc aac gag gct aag gaa gaa ctg ttc aac ctt cgc ttc cag ctt gcc 211
 Leu Asn Glu Ala Lys Glu Glu Leu Phe Asn Leu Arg Phe Gln Leu Ala
 25 30 35

acc ggc cag ctg acc aac aac cgc cgc ctg 241
 Thr Gly Gln Leu Thr Asn Asn Arg Arg Leu
 40 45

<210> 344

<211> 47

<212> PRT

<213> Corynebacterium glutamicum

<400> 344

Met Ala Ile Gly Thr Pro Ala His Glu Phe Arg Glu Leu Asn Glu Glu
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Glu Leu Val Thr Arg Leu Asn Glu Ala Lys Glu Glu Leu Phe Asn Leu
 20 25 30

Arg Phe Gln Leu Ala Thr Gly Gln Leu Thr Asn Asn Arg Arg Leu
 35 40 45

<210> 345

<211> 306

<212> DNA

<213> Corynebacterium glutamicum

<220>

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	Met	Lys	Lys	Asp	Ile	
	1				5	
cac cct gac tac cat gcg gta gtc ttc cag gac gca ggt act ggc ttc						163
His Pro Asp Tyr His Ala Val Val Phe Gln Asp Ala Gly Thr Gly Phe						
			10		15	20
cag ttc ctg acc aag tcc acc gct tcc agc gac cgc acc gtg tcc tgg						211
Gln Phe Leu Thr Lys Ser Thr Ala Ser Ser Asp Arg Thr Val Ser Trp						
			25		30	35
gaa gat ggt aac gag tac cca ctg atc gtc gtt gac gtc acc agc gag						259
Glu Asp Gly Asn Glu Tyr Pro Leu Ile Val Val Asp Val Thr Ser Glu						
			40		45	50
tct cac cca ttc tgg acc ggc gct cag cgt gtc atg gac acc gct ggt						307
Ser His Pro Phe Trp Thr Gly Ala Gln Arg Val Met Asp Thr Ala Gly						
			55		60	65
cgt gtt gag aag ttc gag cgt cgc ttc ggt ggc atg gct cgc cgc aag						355
Arg Val Glu Lys Phe Glu Arg Arg Phe Gly Gly Met Ala Arg Arg Lys						
			70		75	80
aag aag gca taggagggaa aacaatggca gtt						387
Lys Lys Ala						

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<211> 88

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

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Ala	Gly	Thr	Gly	Phe	Gln	Phe	Leu	Thr	Lys	Ser	Thr	Ala	Ser	Ser	Asp
			20					25					30		

Arg	Thr	Val	Ser	Trp	Glu	Asp	Gly	Asn	Glu	Tyr	Pro	Leu	Ile	Val	Val
			35				40					45			

Asp	Val	Thr	Ser	Glu	Ser	His	Pro	Phe	Trp	Thr	Gly	Ala	Gln	Arg	Val
	50					55					60				

Met	Asp	Thr	Ala	Gly	Arg	Val	Glu	Lys	Phe	Glu	Arg	Arg	Phe	Gly	Gly
65					70					75				80	

Met	Ala	Arg	Arg	Lys	Lys	Lys	Ala
				85			

<210> 349

<211> 285

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(262)

<223> RXA02636

<400> 349

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ttgttgctca gattcgcgca cgtggggaga agatctaaag atg gca cgt aat gat 115
 Met Ala Arg Asn Asp
 1 5

atc cgc cct atc atc aag ctg aag tct act gct ggc act ggt tac acc 163
 Ile Arg Pro Ile Ile Lys Leu Lys Ser Thr Ala Gly Thr Gly Tyr Thr
 10 15 20

tat gtc acc cgt aag aac aag cgc aac aac ccg gac cgt att tcc ctc 211
 Tyr Val Thr Arg Lys Asn Lys Arg Asn Asn Pro Asp Arg Ile Ser Leu
 25 30 35

atg aag tac gat cca gta gtc cgt aag cac gtc gaa ttc cgc gag gag 259
 Met Lys Tyr Asp Pro Val Val Arg Lys His Val Glu Phe Arg Glu Glu
 40 45 50

cga taatcaatgg ctaagaagtc aaa 285
 Arg

<210> 350

<211> 54

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

Met Ala Arg Asn Asp Ile Arg Pro Ile Ile Lys Leu Lys Ser Thr Ala
 1 5 10 15

Gly Thr Gly Tyr Thr Tyr Val Thr Arg Lys Asn Lys Arg Asn Asn Pro
 20 25 30

Asp Arg Ile Ser Leu Met Lys Tyr Asp Pro Val Val Arg Lys His Val
 35 40 45

Glu Phe Arg Glu Glu Arg
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<210> 351

<211> 264

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(241)

<223> RXA01423

<400> 351

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gtccggtgat ccgtcaacaa aatatttagg agtgtttcac atg gca aag ggc aag 115
 Met Ala Lys Gly Lys
 1 5

cgg acg ttc cag ccg aac aac cgt cgt cgt gca cgt gtt cac ggt ttc 163
 Arg Thr Phe Gln Pro Asn Asn Arg Arg Arg Ala Arg Val His Gly Phe
 10 15 20
 cgt ctt cgt atg cgt acc cgt gca ggt cgt gca att gtt gcg gct cgt 211
 Arg Leu Arg Met Arg Thr Arg Ala Gly Arg Ala Ile Val Ala Ala Arg
 25 30 35
 cgt cgc aag ggt cgc gca aag ctg acc gcg taatttttta gcgtcaccac 261
 Arg Arg Lys Gly Arg Ala Lys Leu Thr Ala
 40 45
 aat 264

<210> 352
 <211> 47
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 352
 Met Ala Lys Gly Lys Arg Thr Phe Gln Pro Asn Asn Arg Arg Arg Ala
 1 5 10 15
 Arg Val His Gly Phe Arg Leu Arg Met Arg Thr Arg Ala Gly Arg Ala
 20 25 30
 Ile Val Ala Ala Arg Arg Arg Lys Gly Arg Ala Lys Leu Thr Ala
 35 40 45

<210> 353
 <211> 315
 <212> DNA
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<220>
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 <222> (101)..(292)
 <223> RXA02419

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 Met Lys Asn Lys Thr
 1 5
 cac aag ggc acc gca aag cgc gtt aag gtg act ggc tcc ggc aag ctc 163
 His Lys Gly Thr Ala Lys Arg Val Lys Val Thr Gly Ser Gly Lys Leu
 10 15 20
 gtt cgc gag cag gca aac cgc cgc cac ctt ctc gag ggc aag tca tct 211
 Val Arg Glu Gln Ala Asn Arg Arg His Leu Leu Glu Gly Lys Ser Ser
 25 30 35
 acc cgc act cgt cgc ctg aag ggc atc gtt gag gtt gac aag gcc gac 259
 Thr Arg Thr Arg Arg Leu Lys Gly Ile Val Glu Val Asp Lys Ala Asp
 40 45 50

acc aag cgc atg aag cgc ctg ctc ggc aag gct taagtttaaa accttcgcct 312
 Thr Lys Arg Met Lys Arg Leu Leu Gly Lys Ala
 55 60

aaa 315

<210> 354

<211> 64

<212> PRT

<213> Corynebacterium glutamicum

<400> 354

Met Lys Asn Lys Thr His Lys Gly Thr Ala Lys Arg Val Lys Val Thr
 1 5 10 15

Gly Ser Gly Lys Leu Val Arg Glu Gln Ala Asn Arg Arg His Leu Leu
 20 25 30

Glu Gly Lys Ser Ser Thr Arg Thr Arg Arg Leu Lys Gly Ile Val Glu
 35 40 45

Val Asp Lys Ala Asp Thr Lys Arg Met Lys Arg Leu Leu Gly Lys Ala
 50 55 60

<210> 355

<211> 1581

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1558)

<223> RXA02190

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ccattatcta atttcctatc catttcggag caattttacat atg ccc acc aac aat 115
 Met Pro Thr Asn Asn
 1 5

gca cct cag gta gcc atc aac gac att ggc tct gct gag gac ttc ctt 163
 Ala Pro Gln Val Ala Ile Asn Asp Ile Gly Ser Ala Glu Asp Phe Leu
 10 15 20

gca gca atc gac gca acc atc aag tac ttc aac gat ggc gat atc gtt 211
 Ala Ala Ile Asp Ala Thr Ile Lys Tyr Phe Asn Asp Gly Asp Ile Val
 25 30 35

gaa ggc acc gtg gta aag gtc gat cgt gac gag gta ctt ctc gac atc 259
 Glu Gly Thr Val Val Lys Val Asp Arg Asp Glu Val Leu Leu Asp Ile
 40 45 50

gga tac aag acc gag ggt gtc atc cca tcc cgc gag ctg tcc atc aag 307
 Gly Tyr Lys Thr Glu Gly Val Ile Pro Ser Arg Glu Leu Ser Ile Lys
 55 60 65

gagatcaaaa ccccgctctat acagggcatt tgaaagatac tgcatacctgt

cac His 70	gat Asp	gtc Val	gat Asp	cca Pro	gac Asp 75	gag Glu	gtc Val	gtc Val	gaa Glu	gtc Val 80	ggc Gly	gac Asp	caa Gln	att Ile	gac Asp 85	355
gca Ala	ctt Leu	gtc Val	ctc Leu	acc Thr 90	aag Lys	gaa Glu	gac Asp	aaa Lys	gaa Glu 95	ggc Gly	cgt Arg	ctg Leu	atc Ile	ctt Leu 100	tcc Ser	403
aag Lys	aag Lys	cgt Arg	gct Ala 105	cag Gln	tac Tyr	gag Glu	cgt Arg	gct Ala 110	tgg Trp	ggc Gly	gcc Ala	atc Ile	gag Glu 115	gag Glu	ctc Leu	451
aag Lys	gaa Glu	aag Lys 120	gac Asp	gag Glu	cca Pro	gtt Val	acc Thr 125	ggc Gly	acc Thr	gtc Val	atc Ile	gag Glu 130	gtc Val	gtc Val	aag Lys	499
ggc Gly 135	gtc Leu	ctc Ile	atc Ile	atc Ile	gac Asp	atc Ile 140	ggc Gly	ctc Leu	cgt Arg	ggc Gly	ttc Phe 145	ctg Leu	cct Pro	gca Ala	tcc Ser	547
ctc Leu 150	gtt Val	gag Glu	atg Met	cgt Arg	cgc Arg 155	gtc Val	cgc Arg	gac Asp	ctg Leu	gat Asp 160	ccg Pro	tac Tyr	atc Ile	ggc Gly	cag Gln 165	595
gag Glu	ctc Leu	gaa Glu	gct Ala	aag Lys 170	atc Ile	atc Ile	gag Glu	ctg Leu	gac Asp 175	aag Lys	aac Asn	cgc Arg	aac Asn	aac Asn 180	gtc Val	643
gtt Val	ctg Leu	tcc Ser	cgt Arg 185	cgc Arg	gca Ala	ttc Phe	ctc Leu	gag Glu 190	cag Gln	acc Thr	cag Gln	tct Ser	gag Glu 195	gtc Val	cgc Arg	691
tcc Ser	gag Glu	ttc Phe 200	ctg Leu	cac His	cag Gln	ctc Leu	cag Gln 205	aag Lys	ggc Gly	cag Gln	gtc Val	cgc Arg 210	aag Lys	ggc Gly	gtc Val	739
gtc Val 215	tct Ser	tcc Ser	atc Ile	gtc Val	aac Asn	ttc Phe 220	ggc Gly	gca Ala	ttc Phe	gtc Val	gat Asp 225	ctc Leu	ggc Gly	ggc Gly	gtc Val	787
gac Asp 230	gga Gly	ctg Leu	gtt Val	cac His	gtt Val 235	tcc Ser	gag Glu	ctg Leu	tcc Ser	tgg Trp 240	aag Lys	cac His	atc Ile	gac Asp	cac His 245	835
cca Pro	tct Ser	gag Glu	gtt Val	gtc Val 250	acc Thr	gtc Val	ggc Gly	gac Asp	gaa Glu 255	gtc Val	acc Thr	gtt Val	gag Glu	gtt Val 260	ctc Leu	883
gag Glu	gtc Val	gat Asp	ctc Leu 265	gac Asp	cgc Arg	gag Glu	cgc Arg	gtc Val 270	tcc Ser	ctg Leu	tcc Ser	ctg Leu	aag Lys 275	gct Ala	acc Thr	931
cag Gln	gaa Glu	gac Asp 280	cca Pro	tgg Trp	cgc Arg	gtc Val	ttc Phe 285	gct Ala	cgc Arg	act Thr	cac His	gct Ala 290	gtg Val	ggc Gly	cag Gln	979
atc Ile	gtt Val 295	cca Pro	ggc Gly	aag Lys	gtc Val	acc Thr 300	aag Lys	ctg Leu	gtt Val	cca Pro	ttc Phe 305	ggc Gly	gcg Ala	ttc Phe	gtt Val	1027

cgc gtc gaa gag ggc atc gaa ggc ctc gtc cac atc tcc gag ctg gct	1075
Arg Val Glu Glu Gly Ile Glu Gly Leu Val His Ile Ser Glu Leu Ala	
310 315 320 325	
cag cgc cac gtc gag gtt ccg gac cag gtt gtc gca gtt ggc gaa gag	1123
Gln Arg His Val Glu Val Pro Asp Gln Val Val Ala Val Gly Glu Glu	
330 335 340	
gtc atg gtc aag gtc atc gac atc gat ctc gag cgt cgt cgt atc tcc	1171
Val Met Val Lys Val Ile Asp Ile Asp Leu Glu Arg Arg Arg Ile Ser	
345 350 355	
ctg tcc ctc aag cag gct gac gag gac tac acc gaa gag ttc gac cca	1219
Leu Ser Leu Lys Gln Ala Asp Glu Asp Tyr Thr Glu Glu Phe Asp Pro	
360 365 370	
tcc aag tac gga atg gct gac tcc tac gac gag cag ggt aac tac atc	1267
Ser Lys Tyr Gly Met Ala Asp Ser Tyr Asp Glu Gln Gly Asn Tyr Ile	
375 380 385	
ttc cct gag ggc ttc gac gcc gag acc aac gaa tgg ctc gaa ggc ttc	1315
Phe Pro Glu Gly Phe Asp Ala Glu Thr Asn Glu Trp Leu Glu Gly Phe	
390 395 400 405	
gat gag cag cgt cag gct tgg gaa gct cgc tac gcc gag tcc gag cgt	1363
Asp Glu Gln Arg Gln Ala Trp Glu Ala Arg Tyr Ala Glu Ser Glu Arg	
410 415 420	
cgc ttc acc gct cac acc gct cag atc gag cgt cgt cgt cag cag gct	1411
Arg Phe Thr Ala His Thr Ala Gln Ile Glu Arg Arg Arg Gln Gln Ala	
425 430 435	
gaa gag gca gct gcc gag gct ccg gcc ggc aac tac tcc act gat tct	1459
Glu Glu Ala Ala Glu Ala Pro Ala Gly Asn Tyr Ser Thr Asp Ser	
440 445 450	
gca gaa gat gca cct gca gca gaa gca gtt gaa gag tcc gct ggc tcc	1507
Ala Glu Asp Ala Pro Ala Ala Glu Ala Val Glu Glu Ser Ala Gly Ser	
455 460 465	
ctc gct tcc gat gag cag ctc gct gct ctt cgc gag aag ctc gca ggt	1555
Leu Ala Ser Asp Glu Gln Leu Ala Ala Leu Arg Glu Lys Leu Ala Gly	
470 475 480 485	
aac taatagttcc tgcacctctt aag	1581
Asn	

<210> 356

<211> 486

<212> PRT

<213> Corynebacterium glutamicum

<400> 356

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			20					25					30		

Asp Gly Asp Ile Val Glu Gly Thr Val Val Lys Val Asp Arg Asp Glu
 35 40 45
 Val Leu Leu Asp Ile Gly Tyr Lys Thr Glu Gly Val Ile Pro Ser Arg
 50 55 60
 Glu Leu Ser Ile Lys His Asp Val Asp Pro Asp Glu Val Val Glu Val
 65 70 75 80
 Gly Asp Gln Ile Asp Ala Leu Val Leu Thr Lys Glu Asp Lys Glu Gly
 85 90 95
 Arg Leu Ile Leu Ser Lys Lys Arg Ala Gln Tyr Glu Arg Ala Trp Gly
 100 105 110
 Ala Ile Glu Glu Leu Lys Glu Lys Asp Glu Pro Val Thr Gly Thr Val
 115 120 125
 Ile Glu Val Val Lys Gly Gly Leu Ile Ile Asp Ile Gly Leu Arg Gly
 130 135 140
 Phe Leu Pro Ala Ser Leu Val Glu Met Arg Arg Val Arg Asp Leu Asp
 145 150 155 160
 Pro Tyr Ile Gly Gln Glu Leu Glu Ala Lys Ile Ile Glu Leu Asp Lys
 165 170 175
 Asn Arg Asn Asn Val Val Leu Ser Arg Arg Ala Phe Leu Glu Gln Thr
 180 185 190
 Gln Ser Glu Val Arg Ser Glu Phe Leu His Gln Leu Gln Lys Gly Gln
 195 200 205
 Val Arg Lys Gly Val Val Ser Ser Ile Val Asn Phe Gly Ala Phe Val
 210 215 220
 Asp Leu Gly Gly Val Asp Gly Leu Val His Val Ser Glu Leu Ser Trp
 225 230 235 240
 Lys His Ile Asp His Pro Ser Glu Val Val Thr Val Gly Asp Glu Val
 245 250 255
 Thr Val Glu Val Leu Glu Val Asp Leu Asp Arg Glu Arg Val Ser Leu
 260 265 270
 Ser Leu Lys Ala Thr Gln Glu Asp Pro Trp Arg Val Phe Ala Arg Thr
 275 280 285
 His Ala Val Gly Gln Ile Val Pro Gly Lys Val Thr Lys Leu Val Pro
 290 295 300
 Phe Gly Ala Phe Val Arg Val Glu Glu Gly Ile Glu Gly Leu Val His
 305 310 315 320
 Ile Ser Glu Leu Ala Gln Arg His Val Glu Val Pro Asp Gln Val Val
 325 330 335
 Ala Val Gly Glu Glu Val Met Val Lys Val Ile Asp Ile Asp Leu Glu
 340 345 350
 Arg Arg Arg Ile Ser Leu Ser Leu Lys Gln Ala Asp Glu Asp Tyr Thr

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Trp Leu Gly Gly Met Leu Thr Asn Phe Gln Thr Val Ser Lys Arg Leu
 70 75 80 85
 aac cgc atg aag gaa ctg cag gca atg gat gct gca gaa aac ggc tac 403
 Asn Arg Met Lys Glu Leu Gln Ala Met Asp Ala Ala Glu Asn Gly Tyr
 90 95 100
 gag ggt cgc acc aag cgc gaa gtt ctc atg ctg acc cgt gag cgc acc 451
 Glu Gly Arg Thr Lys Arg Glu Val Leu Met Leu Thr Arg Glu Arg Thr
 105 110 115
 aag ctg gag cgc gtc ctc ggt ggt atc gca gag atg acc cgc gtg cct 499
 Lys Leu Glu Arg Val Leu Gly Gly Ile Ala Glu Met Thr Arg Val Pro
 120 125 130
 tcc gca ctg tgg atc att gac acc aac aag gag cac atc gct gtc gct 547
 Ser Ala Leu Trp Ile Ile Asp Thr Asn Lys Glu His Ile Ala Val Ala
 135 140 145
 gag gct cac aag ctg aac atc cca gtt gtt gcc atc ctg gac acc aac 595
 Glu Ala His Lys Leu Asn Ile Pro Val Val Ala Ile Leu Asp Thr Asn
 150 155 160 165
 tgt gac cca gac gtt gtt gac ttc cca gtt cct ggt aac gac gac gca 643
 Cys Asp Pro Asp Val Val Asp Phe Pro Val Pro Gly Asn Asp Asp Ala
 170 175 180
 atc cgc tcc acc gca ctg ctt tcc cgc gtt atc tcc acc gct gtg gaa 691
 Ile Arg Ser Thr Ala Leu Leu Ser Arg Val Ile Ser Thr Ala Val Glu
 185 190 195
 gag ggt aag aag gca cgc gag gag cgt cag ctg gca gct gct aag gat 739
 Glu Gly Lys Lys Ala Arg Glu Glu Arg Gln Leu Ala Ala Ala Lys Asp
 200 205 210
 gca gca ggc gac gca aag cct gag gca gag gaa gca cca gca gca gct 787
 Ala Ala Gly Asp Ala Lys Pro Glu Ala Glu Glu Ala Pro Ala Ala Ala
 215 220 225
 gag gct gaa gag gca cct gca gct gag gct gaa gag gca cct gca gct 835
 Glu Ala Glu Glu Ala Pro Ala Ala Glu Ala Glu Glu Ala Pro Ala Ala
 230 235 240 245
 gag taagctgccc ttaactgcag ttt 861
 Glu

<210> 358

<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

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Glu Thr Val Ala His Gly Gly Thr Val Leu Phe Val Gly Thr Lys Lys

35					40					45					
Gln	Ala	Gln	Glu	Ala	Val	Gln	Val	Glu	Ala	Asp	Arg	Val	Gly	Met	Pro
50						55					60				
Tyr	Val	Asn	His	Arg	Trp	Leu	Gly	Gly	Met	Leu	Thr	Asn	Phe	Gln	Thr
65					70					75					80
Val	Ser	Lys	Arg	Leu	Asn	Arg	Met	Lys	Glu	Leu	Gln	Ala	Met	Asp	Ala
				85					90					95	
Ala	Glu	Asn	Gly	Tyr	Glu	Gly	Arg	Thr	Lys	Arg	Glu	Val	Leu	Met	Leu
			100					105					110		
Thr	Arg	Glu	Arg	Thr	Lys	Leu	Glu	Arg	Val	Leu	Gly	Gly	Ile	Ala	Glu
		115					120					125			
Met	Thr	Arg	Val	Pro	Ser	Ala	Leu	Trp	Ile	Ile	Asp	Thr	Asn	Lys	Glu
	130					135					140				
His	Ile	Ala	Val	Ala	Glu	Ala	His	Lys	Leu	Asn	Ile	Pro	Val	Val	Ala
145					150					155					160
Ile	Leu	Asp	Thr	Asn	Cys	Asp	Pro	Asp	Val	Val	Asp	Phe	Pro	Val	Pro
				165					170					175	
Gly	Asn	Asp	Asp	Ala	Ile	Arg	Ser	Thr	Ala	Leu	Leu	Ser	Arg	Val	Ile
		180						185					190		
Ser	Thr	Ala	Val	Glu	Glu	Gly	Lys	Lys	Ala	Arg	Glu	Glu	Arg	Gln	Leu
		195					200					205			
Ala	Ala	Ala	Lys	Asp	Ala	Ala	Gly	Asp	Ala	Lys	Pro	Glu	Ala	Glu	Glu
	210					215					220				
Ala	Pro	Ala	Ala	Ala	Glu	Ala	Glu	Glu	Ala	Pro	Ala	Ala	Glu	Ala	Glu
225					230					235					240
Glu	Ala	Pro	Ala	Ala	Glu										
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<210> 359

<211> 894

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(871)

<223> FRXA01912

<400> 359

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				Met	Arg	Arg	Phe	Ile	
				1				5	

ttc	acc	gag	cgt	aac	ggc	atc	tac	atc	att	gac	ctt	cag	cag	acc	ctg	163
Phe	Thr	Glu	Arg	Asn	Gly	Ile	Tyr	Ile	Ile	Asp	Leu	Gln	Gln	Thr	Leu	

10										15					20					
acc	tac	atc	gat	cag	gct	ttc	gag	ttc	gtc	aag	gaa	acc	gtt	gct	cac	211				
Thr	Tyr	Ile	Asp	Gln	Ala	Phe	Glu	Phe	Val	Lys	Glu	Thr	Val	Ala	His					
			25				30						35							
ggg	ggc	acc	gtt	ctt	ttc	gtt	ggg	acc	aaa	aag	cag	gct	cag	gaa	gct	259				
Gly	Gly	Thr	Val	Leu	Phe	Val	Gly	Thr	Lys	Lys	Gln	Ala	Gln	Glu	Ala					
			40				45						50							
gtt	cag	gtt	gag	gca	gac	cgc	gtt	ggg	atg	cct	tac	gtg	aac	cac	cgt	307				
Val	Gln	Val	Glu	Ala	Asp	Arg	Val	Gly	Met	Pro	Tyr	Val	Asn	His	Arg					
			55				60						65							
tgg	ctc	ggc	ggc	atg	ctg	acc	aac	ttc	cag	acc	gtt	tcc	aag	cgt	ctg	355				
Trp	Leu	Gly	Gly	Met	Leu	Thr	Asn	Phe	Gln	Thr	Val	Ser	Lys	Arg	Leu					
70				75						80			85							
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Asn	Arg	Met	Lys	Glu	Leu	Gln	Ala	Met	Asp	Ala	Ala	Glu	Asn	Gly	Tyr					
			90						95						100					
gag	ggg	cgc	acc	aag	cgc	gaa	gtt	ctc	atg	ctg	acc	cgt	gag	cgc	acc	451				
Glu	Gly	Arg	Thr	Lys	Arg	Glu	Val	Leu	Met	Leu	Thr	Arg	Glu	Arg	Thr					
			105						110						115					
aag	ctg	gag	cgc	gtc	ctc	ggg	ggg	atc	gca	gag	atg	acc	cgc	gtg	cct	499				
Lys	Leu	Glu	Arg	Val	Leu	Gly	Gly	Ile	Ala	Glu	Met	Thr	Arg	Val	Pro					
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tcc	gca	ctg	tgg	atc	att	gac	acc	aac	aag	gag	cac	atc	gct	gtc	gct	547				
Ser	Ala	Leu	Trp	Ile	Ile	Asp	Thr	Asn	Lys	Glu	His	Ile	Ala	Val	Ala					
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gag	gct	cac	aag	ctg	aac	atc	cca	gtt	gtt	gcc	atc	ctg	gac	acc	aac	595				
Glu	Ala	His	Lys	Leu	Asn	Ile	Pro	Val	Val	Ala	Ile	Leu	Asp	Thr	Asn					
150						155						160			165					
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Cys	Asp	Pro	Asp	Val	Val	Asp	Phe	Pro	Val	Pro	Gly	Asn	Asp	Asp	Ala					
			170						175						180					
atc	cgc	tcc	acc	gca	ctg	ctt	tcc	cgc	gtt	atc	tcc	acc	gct	gtg	gaa	691				
Ile	Arg	Ser	Thr	Ala	Leu	Leu	Ser	Arg	Val	Ile	Ser	Thr	Ala	Val	Glu					
			185						190						195					
gag	ggg	aag	aag	gca	cgc	gag	gag	cgt	cag	ctg	gca	gct	gct	aag	gat	739				
Glu	Gly	Lys	Lys	Ala	Arg	Glu	Glu	Arg	Gln	Leu	Ala	Ala	Ala	Lys	Asp					
			200						205						210					
gca	gca	ggc	gac	gca	aag	cct	gag	gca	gag	gaa	gca	cca	gca	gca	gct	787				
Ala	Ala	Gly	Asp	Ala	Lys	Pro	Glu	Ala	Glu	Glu	Ala	Pro	Ala	Ala	Ala					
215						220						225								
gag	gct	gaa	gag	gca	cct	gca	gct	gag	gct	gaa	gaa	cac	ctg	cag	ctg	835				
Glu	Ala	Glu	Glu	Ala	Pro	Ala	Ala	Glu	Ala	Glu	Glu	His	Leu	Gln	Leu					
230						235						240			245					
agt	aag	ctg	ccc	tta	act	gca	gtt	tct	gca	gtt	agc	tgaccaattt				881				
Ser	Lys	Leu	Pro	Leu	Thr	Ala	Val	Ser	Ala	Val	Ser									
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894

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<400> 360

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Glu Thr Val Ala His Gly Gly Thr Val Leu Phe Val Gly Thr Lys Lys
 35 40 45

Gln Ala Gln Glu Ala Val Gln Val Glu Ala Asp Arg Val Gly Met Pro
 50 55 60

Tyr Val Asn His Arg Trp Leu Gly Gly Met Leu Thr Asn Phe Gln Thr
 65 70 75 80

Val Ser Lys Arg Leu Asn Arg Met Lys Glu Leu Gln Ala Met Asp Ala
 85 90 95

Ala Glu Asn Gly Tyr Glu Gly Arg Thr Lys Arg Glu Val Leu Met Leu
 100 105 110

Thr Arg Glu Arg Thr Lys Leu Glu Arg Val Leu Gly Gly Ile Ala Glu
 115 120 125

Met Thr Arg Val Pro Ser Ala Leu Trp Ile Ile Asp Thr Asn Lys Glu
 130 135 140

His Ile Ala Val Ala Glu Ala His Lys Leu Asn Ile Pro Val Val Ala
 145 150 155 160

Ile Leu Asp Thr Asn Cys Asp Pro Asp Val Val Asp Phe Pro Val Pro
 165 170 175

Gly Asn Asp Asp Ala Ile Arg Ser Thr Ala Leu Leu Ser Arg Val Ile
 180 185 190

Ser Thr Ala Val Glu Glu Gly Lys Lys Ala Arg Glu Glu Arg Gln Leu
 195 200 205

Ala Ala Ala Lys Asp Ala Ala Gly Asp Ala Lys Pro Glu Ala Glu Glu
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Ala Pro Ala Ala Ala Glu Ala Glu Glu Ala Pro Ala Ala Glu Ala Glu
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Ser

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 Ser Tyr Ala Asp Tyr Val Ala Glu Asp Ile Lys Ile Arg Glu Phe Leu
 20 25 30
 tcc aag ggc ctc gac cgt gcc ggc atc gcc gac gtc gtc atc gag cgc 144
 Ser Lys Gly Leu Asp Arg Ala Gly Ile Ala Asp Val Val Ile Glu Arg
 35 40 45
 acc cgc gac cgc gtt cgc gta gac atc cac acc gct cgc cca ggc atc 192
 Thr Arg Asp Arg Val Arg Val Asp Ile His Thr Ala Arg Pro Gly Ile
 50 55 60
 gtc att ggt cgt cgt ggc gct gag gct gac cgc atc cgc cgt gag ctc 240
 Val Ile Gly Arg Arg Gly Ala Glu Ala Asp Arg Ile Arg Arg Glu Leu
 65 70 75 80
 gag aag ctc acc ggc aag cag gtt gcc ctc aac atc ctc gag gtc aag 288
 Glu Lys Leu Thr Gly Lys Gln Val Ala Leu Asn Ile Leu Glu Val Lys
 85 90 95
 aac gtc gat gct aac gct aag ctg gtg gca cag tcc atc gct gag cag 336
 Asn Val Asp Ala Asn Ala Lys Leu Val Ala Gln Ser Ile Ala Glu Gln
 100 105 110
 ctg acc aac cgc gtg gca ttc cgt cgc gca atg cgc aag gct atc cag 384
 Leu Thr Asn Arg Val Ala Phe Arg Arg Ala Met Arg Lys Ala Ile Gln
 115 120 125
 tct gca atg cgt cag cca cag gtt aag ggc atc aag gtc gtg tgc tcc 432
 Ser Ala Met Arg Gln Pro Gln Val Lys Gly Ile Lys Val Val Cys Ser
 130 135 140
 ggt cgt ctc ggc ggt gcc gag atg tcc cgc acc gag cgc tac cac gaa 480
 Gly Arg Leu Gly Gly Ala Glu Met Ser Arg Thr Glu Arg Tyr His Glu
 145 150 155 160
 ggt cgc gtt cca ctg cac acc ctt cgc gca gaa atc gat tac ggc acc 528
 Gly Arg Val Pro Leu His Thr Leu Arg Ala Glu Ile Asp Tyr Gly Thr
 165 170 175
 tac gag gct cac acc act ttc gga cgc atc ggc gtc aag gtg tgg atc 576
 Tyr Glu Ala His Thr Thr Phe Gly Arg Ile Gly Val Lys Val Trp Ile
 180 185 190
 tac aag ggt gac gtc gtt ggt gga cgt cgc gag agc gag atc aat gca 624

Tyr Lys Gly Asp Val Val Gly Gly Arg Arg Glu Ser Glu Ile Asn Ala
 195 200 205

ccc gca gag cgt cgc ggc cgc ggc gac cgc aac gca cgt ccg cgt cgt 672
 Pro Ala Glu Arg Arg Gly Arg Gly Asp Arg Asn Ala Arg Pro Arg Arg
 210 215 220

ggg ggc cag cgt cgt cag cgt gct gag cag aag cag gag ggc 714
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<400> 362

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 20 25 30

Ser Lys Gly Leu Asp Arg Ala Gly Ile Ala Asp Val Val Ile Glu Arg
 35 40 45

Thr Arg Asp Arg Val Arg Val Asp Ile His Thr Ala Arg Pro Gly Ile
 50 55 60

Val Ile Gly Arg Arg Gly Ala Glu Ala Asp Arg Ile Arg Arg Glu Leu
 65 70 75 80

Glu Lys Leu Thr Gly Lys Gln Val Ala Leu Asn Ile Leu Glu Val Lys
 85 90 95

Asn Val Asp Ala Asn Ala Lys Leu Val Ala Gln Ser Ile Ala Glu Gln
 100 105 110

Leu Thr Asn Arg Val Ala Phe Arg Arg Ala Met Arg Lys Ala Ile Gln
 115 120 125

Ser Ala Met Arg Gln Pro Gln Val Lys Gly Ile Lys Val Val Cys Ser
 130 135 140

Gly Arg Leu Gly Gly Ala Glu Met Ser Arg Thr Glu Arg Tyr His Glu
 145 150 155 160

Gly Arg Val Pro Leu His Thr Leu Arg Ala Glu Ile Asp Tyr Gly Thr
 165 170 175

Tyr Glu Ala His Thr Thr Phe Gly Arg Ile Gly Val Lys Val Trp Ile
 180 185 190

Tyr Lys Gly Asp Val Val Gly Gly Arg Arg Glu Ser Glu Ile Asn Ala
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Pro Ala Glu Arg Arg Gly Arg Gly Asp Arg Asn Ala Arg Pro Arg Arg
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Gly Gly Gln Arg Arg Gln Arg Ala Glu Gln Lys Gln Glu Gly
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 Met Ala Arg Tyr Thr
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 ggc cca gca acc cgt aaa tcc cgt cgt ctg cgc gtc gac ctt gtt ggt 163
 Gly Pro Ala Thr Arg Lys Ser Arg Arg Leu Arg Val Asp Leu Val Gly
 10 15 20
 gga gac atg gcg ttt gag cgc cgt cct tac cct cca gga cag gca ggc 211
 Gly Asp Met Ala Phe Glu Arg Arg Pro Tyr Pro Pro Gly Gln Ala Gly
 25 30 35
 cgt gca cgc atc aag gag tcc gag tac ctg ctg cag ctc cag gag aag 259
 Arg Ala Arg Ile Lys Glu Ser Glu Tyr Leu Leu Gln Leu Gln Glu Lys
 40 45 50
 cag aag gct cgt ttc atc tac ggc gtc atg gaa aag cag ttc cgt cgt 307
 Gln Lys Ala Arg Phe Ile Tyr Gly Val Met Glu Lys Gln Phe Arg Arg
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 tac tac gcc gag gct aac cgt cgc gca ggc aag acc ggt gag aac ctg 355
 Tyr Tyr Ala Glu Ala Asn Arg Arg Ala Gly Lys Thr Gly Glu Asn Leu
 70 75 80 85
 gtc gtc ctg ctc gag tcc cgc ctc gac aac gtc gtg tac cgc gca ggt 403
 Val Val Leu Leu Glu Ser Arg Leu Asp Asn Val Val Tyr Arg Ala Gly
 90 95 100
 ctg gca aac acc cgt cgc cag gct cgt cag ctt gtt tcc cac ggt cac 451
 Leu Ala Asn Thr Arg Arg Gln Ala Arg Gln Leu Val Ser His Gly His
 105 110 115
 ttc acc gtg aac ggc aag gca atc gac gtt cca tct ttc cgc gtt tct 499
 Phe Thr Val Asn Gly Lys Ala Ile Asp Val Pro Ser Phe Arg Val Ser
 120 125 130
 cag tac gac atc atc aat gtt cgt gag aag tcc cag aag atg aac tgg 547
 Gln Tyr Asp Ile Ile Asn Val Arg Glu Lys Ser Gln Lys Met Asn Trp
 135 140 145
 ttc gaa gag gct cag gac aac ctg gcc gac gca gtc gtc cca gct tgg 595
 Phe Glu Glu Ala Gln Asp Asn Leu Ala Asp Ala Val Val Pro Ala Trp
 150 155 160 165

ctc cag gtc gtt cct gag aac ctt cgt atc ctc gtg cac cag ctc cca 643
 Leu Gln Val Val Pro Glu Asn Leu Arg Ile Leu Val His Gln Leu Pro
 170 175 180

gag cgc gca cag atc gat atc cca ctg caa gag cag ctc atc gtc gag 691
 Glu Arg Ala Gln Ile Asp Ile Pro Leu Gln Glu Gln Leu Ile Val Glu
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 Phe Tyr Ser Lys
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Pro Gly Gln Ala Gly Arg Ala Arg Ile Lys Glu Ser Glu Tyr Leu Leu
 35 40 45

Gln Leu Gln Glu Lys Gln Lys Ala Arg Phe Ile Tyr Gly Val Met Glu
 50 55 60

Lys Gln Phe Arg Arg Tyr Tyr Ala Glu Ala Asn Arg Arg Ala Gly Lys
 65 70 75 80

Thr Gly Glu Asn Leu Val Val Leu Leu Glu Ser Arg Leu Asp Asn Val
 85 90 95

Val Tyr Arg Ala Gly Leu Ala Asn Thr Arg Arg Gln Ala Arg Gln Leu
 100 105 110

Val Ser His Gly His Phe Thr Val Asn Gly Lys Ala Ile Asp Val Pro
 115 120 125

Ser Phe Arg Val Ser Gln Tyr Asp Ile Ile Asn Val Arg Glu Lys Ser
 130 135 140

Gln Lys Met Asn Trp Phe Glu Glu Ala Gln Asp Asn Leu Ala Asp Ala
 145 150 155 160

Val Val Pro Ala Trp Leu Gln Val Val Pro Glu Asn Leu Arg Ile Leu
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Val His Gln Leu Pro Glu Arg Ala Gln Ile Asp Ile Pro Leu Gln Glu
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Gln Leu Ile Val Glu Phe Tyr Ser Lys
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				Met	Pro	Gly	Arg	Glu								
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cgc	cgt	gac	ggc	gga	cgc	tcc	gcc	gac	gac	aac	aag	caa	aac	gat	cgc	163
Arg	Arg	Asp	Gly	Gly	Arg	Ser	Ala	Asp	Asp	Asn	Lys	Gln	Asn	Asp	Arg	
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aac	gag	cgt	cgt	ggc	gga	ggc	cgc	cgc	gat	gac	cgt	cgc	aat	cag	cag	211
Asn	Glu	Arg	Arg	Gly	Gly	Gly	Arg	Arg	Asp	Asp	Arg	Arg	Asn	Gln	Gln	
			25					30					35			
cag	gac	gag	cgc	tca	cag	tac	atc	gag	cgt	gta	gtc	acc	atc	aac	cgt	259
Gln	Asp	Glu	Arg	Ser	Gln	Tyr	Ile	Glu	Arg	Val	Val	Thr	Ile	Asn	Arg	
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gtg	tcc	aag	gtc	gtc	aag	ggc	ggc	cgt	cgc	ttc	agc	ttc	acc	gca	ctt	307
Val	Ser	Lys	Val	Val	Lys	Gly	Gly	Arg	Arg	Phe	Ser	Phe	Thr	Ala	Leu	
		55				60					65					
gtc	atc	gtt	ggc	gac	ggc	aag	gga	atg	gtc	ggc	gtc	ggc	tac	ggc	aag	355
Val	Ile	Val	Gly	Asp	Gly	Lys	Gly	Met	Val	Gly	Val	Gly	Tyr	Gly	Lys	
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gcc	aag	gaa	gtt	cct	gcc	gca	atc	cag	aag	ggc	gca	gaa	gag	gct	cgt	403
Ala	Lys	Glu	Val	Pro	Ala	Ala	Ile	Gln	Lys	Gly	Ala	Glu	Glu	Ala	Arg	
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aag	aac	ttc	ttc	cgc	gtc	cca	atg	gtc	aac	ggc	acc	atc	acc	cac	cca	451
Lys	Asn	Phe	Phe	Arg	Val	Pro	Met	Val	Asn	Gly	Thr	Ile	Thr	His	Pro	
			105					110					115			
gtt	cag	ggc	gaa	aag	gca	gcc	ggc	atc	gtt	atg	ctg	aag	cca	gct	gct	499
Val	Gln	Gly	Glu	Lys	Ala	Ala	Gly	Ile	Val	Met	Leu	Lys	Pro	Ala	Ala	
		120					125					130				
cca	ggc	acc	ggc	gtt	atc	gcc	ggc	ggc	gca	gca	cgt	cca	gtt	ctt	gag	547
Pro	Gly	Thr	Gly	Val	Ile	Ala	Gly	Gly	Ala	Ala	Arg	Pro	Val	Leu	Glu	
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tgc	gca	ggc	atc	caa	gac	atc	ctg	tcc	aag	tcc	ctt	ggc	tct	gac	aac	595
Cys	Ala	Gly	Ile	Gln	Asp	Ile	Leu	Ser	Lys	Ser	Leu	Gly	Ser	Asp	Asn	
	150				155					160					165	
gct	atc	aac	gtc	gtc	cac	gca	act	gtg	gat	ggc	ctg	aag	cag	ctg	gtc	643
Ala	Ile	Asn	Val	Val	His	Ala	Thr	Val	Asp	Gly	Leu	Lys	Gln	Leu	Val	
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cgc	cct	gaa	gag	gtt	gca	gcc	cgc	cgt	ggc	aag	acc	atc	gaa	gag	gtc	691

Arg Pro Glu Glu Val Ala Ala Arg Arg Gly Lys Thr Ile Glu Glu Val
 185 190 195

gca cca gca cgt att ctg cgt gca cgc gca ggt cag gag gcg 733
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<213> Corynebacterium glutamicum

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Arg Arg Asn Gln Gln Gln Asp Glu Arg Ser Gln Tyr Ile Glu Arg Val
 35 40 45

Val Thr Ile Asn Arg Val Ser Lys Val Val Lys Gly Gly Arg Arg Phe
 50 55 60

Ser Phe Thr Ala Leu Val Ile Val Gly Asp Gly Lys Gly Met Val Gly
 65 70 75 80

Val Gly Tyr Gly Lys Ala Lys Glu Val Pro Ala Ala Ile Gln Lys Gly
 85 90 95

Ala Glu Glu Ala Arg Lys Asn Phe Phe Arg Val Pro Met Val Asn Gly
 100 105 110

Thr Ile Thr His Pro Val Gln Gly Glu Lys Ala Ala Gly Ile Val Met
 115 120 125

Leu Lys Pro Ala Ala Pro Gly Thr Gly Val Ile Ala Gly Gly Ala Ala
 130 135 140

Arg Pro Val Leu Glu Cys Ala Gly Ile Gln Asp Ile Leu Ser Lys Ser
 145 150 155 160

Leu Gly Ser Asp Asn Ala Ile Asn Val Val His Ala Thr Val Asp Gly
 165 170 175

Leu Lys Gln Leu Val Arg Pro Glu Glu Val Ala Ala Arg Arg Gly Lys
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Thr Ile Glu Glu Val Ala Pro Ala Arg Ile Leu Arg Ala Arg Ala Gly
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Gln Glu Ala
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<212> DNA

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 Met Ile Ile Leu Asp
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cct tct cag gat gag cgc act gtt gcc ccg tcc ctg gat aaa ttc ctc 163
 Pro Ser Gln Asp Glu Arg Thr Val Ala Pro Ser Leu Asp Lys Phe Leu
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 Glu Val Val Arg Lys Asp Lys Gly Asp Val Val Lys Val Asp Val Trp
 25 30 35

ggc aag cgc cgt ctt gca tac cca atc gac aag aag gaa gag ggc gtt 259
 Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys Lys Glu Glu Gly Val
 40 45 50

tac gcc gtc gtc gat ctc aag tgt gag tct gcg acc gta ctc gag ctc 307
 Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala Thr Val Leu Glu Leu
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gat cgt gtt ctg aac ctg aat gat ggt gtc ctg cgc acc aag gtt ctg 355
 Asp Arg Val Leu Asn Leu Asn Asp Gly Val Leu Arg Thr Lys Val Leu
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 Arg Leu Asp Lys

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<212> PRT

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<400> 368

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 20 25 30

Lys Val Asp Val Trp Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys
 35 40 45

Lys Glu Glu Gly Val Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala
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Thr Val Leu Glu Leu Asp Arg Val Leu Asn Leu Asn Asp Gly Val Leu
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Arg Thr Lys Val Leu Arg Leu Asp Lys
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Met Ile Ile Leu Asp
1 5

cct tct cag gat gag cgc act gtt gcc ccg tcc ctg gat aaa ttc ctc 163
Pro Ser Gln Asp Glu Arg Thr Val Ala Pro Ser Leu Asp Lys Phe Leu
10 15 20

gag gtt gtc cgc aag gac aag ggt gac gtt gtg aag gtt gat gtt tgg 211
Glu Val Val Arg Lys Asp Lys Gly Asp Val Val Lys Val Asp Val Trp
25 30 35

ggc aag cgc cgt ctt gca tac cca atc gac aag aag gaa gag ggc gtt 259
Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys Lys Glu Glu Gly Val
40 45 50

tac gcc gtc gtc gat ctc aag tgt gag tct gcg acc gta ctc gag ctc 307
Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala Thr Val Leu Glu Leu
55 60 65

gat cgt gtt ctg aac ctg aat gat ggt gtc ctg cgc acc aag gtt ctg 355
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70 75 80 85

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Lys Val Asp Val Trp Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys
35 40 45

Lys Glu Glu Gly Val Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala
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Thr Val Leu Glu Leu Asp Arg Val Leu Asn Leu Asn Asp Gly Val Leu

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70

75

80

Arg Thr Lys Val Leu
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<223> RXA01279

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Met Arg Lys Ser Ala
1 5

gct cct aag cgt cca gta gtt cag gac cct gta tac aag tcc gag ctc 163
Ala Pro Lys Arg Pro Val Val Gln Asp Pro Val Tyr Lys Ser Glu Leu
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gtt acc cag ctc gta aac aag atc ctc atc ggt ggc aag aag tcc acc 211
Val Thr Gln Leu Val Asn Lys Ile Leu Ile Gly Gly Lys Lys Ser Thr
25 30 35

gca gag cgc atc gtc tac ggt gca ctc gag atc tgc cgt gag aag acc 259
Ala Glu Arg Ile Val Tyr Gly Ala Leu Glu Ile Cys Arg Glu Lys Thr
40 45 50

ggc acc gat cca gta gga acc ctc gag aag gct ctc ggc aac gtg cgt 307
Gly Thr Asp Pro Val Gly Thr Leu Glu Lys Ala Leu Gly Asn Val Arg
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Pro Asp Leu Glu Val Arg Ser Arg Arg Val Gly Gly Ala Thr Tyr Gln
70 75 80 85

gtg cca gtg gat gtt cgc cca gag cgc gca aac acc ctc gca ctg cgt 403
Val Pro Val Asp Val Arg Pro Glu Arg Ala Asn Thr Leu Ala Leu Arg
90 95 100

tgg ttg gta acc ttc acc cgt cag cgt cgt gag aac acc atg atc gag 451
Trp Leu Val Thr Phe Thr Arg Gln Arg Arg Glu Asn Thr Met Ile Glu
105 110 115

cgt ctt gca aac gaa ctt ctg gat gca gcc aac ggc ctt ggc gct tcc 499
Arg Leu Ala Asn Glu Leu Leu Asp Ala Ala Asn Gly Leu Gly Ala Ser
120 125 130

gtg aag cgt cgc gaa gac acc cac aag atg gca gag gcc aac cgc gcc 547
Val Lys Arg Arg Glu Asp Thr His Lys Met Ala Glu Ala Asn Arg Ala
135 140 145

ttc gct cac tac cgc tgg tagtactgcc aagacatgaa agc 588
Phe Ala His Tyr Arg Trp

150

155

<210> 372

<211> 155

<212> PRT

<213> Corynebacterium glutamicum

<400> 372

Met Arg Lys Ser Ala Ala Pro Lys Arg Pro Val Val Gln Asp Pro Val
 1 5 10 15

Tyr Lys Ser Glu Leu Val Thr Gln Leu Val Asn Lys Ile Leu Ile Gly
 20 25 30

Gly Lys Lys Ser Thr Ala Glu Arg Ile Val Tyr Gly Ala Leu Glu Ile
 35 40 45

Cys Arg Glu Lys Thr Gly Thr Asp Pro Val Gly Thr Leu Glu Lys Ala
 50 55 60

Leu Gly Asn Val Arg Pro Asp Leu Glu Val Arg Ser Arg Arg Val Gly
 65 70 75 80

Gly Ala Thr Tyr Gln Val Pro Val Asp Val Arg Pro Glu Arg Ala Asn
 85 90 95

Thr Leu Ala Leu Arg Trp Leu Val Thr Phe Thr Arg Gln Arg Arg Glu
 100 105 110

Asn Thr Met Ile Glu Arg Leu Ala Asn Glu Leu Leu Asp Ala Ala Asn
 115 120 125

Gly Leu Gly Ala Ser Val Lys Arg Arg Glu Asp Thr His Lys Met Ala
 130 135 140

Glu Ala Asn Arg Ala Phe Ala His Tyr Arg Trp
 145 150 155

<210> 373

<211> 519

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(496)

<223> RXA00694

<400> 373

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ggaaggggaac cccaacgaga aaggcatcag gtcgtctcta atg aca atg act gat 115
 Met Thr Met Thr Asp
 1 5

cca atc gcc gac atg ctg tcg cgc gtg cgc aat gct agc aat gcg cac 163
 Pro Ile Ala Asp Met Leu Ser Arg Val Arg Asn Ala Ser Asn Ala His
 10 15 20

<400> 374																
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Ala	Ser	Asn	Ala	His	His	Asp	Thr	Val	Ser	Met	Pro	Ser	Ser	Lys	Ile	
			20					25					30			
Lys	Ala	Asn	Ile	Ala	Glu	Ile	Leu	Lys	Gln	Glu	Gly	Tyr	Ile	Ala	Asn	
		35					40					45				
Tyr	Thr	Val	Glu	Asp	Ala	Lys	Val	Gly	Lys	Thr	Leu	Ser	Leu	Glu	Leu	
	50					55					60					
Lys	Tyr	Ser	Asn	Thr	Arg	Glu	Arg	Ser	Ile	Ala	Gly	Leu	Arg	Arg	Val	
65					70					75					80	
Ser	Lys	Pro	Gly	Leu	Arg	Val	Tyr	Ala	Lys	Ser	Thr	Asn	Leu	Pro	Gln	
				85					90					95		
Val	Leu	Gly	Gly	Leu	Gly	Val	Ala	Ile	Ile	Ser	Thr	Ser	Gln	Gly	Leu	
			100					105					110			
Leu	Thr	Asp	Arg	Gln	Ala	Thr	Glu	Lys	Gly	Val	Gly	Gly	Glu	Val	Leu	
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Ala Tyr Val Trp
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<210> 375
<211> 492
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(469)
<223> RXN02038

<400> 375
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agaagcctga ggcctacgag atcaagaagg tggcccagta atg tca gag cct atc 115
Met Ser Glu Pro Ile
1 5

cag aac gag aac gta gag agc aac gtc gca gac gct gct gac atc gct 163
Gln Asn Glu Asn Val Glu Ser Asn Val Ala Asp Ala Ala Asp Ile Ala
10 15 20

gca gca acc gct gca acc gag gag ttc acc aac acc atc ggc gat gca 211
Ala Ala Thr Ala Ala Thr Glu Glu Phe Thr Asn Thr Ile Gly Asp Ala
25 30 35

att gct act gct tcc gaa gaa gag acc atc gag gct gca cca gta gta 259
Ile Ala Thr Ala Ser Glu Glu Glu Thr Ile Glu Ala Ala Pro Val Val
40 45 50

ctc gac ggc cca atc cag acc gtt ggt cgc cgt aag cgc gcc atc gtt 307
Leu Asp Gly Pro Ile Gln Thr Val Gly Arg Arg Lys Arg Ala Ile Val
55 60 65

cgc gtc cgc ctt gta gct ggc tcc ggc gag ttc aag tgc aac ggt cgc 355
Arg Val Arg Leu Val Ala Gly Ser Gly Glu Phe Lys Cys Asn Gly Arg
70 75 80 85

acc ctg gaa gag tac ttc cct aac aag ctg cac cag cag ctg atc aag 403
Thr Leu Glu Glu Tyr Phe Pro Asn Lys Leu His Gln Gln Leu Ile Lys
90 95 100

gct cct ttg gtc ctt ctg gac cgc ctg aac caa tgc aac atc gag gct 451
Ala Pro Leu Val Leu Leu Asp Arg Leu Asn Gln Cys Asn Ile Glu Ala
105 110 115

tct ata aag gga cct aaa tagatcggcc aggttatggc aat 492
Ser Ile Lys Gly Pro Lys
120

<210> 376
<211> 123
<212> PRT
<213> Corynebacterium glutamicum

<400> 376
Met Ser Glu Pro Ile Gln Asn Glu Asn Val Glu Ser Asn Val Ala Asp

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Ala Ala Asp Ile	Ala Ala Ala Thr	Ala Ala Thr Glu Glu	Phe Thr Asn
20	25	30	
Thr Ile Gly Asp	Ala Ile Ala Thr	Ala Ser Glu Glu Glu	Thr Ile Glu
35	40	45	
Ala Ala Pro Val	Val Leu Asp Gly	Pro Ile Gln Thr	Val Gly Arg Arg
50	55	60	
Lys Arg Ala Ile	Val Arg Val Arg	Leu Val Ala Gly	Ser Gly Glu Phe
65	70	75	80
Lys Cys Asn Gly	Arg Thr Leu Glu	Glu Tyr Phe Pro	Asn Lys Leu His
85	90	95	
Gln Gln Leu Ile	Lys Ala Pro Leu	Val Leu Leu Asp	Arg Leu Asn Gln
100	105	110	
Cys Asn Ile Glu	Ala Ser Ile Lys	Gly Pro Lys	
115	120		

<210> 377

<211> 409

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(409)

<223> FRXA02038

<400> 377

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agaagcctga ggcctacgag atcaagaagg tggcccagta	atg tca gag cct atc	115
	Met Ser Glu Pro Ile	
	1 5	

cag aac gag aac gta gag agc aac gtc gca gac gct gct gac atc gct	163
Gln Asn Glu Asn Val Glu Ser Asn Val Ala Asp Ala Ala Asp Ile Ala	
10 15 20	

gca gca acc gct gca acc gag gag ttc acc aac acc atc ggc gat gca	211
Ala Ala Thr Ala Ala Thr Glu Glu Phe Thr Asn Thr Ile Gly Asp Ala	
25 30 35	

att gct act gct tcc gaa gaa gag acc atc gag gct gca cca gta gta	259
Ile Ala Thr Ala Ser Glu Glu Glu Thr Ile Glu Ala Ala Pro Val Val	
40 45 50	

ctc gac ggc cca atc cag acc gtt ggt cgc cgt aag cgc gcc atc gtt	307
Leu Asp Gly Pro Ile Gln Thr Val Gly Arg Arg Lys Arg Ala Ile Val	
55 60 65	

cgc gtc cgc ctt gta gct ggc tcc ggc gag ttc aag tgc aac ggt cgc	355
Arg Val Arg Leu Val Ala Gly Ser Gly Glu Phe Lys Cys Asn Gly Arg	
70 75 80 85	

gct cct 409
Ala Pro

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<400> 378
Met Ser Glu Pro Ile Gln Asn Glu Asn Val Glu Ser Asn Val Ala Asp
  1             5             10             15

Ala Ala Asp Ile Ala Ala Ala Thr Ala Ala Thr Glu Glu Phe Thr Asn
             20             25             30

Thr Ile Gly Asp Ala Ile Ala Thr Ala Ser Glu Glu Glu Thr Ile Glu
      35             40             45

Ala Ala Pro Val Val Leu Asp Gly Pro Ile Gln Thr Val Gly Arg Arg
  50             55             60

Lys Arg Ala Ile Val Arg Val Arg Leu Val Ala Gly Ser Gly Glu Phe
  65             70             75             80

Lys Cys Asn Gly Arg Thr Leu Glu Glu Tyr Phe Pro Asn Lys Leu His
             85             90             95

Gln Gln Leu Ile Lys Ala Pro
      100

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<220>  
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<222> (101)..(403)  
<223> RXA01287
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caaaatggaa gatgtgggac gagcggaggaa gaggataagc gtg gcg gga caa aag      115
                                     Val Ala Gly Gln Lys
                                           1           5

atc cgc att agg ctg aag gcc tac gac cac gaa gcg att gat gcg tct      163
Ile Arg Ile Arg Leu Lys Ala Tyr Asp His Glu Ala Ile Asp Ala Ser
                        10                      15                  20

gca cgc aag atc gtt gag acg gtc acc cgt acg ggt gcc cga gtc gtt      211
Ala Arg Lys Ile Val Glu Thr Val Thr Arg Thr Gly Ala Arg Val Val
                25                     30                   35
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gga ccg gtg cct ttg cct acc gaa aag aac gta tac gcc gtt att cgt 259
 Gly Pro Val Pro Leu Pro Thr Glu Lys Asn Val Tyr Ala Val Ile Arg
 40 45 50

 tct cca cat aag tac aag gac tct cgc gag cac ttc gag atg cgc act 307
 Ser Pro His Lys Tyr Lys Asp Ser Arg Glu His Phe Glu Met Arg Thr
 55 60 65

 cac aag cgc ctg atc gac atc ctc gac ccg acg ccg aag act gtt gat 355
 His Lys Arg Leu Ile Asp Ile Leu Asp Pro Thr Pro Lys Thr Val Asp
 70 75 80 85

 gcc ctt atg cgc atc gac ctt ccg gcc agc gtc gac gtg aac att cag 403
 Ala Leu Met Arg Ile Asp Leu Pro Ala Ser Val Asp Val Asn Ile Gln
 90 95 100

 tgatcgacgg aatttttggc agc 426

<210> 380
 <211> 101
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 380
 Val Ala Gly Gln Lys Ile Arg Ile Arg Leu Lys Ala Tyr Asp His Glu
 1 5 10 15

 Ala Ile Asp Ala Ser Ala Arg Lys Ile Val Glu Thr Val Thr Arg Thr
 20 25 30

 Gly Ala Arg Val Val Gly Pro Val Pro Leu Pro Thr Glu Lys Asn Val
 35 40 45

 Tyr Ala Val Ile Arg Ser Pro His Lys Tyr Lys Asp Ser Arg Glu His
 50 55 60

 Phe Glu Met Arg Thr His Lys Arg Leu Ile Asp Ile Leu Asp Pro Thr
 65 70 75 80

 Pro Lys Thr Val Asp Ala Leu Met Arg Ile Asp Leu Pro Ala Ser Val
 85 90 95

 Asp Val Asn Ile Gln
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<210> 381
 <211> 113
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(90)
 <223> RXA00673

<400> 381
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 Leu Gln Ala Ala Gly Leu Glu Ile Gly Ser Ile Ser Asp Val Thr Pro

1	5	10	15	
cag cca cac aac ggc tgc cgt cca cca aag cgt cgt cgc gtt				90
Gln Pro His Asn Gly Cys Arg Pro Pro Lys Arg Arg Arg Val				
20	25	30		

taatagggaa ggaaaggtaa tac	113
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<210> 382

<211> 30

<212> PRT

<213> Corynebacterium glutamicum

<400> 382

Leu Gln Ala Ala Gly Leu Glu Ile Gly Ser Ile Ser Asp Val Thr Pro
1 5 10 15

Gln Pro His Asn Gly Cys Arg Pro Pro Lys Arg Arg Arg Val
20 25 30

<210> 383

<211> 489

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(466)

<223> RXA01280

<400> 383

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cgtcagcagt taaagaacaa ctccgaaata aggatgggttc atg cca act att cag	115
Met Pro Thr Ile Gln	
1 5	

cag ctg gtc cgt aag gcc cgc cac gat aag tcc gac aag gtg gct acc	163
Gln Leu Val Arg Lys Ala Arg His Asp Lys Ser Asp Lys Val Ala Thr	
10 15 20	

gcg gca ctg aag ggt tcc cct cag cgt cgt ggc gta tgc acc cgt gtg	211
Ala Ala Leu Lys Gly Ser Pro Gln Arg Arg Gly Val Cys Thr Arg Val	
25 30 35	

tac acc acc acc cct aag aag cct aac tct gct ctt cgt aag gtc gct	259
Tyr Thr Thr Thr Pro Lys Lys Pro Asn Ser Ala Leu Arg Lys Val Ala	
40 45 50	

cgt gtg cgc ctt acc tcc ggc atc gag gtt tcc gct tac atc cct ggt	307
Arg Val Arg Leu Thr Ser Gly Ile Glu Val Ser Ala Tyr Ile Pro Gly	
55 60 65	

gag ggc cac aac ctg cag gag cac tcc atg gtg ctc gtt cgc ggt ggt	355
Glu Gly His Asn Leu Gln Glu His Ser Met Val Leu Val Arg Gly Gly	
70 75 80 85	

cgt gtt aag gac ctc cca ggt gtc cgt tac aag atc gtc cgt ggc gca	403
Arg Val Lys Asp Leu Pro Gly Val Arg Tyr Lys Ile Val Arg Gly Ala	

90 95 100
 ctg gat acc cag ggt gtt aag gac cgc aag cag gct cgt tcc cgc tac 451
 Leu Asp Thr Gln Gly Val Lys Asp Arg Lys Gln Ala Arg Ser Arg Tyr
 105 110 115

ggc gcg aag agg gga taattaaaaa tgcgtaaadc agc 489
 Gly Ala Lys Arg Gly
 120

<210> 384
 <211> 122
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 384
 Met Pro Thr Ile Gln Gln Leu Val Arg Lys Ala Arg His Asp Lys Ser
 1 5 10 15
 Asp Lys Val Ala Thr Ala Ala Leu Lys Gly Ser Pro Gln Arg Arg Gly
 20 25 30
 Val Cys Thr Arg Val Tyr Thr Thr Thr Pro Lys Lys Pro Asn Ser Ala
 35 40 45
 Leu Arg Lys Val Ala Arg Val Arg Leu Thr Ser Gly Ile Glu Val Ser
 50 55 60
 Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln Glu His Ser Met Val
 65 70 75 80
 Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr Lys
 85 90 95
 Ile Val Arg Gly Ala Leu Asp Thr Gln Gly Val Lys Asp Arg Lys Gln
 100 105 110
 Ala Arg Ser Arg Tyr Gly Ala Lys Arg Gly
 115 120

<210> 385
 <211> 426
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(403)
 <223> RXA02637

<400> 385
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 agtccgcgaag cagctcgaat tccgcgagga gcgataatca atg gct aag aag tca 115
 Met Ala Lys Lys Ser
 1 5
 aag atc gcc aag aac gag aag cgc aag gaa atc gtc gcc cgc tac gcg 163
 Lys Ile Ala Lys Asn Glu Lys Arg Lys Glu Ile Val Ala Arg Tyr Ala

	10	15	20	
gag cgt cgc gct gag ctc aag gca att atc agt aac cca aac acc tct				211
Glu Arg Arg Ala Glu Leu Lys Ala Ile Ile Ser Asn Pro Asn Thr Ser				
	25	30	35	
gac gag gat cgt ctg gat gca cag ttc gaa ctg aac agc cag cca cgt				259
Asp Glu Asp Arg Leu Asp Ala Gln Phe Glu Leu Asn Ser Gln Pro Arg				
	40	45	50	
gat gct gct gct gtc cgc gtt cgt aac cgc gac tca cac gat ggt cgc				307
Asp Ala Ala Ala Val Arg Val Arg Asn Arg Asp Ser His Asp Gly Arg				
	55	60	65	
cca cgc ggc tac ctc cgt aag ttc ggt ctt tcc cgt gtc cgt atg cgc				355
Pro Arg Gly Tyr Leu Arg Lys Phe Gly Leu Ser Arg Val Arg Met Arg				
	70	75	80	85
gag atg gct cac cgt ggt gag ctg ccg ggc gtt cgt aag tcc agc tgg				403
Glu Met Ala His Arg Gly Glu Leu Pro Gly Val Arg Lys Ser Ser Trp				
	90	95	100	
taagggagtt tttaccaatg aag				426

<210> 386

<211> 101

<212> PRT

<213> Corynebacterium glutamicum

<400> 386

Met Ala Lys Lys Ser Lys Ile Ala Lys Asn Glu Lys Arg Lys Glu Ile	
1 5 10 15	

Val Ala Arg Tyr Ala Glu Arg Arg Ala Glu Leu Lys Ala Ile Ile Ser	
20 25 30	

Asn Pro Asn Thr Ser Asp Glu Asp Arg Leu Asp Ala Gln Phe Glu Leu	
35 40 45	

Asn Ser Gln Pro Arg Asp Ala Ala Ala Val Arg Val Arg Asn Arg Asp	
50 55 60	

Ser His Asp Gly Arg Pro Arg Gly Tyr Leu Arg Lys Phe Gly Leu Ser	
65 70 75 80	

Arg Val Arg Met Arg Glu Met Ala His Arg Gly Glu Leu Pro Gly Val	
85 90 95	

Arg Lys Ser Ser Trp	
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<210> 387

<211> 390

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(367)

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<400> 387

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aaatttttca tgcggactga aataactttt aggagacacc atg gct ctt act tct 115
 Met Ala Leu Thr Ser
 1 5

gag cag aag aag tcc atc ctt tcc gag ttc ggc ctc cac gag acc gac 163
 Glu Gln Lys Lys Ser Ile Leu Ser Glu Phe Gly Leu His Glu Thr Asp
 10 15 20

acc ggt tcc cca gaa gca cag atc gcg ctt ctg acc aac cgc atc aac 211
 Thr Gly Ser Pro Glu Ala Gln Ile Ala Leu Leu Thr Asn Arg Ile Asn
 25 30 35

aac ctc acc gag cac ctc aag ttc cac aag cac gat cac cac tcc cgt 259
 Asn Leu Thr Glu His Leu Lys Phe His Lys His Asp His His Ser Arg
 40 45 50

cgt ggt ctg ctg ctg ctc gtt ggt cgt cgt cgt ggt ctg ctg aag tac 307
 Arg Gly Leu Leu Leu Leu Val Gly Arg Arg Arg Gly Leu Leu Lys Tyr
 55 60 65

ctg gct gac aac aac gtt gat cgc tac cgt gat ctg atc gca cgc ctc 355
 Leu Ala Asp Asn Asn Val Asp Arg Tyr Arg Asp Leu Ile Ala Arg Leu
 70 75 80 85

ggc ctg cgt cga taagcctggt ttttccagtc ttt 390
 Gly Leu Arg Arg

<210> 388

<211> 89

<212> PRT

<213> Corynebacterium glutamicum

<400> 388

Met Ala Leu Thr Ser Glu Gln Lys Lys Ser Ile Leu Ser Glu Phe Gly
 1 5 10 15

Leu His Glu Thr Asp Thr Gly Ser Pro Glu Ala Gln Ile Ala Leu Leu
 20 25 30

Thr Asn Arg Ile Asn Asn Leu Thr Glu His Leu Lys Phe His Lys His
 35 40 45

Asp His His Ser Arg Arg Gly Leu Leu Leu Leu Val Gly Arg Arg Arg
 50 55 60

Gly Leu Leu Lys Tyr Leu Ala Asp Asn Asn Val Asp Arg Tyr Arg Asp
 65 70 75 80

Leu Ile Ala Arg Leu Gly Leu Arg Arg
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<210> 389

<211> 618

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(595)

<223> RXA02752

<400> 389

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agtgactgta ctgcccagtg acctagttag gaaaattcac atg gct gta aag att 115
                               Met Ala Val Lys Ile
                               1 5

aag ctc cag cgc ctc ggc aag atc cgt acc ccg cac tac cgc gtt gtc 163
Lys Leu Gln Arg Leu Gly Lys Ile Arg Thr Pro His Tyr Arg Val Val
                               10 15 20

atc gct gat gca cgc acc aag cgc gac ggc aag gtt atc gag aac atc 211
Ile Ala Asp Ala Arg Thr Lys Arg Asp Gly Lys Val Ile Glu Asn Ile
                               25 30 35

ggg atc tac gag cca aag gct gag cct tcc gta atc aag atc aac tcc 259
Gly Ile Tyr Glu Pro Lys Ala Glu Pro Ser Val Ile Lys Ile Asn Ser
                               40 45 50

gag cgt gcg cag cac tgg ctc tcc gtt ggc gct cag cca acc gag gct 307
Glu Arg Ala Gln His Trp Leu Ser Val Gly Ala Gln Pro Thr Glu Ala
                               55 60 65

gtt gca gcg ctg ctc aag gtg acc ggc gac tgg cag aag ttc aag ggc 355
Val Ala Ala Leu Leu Lys Val Thr Gly Asp Trp Gln Lys Phe Lys Gly
                               70 75 80 85

atc gag ggc gca gaa ggc acc ctc cgt gtt gca gag cct aag cca tcc 403
Ile Glu Gly Ala Glu Gly Thr Leu Arg Val Ala Glu Pro Lys Pro Ser
                               90 95 100

aag ctt gag ctg ttc aac cag gct ctt tct gag gct aac aac ggc cca 451
Lys Leu Glu Leu Phe Asn Gln Ala Leu Ser Glu Ala Asn Asn Gly Pro
                               105 110 115

acc gct gaa gcc atc act gaa aag aag aag aag gct cgc gag gac aag 499
Thr Ala Glu Ala Ile Thr Glu Lys Lys Lys Lys Ala Arg Glu Asp Lys
                               120 125 130

gaa gct aag gaa gca gct gag aag gct gct gct gaa aag gct gcc gct 547
Glu Ala Lys Glu Ala Ala Glu Lys Ala Ala Ala Glu Lys Ala Ala Ala
                               135 140 145

gca gag tcc gaa gag gct cca gct gag gaa gct gct gca gaa gag gca 595
Ala Glu Ser Glu Glu Ala Pro Ala Glu Glu Ala Ala Ala Glu Glu Ala
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<210> 390

<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 390

Met Ala Val Lys Ile Lys Leu Gln Arg Leu Gly Lys Ile Arg Thr Pro
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His Tyr Arg Val Val Ile Ala Asp Ala Arg Thr Lys Arg Asp Gly Lys
20 25 30

Val Ile Glu Asn Ile Gly Ile Tyr Glu Pro Lys Ala Glu Pro Ser Val
35 40 45

Ile Lys Ile Asn Ser Glu Arg Ala Gln His Trp Leu Ser Val Gly Ala
50 55 60

Gln Pro Thr Glu Ala Val Ala Ala Leu Leu Lys Val Thr Gly Asp Trp
65 70 75 80

Gln Lys Phe Lys Gly Ile Glu Gly Ala Glu Gly Thr Leu Arg Val Ala
85 90 95

Glu Pro Lys Pro Ser Lys Leu Glu Leu Phe Asn Gln Ala Leu Ser Glu
100 105 110

Ala Asn Asn Gly Pro Thr Ala Glu Ala Ile Thr Glu Lys Lys Lys Lys
115 120 125

Ala Arg Glu Asp Lys Glu Ala Lys Glu Ala Ala Glu Lys Ala Ala Ala
130 135 140

Glu Lys Ala Ala Ala Ala Glu Ser Glu Glu Ala Pro Ala Glu Glu Ala
145 150 155 160

Ala Ala Glu Glu Ala
165

<210> 391

<211> 384

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(361)

<223> RXA02389

<400> 391

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tgtacacaac tttaactaga aagttcaaga ggtatttgcg atg gca aac atc aag 115
Met Ala Asn Ile Lys
1 5

tct cag atc aag cgt aac aag acc aac gag aag gct cgt ctg cgt aac 163
Ser Gln Ile Lys Arg Asn Lys Thr Asn Glu Lys Ala Arg Leu Arg Asn
10 15 20

cag gca gtt cgc tcc gca gtc cgc acc gag atc cgc aag ttc aac gct 211
Gln Ala Val Arg Ser Ala Val Arg Thr Glu Ile Arg Lys Phe Asn Ala
25 30 35

gcg att gaa gca ggc gac aag gat gca gct cag gct cag ctc cgt acc 259
 Ala Ile Glu Ala Gly Asp Lys Asp Ala Ala Gln Ala Gln Leu Arg Thr
 40 45 50

gct tcc cgc gca ctg gac aag gca gta acc aag ggt gtc ttc cac atc 307
 Ala Ser Arg Ala Leu Asp Lys Ala Val Thr Lys Gly Val Phe His Ile
 55 60 65

aac aac gct gct aac aag aag tcc aac atg gct acc gct ttc aac aag 355
 Asn Asn Ala Ala Asn Lys Lys Ser Asn Met Ala Thr Ala Phe Asn Lys
 70 75 80 85

ctt ggc taatttttgg ctcttttgaa aat 384
 Leu Gly

<210> 392
 <211> 87
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 392
 Met Ala Asn Ile Lys Ser Gln Ile Lys Arg Asn Lys Thr Asn Glu Lys
 1 5 10 15

Ala Arg Leu Arg Asn Gln Ala Val Arg Ser Ala Val Arg Thr Glu Ile
 20 25 30

Arg Lys Phe Asn Ala Ala Ile Glu Ala Gly Asp Lys Asp Ala Ala Gln
 35 40 45

Ala Gln Leu Arg Thr Ala Ser Arg Ala Leu Asp Lys Ala Val Thr Lys
 50 55 60

Gly Val Phe His Ile Asn Asn Ala Ala Asn Lys Lys Ser Asn Met Ala
 65 70 75 80

Thr Ala Phe Asn Lys Leu Gly
 85

<210> 393
 <211> 1137
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1114)
 <223> RXA00671

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taccgacgtc aaatagcggg cgctcactcaa ggagagttca atg ctc att tca cag 115
 Met Leu Ile Ser Gln
 1 5

cgc cca acc atc acc gag gaa ttt gtt aat aac gca cgt tcc cgg ttt 163

Arg	Pro	Thr	Ile	Thr	Glu	Glu	Phe	Val	Asn	Asn	Ala	Arg	Ser	Arg	Phe	
				10					15					20		
gtc	atc	gag	cca	ctg	gag	cca	ggg	ttt	ggc	tac	acc	ctc	ggg	aac	tcc	211
Val	Ile	Glu	Pro	Leu	Glu	Pro	Gly	Phe	Gly	Tyr	Thr	Leu	Gly	Asn	Ser	
			25					30					35			
ctg	cgc	cgt	acc	ctg	ctg	tcc	tcc	att	cct	gga	gca	gca	gta	acc	agc	259
Leu	Arg	Arg	Thr	Leu	Leu	Ser	Ser	Ile	Pro	Gly	Ala	Ala	Val	Thr	Ser	
			40				45					50				
gtc	aag	att	gac	ggg	gta	ctc	cac	gag	ttc	acc	acc	atc	agc	ggg	gtt	307
Val	Lys	Ile	Asp	Gly	Val	Leu	His	Glu	Phe	Thr	Thr	Ile	Ser	Gly	Val	
	55					60					65					
aag	gaa	gat	gtc	tct	gac	atc	atc	ttg	aac	atc	aag	gga	ttg	gtt	ttg	355
Lys	Glu	Asp	Val	Ser	Asp	Ile	Ile	Leu	Asn	Ile	Lys	Gly	Leu	Val	Leu	
	70				75				80						85	
tct	tct	gat	tcc	gat	gag	cca	gtt	gtt	atg	cag	ctg	gtc	aag	gaa	ggc	403
Ser	Ser	Asp	Ser	Asp	Glu	Pro	Val	Val	Met	Gln	Leu	Val	Lys	Glu	Gly	
				90					95					100		
cca	gga	gtt	gta	act	gca	ggg	gac	att	cag	cca	cca	gca	ggc	gtg	gag	451
Pro	Gly	Val	Val	Thr	Ala	Gly	Asp	Ile	Gln	Pro	Pro	Ala	Gly	Val	Glu	
			105					110					115			
atc	cac	aac	ccg	gat	ctg	cac	att	gca	acc	ctg	aac	gag	acc	gcc	aag	499
Ile	His	Asn	Pro	Asp	Leu	His	Ile	Ala	Thr	Leu	Asn	Glu	Thr	Ala	Lys	
		120					125					130				
att	gag	atc	gag	ctc	atc	gtc	gag	cgt	gga	cgt	ggc	tac	gtt	ccc	gca	547
Ile	Glu	Ile	Glu	Leu	Ile	Val	Glu	Arg	Gly	Arg	Gly	Tyr	Val	Pro	Ala	
	135					140					145					
act	gtt	act	gca	acc	ggg	gga	gag	atc	ggc	cgc	att	ccg	gtc	gat	cag	595
Thr	Val	Thr	Ala	Thr	Gly	Gly	Glu	Ile	Gly	Arg	Ile	Pro	Val	Asp	Gln	
	150				155				160						165	
atc	tac	tcc	cca	gta	ctg	aag	gtc	agc	tac	aag	gtt	gaa	gct	act	cgt	643
Ile	Tyr	Ser	Pro	Val	Leu	Lys	Val	Ser	Tyr	Lys	Val	Glu	Ala	Thr	Arg	
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gtt	gag	cag	cgc	acc	gac	ttt	gac	aag	ctg	gtc	atc	gac	gtt	gag	acc	691
Val	Glu	Gln	Arg	Thr	Asp	Phe	Asp	Lys	Leu	Val	Ile	Asp	Val	Glu	Thr	
			185					190					195			
aag	aac	tct	att	acc	gca	cgt	gac	gcc	ctg	gcg	tcg	gca	ggg	aag	acc	739
Lys	Asn	Ser	Ile	Thr	Ala	Arg	Asp	Ala	Leu	Ala	Ser	Ala	Gly	Lys	Thr	
		200					205					210				
ctg	gtt	gag	ctg	ttc	ggc	ctc	gca	cgc	gag	ctg	aac	atc	gca	gcc	gag	787
Leu	Val	Glu	Leu	Phe	Gly	Leu	Ala	Arg	Glu	Leu	Asn	Ile	Ala	Ala	Glu	
	215					220					225					
ggc	atc	gag	atc	gga	cca	tct	cct	cag	gag	acc	gag	tac	atc	gct	gcc	835
Gly	Ile	Glu	Ile	Gly	Pro	Ser	Pro	Gln	Glu	Thr	Glu	Tyr	Ile	Ala	Ala	
	230				235				240					245		
tac	agc	atg	cca	atc	gag	gat	ctg	gac	ttc	tct	gtc	cgt	tcc	tac	aac	883
Tyr	Ser	Met	Pro	Ile	Glu	Asp	Leu	Asp	Phe	Ser	Val	Arg	Ser	Tyr	Asn	

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tgc	ctc	aag	cgc	gaa	gac	atc	cac	acc	gtg	ggc	gaa	ctc	gca	gag	cgc		931
Cys	Leu	Lys	Arg	Glu	Asp	Ile	His	Thr	Val	Gly	Glu	Leu	Ala	Glu	Arg		
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gct	gag	tcc	gat	ttg	ctg	gat	atc	cgc	aac	ttc	gga	cag	aag	tcg	atc		979
Ala	Glu	Ser	Asp	Leu	Leu	Asp	Ile	Arg	Asn	Phe	Gly	Gln	Lys	Ser	Ile		
		280					285					290					
aac	gag	gta	aag	atc	aag	ctt	gct	ggc	ctg	ggc	ctg	acc	ctg	aag	gat		1027
Asn	Glu	Val	Lys	Ile	Lys	Leu	Ala	Gly	Leu	Gly	Leu	Thr	Leu	Lys	Asp		
		295				300					305						
gct	cct	gaa	gac	ttc	gat	cct	tca	act	ctt	gaa	ggc	tat	gac	gcc	gaa		1075
Ala	Pro	Glu	Asp	Phe	Asp	Pro	Ser	Thr	Leu	Glu	Gly	Tyr	Asp	Ala	Glu		
310					315					320					325		
act	ggc	ggc	tac	atc	gat	gtc	gag	gcg	gaa	gat	tcc	gag	taagt	cgcat			1124
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Thr	Leu	Gly	Asn	Ser	Leu	Arg	Arg	Thr	Leu	Leu	Ser	Ser	Ile	Pro	Gly		
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Ala	Ala	Val	Thr	Ser	Val	Lys	Ile	Asp	Gly	Val	Leu	His	Glu	Phe	Thr		
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Thr	Ile	Ser	Gly	Val	Lys	Glu	Asp	Val	Ser	Asp	Ile	Ile	Leu	Asn	Ile		
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Lys	Gly	Leu	Val	Leu	Ser	Ser	Asp	Ser	Asp	Glu	Pro	Val	Val	Met	Gln		
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Leu	Val	Lys	Glu	Gly	Pro	Gly	Val	Val	Thr	Ala	Gly	Asp	Ile	Gln	Pro		
			100					105					110				
Pro	Ala	Gly	Val	Glu	Ile	His	Asn	Pro	Asp	Leu	His	Ile	Ala	Thr	Leu		
		115					120					125					
Asn	Glu	Thr	Ala	Lys	Ile	Glu	Ile	Glu	Leu	Ile	Val	Glu	Arg	Gly	Arg		
	130					135					140						
Gly	Tyr	Val	Pro	Ala	Thr	Val											

Ile Pro Val Asp Gln Ile Tyr Ser Pro Val Leu Lys Val Ser Tyr Lys
 165 170 175
 Val Glu Ala Thr Arg Val Glu Gln Arg Thr Asp Phe Asp Lys Leu Val
 180 185 190
 Ile Asp Val Glu Thr Lys Asn Ser Ile Thr Ala Arg Asp Ala Leu Ala
 195 200 205
 Ser Ala Gly Lys Thr Leu Val Glu Leu Phe Gly Leu Ala Arg Glu Leu
 210 215 220
 Asn Ile Ala Ala Glu Gly Ile Glu Ile Gly Pro Ser Pro Gln Glu Thr
 225 230 235 240
 Glu Tyr Ile Ala Ala Tyr Ser Met Pro Ile Glu Asp Leu Asp Phe Ser
 245 250 255
 Val Arg Ser Tyr Asn Cys Leu Lys Arg Glu Asp Ile His Thr Val Gly
 260 265 270
 Glu Leu Ala Glu Arg Ala Glu Ser Asp Leu Leu Asp Ile Arg Asn Phe
 275 280 285
 Gly Gln Lys Ser Ile Asn Glu Val Lys Ile Lys Leu Ala Gly Leu Gly
 290 295 300
 Leu Thr Leu Lys Asp Ala Pro Glu Asp Phe Asp Pro Ser Thr Leu Glu
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 Gly Tyr Asp Ala Glu Thr Gly Gly Tyr Ile Asp Val Glu Ala Glu Asp
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 Ser Glu

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ggggaaaacc atcgcaacaa ccggaagg gtaactgccac atg gca cgt cta gct 115
 Met Ala Arg Leu Ala
 1 5

ggt gtt gac ctc cca cgc aac aag cgt atg gaa gtc gct ctc acc tac 163
 Gly Val Asp Leu Pro Arg Asn Lys Arg Met Glu Val Ala Leu Thr Tyr
 10 15 20

atc tac gga atc ggc cca gcc cgt tcc aag cag ctt ctc gag gag acc 211
 Ile Tyr Gly Ile Gly Pro Ala Arg Ser Lys Gln Leu Leu Glu Glu Thr
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cgggcggttcg taagtccagc tggtaaggga gtttttacca atg aag cag cgt aac 115
 Met Lys Gln Arg Asn
 1 5

aac gct aag cgc gtc cgc ctt gag cag act cgc cgc cca aag aag aac 163
 Asn Ala Lys Arg Val Arg Leu Glu Gln Thr Arg Arg Pro Lys Lys Asn
 10 15 20

ccg ctg aag gca gcg ggc atc gag aag gtg gac tac aag gac atc aac 211
 Pro Leu Lys Ala Ala Gly Ile Glu Lys Val Asp Tyr Lys Asp Ile Asn
 25 30 35

acc ctt cgt cag ttc atc tcc gac cgc cac aag atc cgt tca cgt cgt 259
 Thr Leu Arg Gln Phe Ile Ser Asp Arg His Lys Ile Arg Ser Arg Arg
 40 45 50

gtc acc ggt ctg acc ccg cag cag cag cgc gag gtt gca acc gcc gtg 307
 Val Thr Gly Leu Thr Pro Gln Gln Gln Arg Glu Val Ala Thr Ala Val
 55 60 65

aag aac gca cgc gaa atg gct ctc ctg ccg ttc acc agc cgc 349
 Lys Asn Ala Arg Glu Met Ala Leu Leu Pro Phe Thr Ser Arg
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taagactggg aataacgtaa cag 372

<210> 398

<211> 83

<212> PRT

<213> Corynebacterium glutamicum

<400> 398

Met Lys Gln Arg Asn Asn Ala Lys Arg Val Arg Leu Glu Gln Thr Arg
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 20 25 30

Tyr Lys Asp Ile Asn Thr Leu Arg Gln Phe Ile Ser Asp Arg His Lys
 35 40 45

Ile Arg Ser Arg Arg Val Thr Gly Leu Thr Pro Gln Gln Arg Glu
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Val Ala Thr Ala Val Lys Asn Ala Arg Glu Met Ala Leu Leu Pro Phe
 65 70 75 80

Thr Ser Arg

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cgc act aac gcg cgc cgc aca ggc cgt cgc gtt gta aaa aag aac gtt 163
 Arg Thr Asn Ala Arg Arg Thr Gly Arg Arg Val Val Lys Lys Asn Val
 10 15 20

tcg atc act gat acc aac ggt gct gta atc tct tgg gct tcc tct ggg 259
Ser Ile Thr Asp Thr Asn Gly Ala Val Ile Ser Trp Ala Ser Ser Gly
40 45 50

atg gct gca gag aac gct gcc cgc aag gca atg gat cac ggc atg aag 355
Met Ala Ala Glu Asn Ala Ala Arg Lys Ala Met Asp His Gly Met Lys
70 75 80 85

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atc cgt tcc ctt cag gct gca ggc ctg gag atc ggt tca atc tcc gac    451
Ile Arg Ser Leu Gln Ala Ala Gly Leu Glu Ile Gly Ser Ile Ser Asp
          105                      110                      115

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gtg acc cca cag cca cac aac ggc tgc cgt cca cca aag cgt cgt cgc 499
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<210> 400
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<213> Corynebacterium glutamicum
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20	25	30	
Asn Asn Thr Ile	Val Ser Ile Thr	Asn Gly Ala Val	Ile Ser
35	40	45	
Trp Ala Ser Ser	Gly His Val Gly	Phe Lys Gly Ser	Arg Lys Ser Thr
50	55	60	
Pro Phe Ala Ala	Gln Met Ala Ala	Glu Asn Ala Ala	Arg Lys Ala Met
65	70	75	80
Asp His Gly Met	Lys Lys Val Asp	Val Phe Val Lys	Gly Pro Gly Ser
85	90	95	
Gly Arg Glu Thr	Ala Ile Arg Ser	Leu Gln Ala Ala	Gly Leu Glu Ile
100	105	110	
Gly Ser Ile Ser	Asp Val Thr Pro	Gln Pro His Asn	Gly Cys Arg Pro
115	120	125	
Pro Lys Arg Arg	Arg Val		
130			

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(661)
 <223> RXN00714

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 accatcacat ataagacatc tcatgatcta acatttcttc atg gct acg att aca 115
 Met Ala Thr Ile Thr
 1 5

 cgc acc gac aga ctg atc ctc gta ccg ctc act gtt gag ctc gaa gac 163
 Arg Thr Asp Arg Leu Ile Leu Val Pro Leu Thr Val Glu Leu Glu Asp
 10 15 20

 gag gcc cac cag att tac tct gat tct cga atc tgg gaa cac cgc ccc 211
 Glu Ala His Gln Ile Tyr Ser Asp Ser Arg Ile Trp Glu His Arg Pro
 25 30 35

 cag gcg cgt cac acc aac gtg cgt gtc acg cgc gac atc atc aag cgc 259
 Gln Ala Arg His Thr Asn Val Arg Val Thr Arg Asp Ile Ile Lys Arg
 40 45 50

 acc aat gaa agc tgg ggc aag aaa gac ctt ggc ccc tgg ggt gtt tac 307
 Thr Asn Glu Ser Trp Gly Lys Lys Asp Leu Gly Pro Trp Gly Val Tyr
 55 60 65

 ctc cgt gac cgc cca tcg gaa ttc gtt ggc gtt ggt ggc gtt gaa ctc 355

Leu Arg Asp Arg Pro Ser Glu Phe Val Gly Val Gly Gly Val Glu Leu
 70 75 80 85
 atc gac gga aaa gta tgg gac ctc aag tac cgc ctc cgc ccc gac cta 403
 Ile Asp Gly Lys Val Trp Asp Leu Lys Tyr Arg Leu Arg Pro Asp Leu
 90 95 100
 tgg ggc aat gga tac gcc acg gaa atc tcc aac gcc gca aca ctg gcc 451
 Trp Gly Asn Gly Tyr Ala Thr Glu Ile Ser Asn Ala Ala Thr Leu Ala
 105 110 115
 acc aag cgt atc gac gac agc ctc cca ctc acg gcc agg gtg act acc 499
 Thr Lys Arg Ile Asp Asp Ser Leu Pro Leu Thr Ala Arg Val Thr Thr
 120 125 130
 aac cac cct gcc tca ttc cgt att ttg gaa aaa ctg gga ctc acc ccc 547
 Asn His Pro Ala Ser Phe Arg Ile Leu Glu Lys Leu Gly Leu Thr Pro
 135 140 145
 gta tgg gaa ggc cga cga gtc gga acg gaa gat gac ccc aac gag cct 595
 Val Trp Glu Gly Arg Arg Val Gly Thr Glu Asp Asp Pro Asn Glu Pro
 150 155 160 165
 gat gtg aga att tat tct gac cgt ccg cta tcg gat gaa att ctt gaa 643
 Asp Val Arg Ile Tyr Ser Asp Arg Pro Leu Ser Asp Glu Ile Leu Glu
 170 175 180
 atg ctc aag caa cga cca tagaccagaa aatctcacc ctt 684
 Met Leu Lys Gln Arg Pro
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<210> 402

<211> 187

<212> PRT

<213> Corynebacterium glutamicum

<400> 402

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 Val Glu Leu Glu Asp Glu Ala His Gln Ile Tyr Ser Asp Ser Arg Ile
 20 25 30
 Trp Glu His Arg Pro Gln Ala Arg His Thr Asn Val Arg Val Thr Arg
 35 40 45
 Asp Ile Ile Lys Arg Thr Asn Glu Ser Trp Gly Lys Lys Asp Leu Gly
 50 55 60
 Pro Trp Gly Val Tyr Leu Arg Asp Arg Pro Ser Glu Phe Val Gly Val
 65 70 75 80
 Gly Gly Val Glu Leu Ile Asp Gly Lys Val Trp Asp Leu Lys Tyr Arg
 85 90 95
 Leu Arg Pro Asp Leu Trp Gly Asn Gly Tyr Ala Thr Glu Ile Ser Asn
 100 105 110
 Ala Ala Thr Leu Ala Thr Lys Arg Ile Asp Asp Ser Leu Pro Leu Thr
 115 120 125

Ala Arg Val Thr Thr Asn His Pro Ala Ser Phe Arg Ile Leu Glu Lys
 130 135 140

Leu Gly Leu Thr Pro Val Trp Glu Gly Arg Arg Val Gly Thr Glu Asp
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Asp Pro Asn Glu Pro Asp Val Arg Ile Tyr Ser Asp Arg Pro Leu Ser
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Asp Glu Ile Leu Glu Met Leu Lys Gln Arg Pro
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<210> 403

<211> 1128

<212> DNA

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<222> (101)..(1105)

<223> RXN00897

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ttgacctgga tgccgggtga agatgaggat cctttcgggc atg acg cct agt ctt 115
 Met Thr Pro Ser Leu
 1 5

ccc cgt ttc cgc agc cag aaa cct gcc gtc ggc gat cgt gtt gtt gca 163
 Pro Arg Phe Arg Ser Gln Lys Pro Ala Val Gly Asp Arg Val Val Ala
 10 15 20

cgt cgc cgg att cct ggt gcc aat gtg cat tgg aca gat gtc att ggc 211
 Arg Arg Arg Ile Pro Gly Ala Asn Val His Trp Thr Asp Val Ile Gly
 25 30 35

cat gtg att ggg gtg gat ccg ttg gtg gtt cgc ccg cag tcg gtt ggt 259
 His Val Ile Gly Val Asp Pro Leu Val Val Arg Pro Gln Ser Val Gly
 40 45 50

ggg atg ccg tct gat gcg gaa gaa att gtc att cct gat gat cag ctt 307
 Gly Met Pro Ser Asp Ala Glu Glu Ile Val Ile Pro Asp Asp Gln Leu
 55 60 65

gag gtg att aag att ttg tcg ccg cgc acc att agg aat tcg gat att 355
 Glu Val Ile Lys Ile Leu Ser Pro Arg Thr Ile Arg Asn Ser Asp Ile
 70 75 80 85

cgt gcg gtg gag gtt gcc acg gcg aag gcc ttt ccg ggg ctg gtc aat 403
 Arg Ala Val Glu Val Ala Thr Ala Lys Ala Phe Pro Gly Leu Val Asn
 90 95 100

gag tgg cat gat ggt tgg ctg ctg cgt gcc ggt gat ggc att gcg gag 451
 Glu Trp His Asp Gly Trp Leu Leu Arg Ala Gly Asp Gly Ile Ala Glu
 105 110 115

cgt tct aat tct gcg tcg cca ctc ggc cca agt gtc ggt tct gag ccg 499
 Arg Ser Asn Ser Ala Ser Pro Leu Gly Pro Ser Val Gly Ser Glu Pro

120	125	130	
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gtg aag ctg cac att ccg gag cgg att ggt cgg cct gcg cag aaa gtc Val Lys Leu His Ile Pro Glu Arg Ile Gly Arg Pro Ala Gln Lys Val 150 155 160 165			595
att gac gcc gat ccc cag aaa tgg gtg atg ggc ccg gag att ttg gtg Ile Asp Ala Asp Pro Gln Lys Trp Val Met Gly Pro Glu Ile Leu Val 170 175 180			643
atg acg aaa tct ttg gac cat gtg gag tcg cac gaa ttg ccc ggt ggc Met Thr Lys Ser Leu Asp His Val Glu Ser His Glu Leu Pro Gly Gly 185 190 195			691
cta gaa ttt agc gtc gat aag cag cct gac cag gag tgg ctg ggc atg Leu Glu Phe Ser Val Asp Lys Gln Pro Asp Gln Glu Trp Leu Gly Met 200 205 210			739
tac cat ttc cgc gga cag gcg ttg ccc gct cac gcc ctt gag ctt ttg Tyr His Phe Arg Gly Gln Ala Leu Pro Ala His Ala Leu Glu Leu Leu 215 220 225			787
cgc acg caa atc gag ggc cgc atg ggg ttc ggg cgc ctg acc acg ccg Arg Thr Gln Ile Glu Gly Arg Met Gly Phe Gly Arg Leu Thr Thr Pro 230 235 240 245			835
gcg ggg caa acc gtc gcg atc acg cgc gcc acc atc acg gct gcg gag Ala Gly Gln Thr Val Ala Ile Thr Arg Ala Thr Ile Thr Ala Ala Glu 250 255 260			883
gag cgc ata ttt ttg ggc tat tca gcg gtc gag gtg gat cct gct ttt Glu Arg Ile Phe Leu Gly Tyr Ser Ala Val Glu Val Asp Pro Ala Phe 265 270 275			931
cga cgt cag ggg ctg ggc acc gcg ctc ggc tcg cgc atc cag gag tgg Arg Arg Gln Gly Leu Gly Thr Ala Leu Gly Ser Arg Ile Gln Glu Trp 280 285 290			979
ggc gcc gag caa cac gca cag gag gca tat ctc cag gtt gtc gcc cat Gly Ala Glu Gln His Ala Gln Glu Ala Tyr Leu Gln Val Val Ala His 295 300 305			1027
aat gaa gca ggt atc ggc ctg tat caa aag ctc ggg ttc agt gaa cac Asn Glu Ala Gly Ile Gly Leu Tyr Gln Lys Leu Gly Phe Ser Glu His 310 315 320 325			1075
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gta			1128

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<211> 335

<212> PRT

<213> Corynebacterium glutamicum

<400> 404

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Thr	Asp	Val	Ile	Gly	His	Val	Ile	Gly	Val	Asp	Pro	Leu	Val	Val	Arg	35	40	45	
Pro	Gln	Ser	Val	Gly	Gly	Met	Pro	Ser	Asp	Ala	Glu	Glu	Ile	Val	Ile	50	55	60	
Pro	Asp	Asp	Gln	Leu	Glu	Val	Ile	Lys	Ile	Leu	Ser	Pro	Arg	Thr	Ile	65	70	75	80
Arg	Asn	Ser	Asp	Ile	Arg	Ala	Val	Glu	Val	Ala	Thr	Ala	Lys	Ala	Phe	85	90	95	
Pro	Gly	Leu	Val	Asn	Glu	Trp	His	Asp	Gly	Trp	Leu	Leu	Arg	Ala	Gly	100	105	110	
Asp	Gly	Ile	Ala	Glu	Arg	Ser	Asn	Ser	Ala	Ser	Pro	Leu	Gly	Pro	Ser	115	120	125	
Val	Gly	Ser	Glu	Pro	Val	Pro	Met	Glu	Asp	Ile	Ser	Arg	Phe	Tyr	Ala	130	135	140	
Arg	His	Asp	Leu	Pro	Val	Lys	Leu	His	Ile	Pro	Glu	Arg	Ile	Gly	Arg	145	150	155	160
Pro	Ala	Gln	Lys	Val	Ile	Asp	Ala	Asp	Pro	Gln	Lys	Trp	Val	Met	Gly	165	170	175	
Pro	Glu	Ile	Leu	Val	Met	Thr	Lys	Ser	Leu	Asp	His	Val	Glu	Ser	His	180	185	190	
Glu	Leu	Pro	Gly	Gly	Leu	Glu	Phe	Ser	Val	Asp	Lys	Gln	Pro	Asp	Gln	195	200	205	
Glu	Trp	Leu	Gly	Met	Tyr	His	Phe	Arg	Gly	Gln	Ala	Leu	Pro	Ala	His	210	215	220	
Ala	Leu	Glu	Leu	Leu	Arg	Thr	Gln	Ile	Glu	Gly	Arg	Met	Gly	Phe	Gly	225	230	235	240
Arg	Leu	Thr	Thr	Pro	Ala	Gly	Gln	Thr	Val	Ala	Ile	Thr	Arg	Ala	Thr	245	250	255	
Ile	Thr	Ala	Ala	Glu	Glu	Arg	Ile	Phe	Leu	Gly	Tyr	Ser	Ala	Val	Glu	260	265	270	
Val	Asp	Pro	Ala	Phe	Arg	Arg	Gln	Gly	Leu	Gly	Thr	Ala	Leu	Gly	Ser	275	280	285	
Arg	Ile	Gln	Glu	Trp	Gly	Ala	Glu	Gln	His	Ala	Gln	Glu	Ala	Tyr	Leu	290	295	300	
Gln	Val	Val	Ala	His	Asn	Glu	Ala	Gly	Ile	Gly	Leu	Tyr	Gln	Lys	Leu	305	310	315	320

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<210> 405

<211> 2322

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(2299)

<223> RXN01380

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acc gtt ccg ttc atc gcc agg tac cgc aag gaa atc act ggg gga ctc 163
 Thr Val Pro Phe Ile Ala Arg Tyr Arg Lys Glu Ile Thr Gly Gly Leu
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gat gat acc caa ctg cgt gac ctg gaa gaa cgc ctc agt tac ctc cgt 211
 Asp Asp Thr Gln Leu Arg Asp Leu Glu Arg Leu Ser Tyr Leu Arg
 25 30 35

gag ctg gag gat cgt aaa caa agc atc ctc gcc gcg att gag gaa caa 259
 Glu Leu Glu Asp Arg Lys Gln Ser Ile Leu Ala Ala Ile Glu Glu Gln
 40 45 50

ggc aaa ctc acc gac gat tta cgc tcg ctg att ttg gga tgc gac acc 307
 Gly Lys Leu Thr Asp Asp Leu Arg Ser Leu Ile Leu Gly Cys Asp Thr
 55 60 65

aag gct cgc ctg gag gat ctg tac ctg ccg ttc aaa aaa cgg cgc aag 355
 Lys Ala Arg Leu Glu Asp Leu Tyr Leu Pro Phe Lys Lys Arg Arg Lys
 70 75 80 85

acg aag gcc gat atc gct agg gag gcg ggc ctg gag ggg ctc gtc gat 403
 Thr Lys Ala Asp Ile Ala Arg Glu Ala Gly Leu Glu Gly Leu Val Asp
 90 95 100

aag ctt atc gac gcc ccg tcc ctc gac gcc gca gcg cag gca gct gca 451
 Lys Leu Ile Asp Ala Pro Ser Leu Asp Ala Ala Ala Gln Ala Ala Ala
 105 110 115

ttt acg act gag ggc ttt gag gat tcc aaa aaa gtt ttg gat ggc gct 499
 Phe Thr Thr Glu Gly Phe Glu Asp Ser Lys Lys Val Leu Asp Gly Ala
 120 125 130

cgc gcc att ttg att gac cgc ttc gcg ctc gat gcc gat ttg gtg ggc 547
 Arg Ala Ile Leu Ile Asp Arg Phe Ala Leu Asp Ala Asp Leu Val Gly
 135 140 145

gag gtg cgt gag caa atg tat cgc gcg ggt tcc atg gcg gca tcg gtg 595
 Glu Val Arg Glu Gln Met Tyr Arg Ala Gly Ser Met Ala Ala Ser Val
 150 155 160 165

gtg gcg ggc aag gag cag gaa ggc gca aag ttc aag gac tac ttt gag	643
Val Ala Gly Lys Glu Gln Glu Gly Ala Lys Phe Lys Asp Tyr Phe Glu	
170 175 180	
ttt tcc gaa cct ttt gac aag ctt cca tct cac cga att ttg gcg ctg	691
Phe Ser Glu Pro Phe Asp Lys Leu Pro Ser His Arg Ile Leu Ala Leu	
185 190 195	
ctg cgc ggt gaa aac gaa ggt gtg ctg agc ctc aac ctc gat gcg ggc	739
Leu Arg Gly Glu Asn Glu Gly Val Leu Ser Leu Asn Leu Asp Ala Gly	
200 205 210	
gac gac ata atc tac gaa ggt ttg atc gcc gac cga ttc tcc ctg gac	787
Asp Asp Ile Ile Tyr Glu Gly Leu Ile Ala Asp Arg Phe Ser Leu Asp	
215 220 225	
acc cac act tct agc tgg ctg gct gag gct gtg cgc tgg ggt tgg cgc	835
Thr His Thr Ser Ser Trp Leu Ala Glu Ala Val Arg Trp Gly Trp Arg	
230 235 240 245	
acc aaa ctg tat gtg tcc tcc gga ttg gat gtg cgc atg cgt ctg aaa	883
Thr Lys Leu Tyr Val Ser Ser Gly Leu Asp Val Arg Met Arg Leu Lys	
250 255 260	
gaa aaa gca gag gaa ggc gca ctc gat gtg ttt gcc acc aac ctc cgc	931
Glu Lys Ala Glu Glu Gly Ala Leu Asp Val Phe Ala Thr Asn Leu Arg	
265 270 275	
gac gtt ctc ctt gca gct ccc gct ggt cag cgc tcc aca att ggc ctt	979
Asp Val Leu Leu Ala Ala Pro Ala Gly Gln Arg Ser Thr Ile Gly Leu	
280 285 290	
gac ccg gga ttc cgc aac ggt gtg aaa gta gct gtc gtg gat tcc acc	1027
Asp Pro Gly Phe Arg Asn Gly Val Lys Val Ala Val Val Asp Ser Thr	
295 300 305	
ggt aag gat gtt gcc acc acg atc gtc tac cca cac cag ccc caa aac	1075
Gly Lys Asp Val Ala Thr Thr Ile Val Tyr Pro His Gln Pro Gln Asn	
310 315 320 325	
cgc tgg aag gaa gcc gta tcc gaa ctg gct aac ctg tgc gcg acc cac	1123
Arg Trp Lys Glu Ala Val Ser Glu Leu Ala Asn Leu Cys Ala Thr His	
330 335 340	
ggt gtg gaa ctc atg gcg atc ggc aac gga acc gcc tcg agg gaa acg	1171
Gly Val Glu Leu Met Ala Ile Gly Asn Gly Thr Ala Ser Arg Glu Thr	
345 350 355	
gaa aaa ctc gcc ggc gaa gta gct gac atg atc aaa gcc gca ggt ggc	1219
Glu Lys Leu Ala Gly Glu Val Ala Asp Met Ile Lys Ala Ala Gly Gly	
360 365 370	
acg cga cca acc ccc gtg gtg gtc tcc gaa tcg ggc gca tcc gtg tac	1267
Thr Arg Pro Thr Pro Val Val Ser Glu Ser Gly Ala Ser Val Tyr	
375 380 385	
tcg gca tca ccg atc gca gcc gaa gaa ttc ccc gac atg gac gtc tcc	1315
Ser Ala Ser Pro Ile Ala Ala Glu Glu Phe Pro Asp Met Asp Val Ser	
390 395 400 405	

ctc cgc ggt gca gtt tct atc gcg agg cga ctc cag gat cca ctg gcg 1363
 Leu Arg Gly Ala Val Ser Ile Ala Arg Arg Leu Gln Asp Pro Leu Ala
 410 415 420

gag ctc gtc aag att gag ccc aaa gcc atc gga gtc ggc cag tac caa 1411
 Glu Leu Val Lys Ile Glu Pro Lys Ala Ile Gly Val Gly Gln Tyr Gln
 425 430 435

cac gat gtc aac cag gtt gca ctt gcc aaa acc ctt gat ggt gtc gtc 1459
 His Asp Val Asn Gln Val Ala Leu Ala Lys Thr Leu Asp Gly Val Val
 440 445 450

gaa gac gca gta aac gca gtc gga gtt aac ctc aac acc gca tcc gca 1507
 Glu Asp Ala Val Asn Ala Val Gly Val Asn Leu Asn Thr Ala Ser Ala
 455 460 465

cca ctt ctt acc cga gtt gcc gga gtg acc tcc acc ttg gca aac aat 1555
 Pro Leu Leu Thr Arg Val Ala Gly Val Thr Ser Thr Leu Ala Asn Asn
 470 475 480 485

atc gtg gcc tac cgc aac gaa aac ggt gga ttc tcc tcc cga aaa gaa 1603
 Ile Val Ala Tyr Arg Asn Glu Asn Gly Gly Phe Ser Ser Arg Lys Glu
 490 495 500

ctg aac aaa gtt cct cgc ctg gga ccc aaa gcc ttt gaa cag tgt gct 1651
 Leu Asn Lys Val Pro Arg Leu Gly Pro Lys Ala Phe Glu Gln Cys Ala
 505 510 515

ggc ttc ctc cgc att tct gga tcc acc gac cct ctc gac gcc tcc gct 1699
 Gly Phe Leu Arg Ile Ser Gly Ser Thr Asp Pro Leu Asp Ala Ser Ala
 520 525 530

gtt cac ccc gag gcg tac cca gtt gtt cgc aac att gcg aaa gcc aca 1747
 Val His Pro Glu Ala Tyr Pro Val Val Arg Asn Ile Ala Lys Ala Thr
 535 540 545

gga ttg gat gtc tcg gga ctg atc gga aac tct gcg gtg ctc acc aaa 1795
 Gly Leu Asp Val Ser Gly Leu Ile Gly Asn Ser Ala Val Leu Thr Lys
 550 555 560 565

ttg aag ccc gct gat ttc gct gat gaa cga ttc ggc atc ccc acc gtc 1843
 Leu Lys Pro Ala Asp Phe Ala Asp Glu Arg Phe Gly Ile Pro Thr Val
 570 575 580

acc gac atc atc gcc gag ctg gat aaa ccc gga cgt gac ccc cgc cca 1891
 Thr Asp Ile Ile Ala Glu Leu Asp Lys Pro Gly Arg Asp Pro Arg Pro
 585 590 595

gaa ttc aaa acc gcc agc ttc aaa gaa ggc gtg gag aaa atc tcc gac 1939
 Glu Phe Lys Thr Ala Ser Phe Lys Glu Gly Val Glu Lys Ile Ser Asp
 600 605 610

ctc aca ccc ggc atg atc ctg gaa gga act gtc acc aac gtt gcg gcg 1987
 Leu Thr Pro Gly Met Ile Leu Glu Gly Thr Val Thr Asn Val Ala Ala
 615 620 625

ttc ggc gca ttc gtt gac gtg gga gtg cac cga gat ggc ctc gtt cac 2035
 Phe Gly Ala Phe Val Asp Val Gly Val His Arg Asp Gly Leu Val His
 630 635 640 645

gtt tcc gcg atg agc gac aaa ttc atc tcc aac ccc cac gaa gtt gtt 2083

Val Ser Ala Met Ser Asp Lys Phe Ile Ser Asn Pro His Glu Val Val
650 655 660

cgc tct ggt gag gtc gtg aag gta aag gtc atg gaa gtt gac gtc gac 2131
Arg Ser Gly Glu Val Val Lys Val Lys Val Met Glu Val Asp Val Asp
665 670 675

cgc aaa cgc atc ggc ctt tcc ctc cgc ttg acc gat gaa ccc ggt gcc 2179
Arg Lys Arg Ile Gly Leu Ser Leu Arg Leu Thr Asp Glu Pro Gly Ala
680 685 690

cca gct ccg caa aag cgc gga aac cga cca gcc aaa cag cag cga gct 2227
Pro Ala Pro Gln Lys Arg Gly Asn Arg Pro Ala Lys Gln Gln Arg Ala
695 700 705

ccg caa aaa cag tcc gct aag ccc gcc aca ggt tcc atg gca gat gct 2275
Pro Gln Lys Gln Ser Ala Lys Pro Ala Thr Gly Ser Met Ala Asp Ala
710 715 720 725

tta cga cgc gcc ggc ctc ggt ggc taaggcaact ttcaaaccac gcg 2322
Leu Arg Arg Ala Gly Leu Gly Gly
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<210> 406

<211> 733

<212> PRT

<213> Corynebacterium glutamicum

<400> 406

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Ile Thr Gly Gly Leu Asp Asp Thr Gln Leu Arg Asp Leu Glu Glu Arg
20 25 30

Leu Ser Tyr Leu Arg Glu Leu Glu Asp Arg Lys Gln Ser Ile Leu Ala
35 40 45

Ala Ile Glu Glu Gln Gly Lys Leu Thr Asp Asp Leu Arg Ser Leu Ile
50 55 60

Leu Gly Cys Asp Thr Lys Ala Arg Leu Glu Asp Leu Tyr Leu Pro Phe
65 70 75 80

Lys Lys Arg Arg Lys Thr Lys Ala Asp Ile Ala Arg Glu Ala Gly Leu
85 90 95

Glu Gly Leu Val Asp Lys Leu Ile Asp Ala Pro Ser Leu Asp Ala Ala
100 105 110

Ala Gln Ala Ala Ala Phe Thr Thr Glu Gly Phe Glu Asp Ser Lys Lys
115 120 125

Val Leu Asp Gly Ala Arg Ala Ile Leu Ile Asp Arg Phe Ala Leu Asp
130 135 140

Ala Asp Leu Val Gly Glu Val Arg Glu Gln Met Tyr Arg Ala Gly Ser
145 150 155 160

Met Ala Ala Ser Val Val Ala Gly Lys Glu Gln Glu Gly Ala Lys Phe

			165					170					175				
Lys	Asp	Tyr	Phe 180	Glu	Phe	Ser	Glu	Pro 185	Phe	Asp	Lys	Leu	Pro 190	Ser	His		
Arg	Ile	Leu 195	Ala	Leu	Leu	Arg	Gly 200	Glu	Asn	Glu	Gly	Val 205	Leu	Ser	Leu		
Asn	Leu 210	Asp	Ala	Gly	Asp	Asp 215	Ile	Ile	Tyr	Glu	Gly 220	Leu	Ile	Ala	Asp		
Arg 225	Phe	Ser	Leu	Asp	Thr 230	His	Thr	Ser	Ser	Trp 235	Leu	Ala	Glu	Ala	Val 240		
Arg	Trp	Gly	Trp	Arg 245	Thr	Lys	Leu	Tyr	Val 250	Ser	Ser	Gly	Leu	Asp 255	Val		
Arg	Met	Arg	Leu 260	Lys	Glu	Lys	Ala	Glu 265	Glu	Gly	Ala	Leu	Asp 270	Val	Phe		
Ala	Thr	Asn 275	Leu	Arg	Asp	Val	Leu 280	Leu	Ala	Ala	Pro	Ala 285	Gly	Gln	Arg		
Ser	Thr 290	Ile	Gly	Leu	Asp	Pro 295	Gly	Phe	Arg	Asn	Gly 300	Val	Lys	Val	Ala		
Val 305	Val	Asp	Ser	Thr	Gly 310	Lys	Asp	Val	Ala	Thr 315	Thr	Ile	Val	Tyr	Pro 320		
His	Gln	Pro	Gln	Asn 325	Arg	Trp	Lys	Glu	Ala 330	Val	Ser	Glu	Leu	Ala 335	Asn		
Leu	Cys	Ala	Thr 340	His	Gly	Val	Glu	Leu 345	Met	Ala	Ile	Gly 350	Asn	Gly	Thr		
Ala	Ser	Arg 355	Glu	Thr	Glu	Lys	Leu 360	Ala	Gly	Glu	Val	Ala 365	Asp	Met	Ile		
Lys	Ala 370	Ala	Gly	Gly	Thr	Arg 375	Pro	Thr	Pro	Val	Val 380	Val	Ser	Glu	Ser		
Gly 385	Ala	Ser	Val	Tyr	Ser	Ala 390	Ser	Pro	Ile	Ala 395	Ala	Glu	Glu	Phe	Pro 400		
Asp	Met	Asp	Val	Ser 405	Leu	Arg	Gly	Ala	Val 410	Ser	Ile	Ala	Arg	Arg 415	Leu		
Gln	Asp	Pro	Leu 420	Ala	Glu	Leu	Val	Lys 425	Ile	Glu	Pro	Lys	Ala 430	Ile	Gly		
Val	Gly 435	Gln	Tyr	Gln	His	Asp	Val 440	Asn	Gln	Val	Ala	Leu 445	Ala	Lys	Thr		
Leu	Asp 450	Gly	Val	Val	Glu	Asp 455	Ala	Val	Asn	Ala	Val 460	Gly	Val	Asn	Leu		
Asn 465	Thr	Ala	Ser	Ala	Pro 470	Leu	Leu	Thr	Arg	Val 475	Ala	Gly	Val	Thr	Ser 480		
Thr	Leu	Ala	Asn	Asn 485	Ile	Val	Ala	Tyr	Arg 490	Asn	Glu	Asn	Gly	Gly 495	Phe		

Ser Ser Arg Lys Glu Leu Asn Lys Val Pro Arg Leu Gly Pro Lys Ala
 500 505 510
 Phe Glu Gln Cys Ala Gly Phe Leu Arg Ile Ser Gly Ser Thr Asp Pro
 515 520 525
 Leu Asp Ala Ser Ala Val His Pro Glu Ala Tyr Pro Val Val Arg Asn
 530 535 540
 Ile Ala Lys Ala Thr Gly Leu Asp Val Ser Gly Leu Ile Gly Asn Ser
 545 550 555 560
 Ala Val Leu Thr Lys Leu Lys Pro Ala Asp Phe Ala Asp Glu Arg Phe
 565 570 575
 Gly Ile Pro Thr Val Thr Asp Ile Ile Ala Glu Leu Asp Lys Pro Gly
 580 585 590
 Arg Asp Pro Arg Pro Glu Phe Lys Thr Ala Ser Phe Lys Glu Gly Val
 595 600 605
 Glu Lys Ile Ser Asp Leu Thr Pro Gly Met Ile Leu Glu Gly Thr Val
 610 615 620
 Thr Asn Val Ala Ala Phe Gly Ala Phe Val Asp Val Gly Val His Arg
 625 630 635 640
 Asp Gly Leu Val His Val Ser Ala Met Ser Asp Lys Phe Ile Ser Asn
 645 650 655
 Pro His Glu Val Val Arg Ser Gly Glu Val Val Lys Val Lys Val Met
 660 665 670
 Glu Val Asp Val Asp Arg Lys Arg Ile Gly Leu Ser Leu Arg Leu Thr
 675 680 685
 Asp Glu Pro Gly Ala Pro Ala Pro Gln Lys Arg Gly Asn Arg Pro Ala
 690 695 700
 Lys Gln Gln Arg Ala Pro Gln Lys Gln Ser Ala Lys Pro Ala Thr Gly
 705 710 715 720
 Ser Met Ala Asp Ala Leu Arg Arg Ala Gly Leu Gly Gly
 725 730

<210> 407

<211> 1286

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1) .. (1263)

<223> RXA00157

<400> 407

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 Ala Arg Ile Val Ala Glu Gln Arg Glu Ala Glu Ala Val Glu Lys Lys
 1 5 10 15

gtc cag acc gag gct gca att gcc gca aac agc gag cag ctc aat gtc	96
Val Gln Thr Glu Ala Ala Ile Ala Ala Asn Ser Glu Gln Leu Asn Val	
20 25 30	
ttg act acc aat cgc agt acc ttg gtt gcc cag cgt gat ggg gct gag	144
Leu Thr Thr Asn Arg Ser Thr Leu Val Ala Gln Arg Asp Gly Ala Glu	
35 40 45	
cgc aac ttg gcc atc gct cgt gcg cag gcg gat aat ctg caa ggt cag	192
Arg Asn Leu Ala Ile Ala Arg Ala Gln Ala Asp Asn Leu Gln Gly Gln	
50 55 60	
cgt gct gag tac gag gaa ttc cag cag gca gag cag gct cgc atc cag	240
Arg Ala Glu Tyr Glu Glu Phe Gln Gln Ala Glu Gln Ala Arg Ile Gln	
65 70 75 80	
gcg gaa gcg gaa gct cag gct gct gcg gag gag aag cgt cgt gcc gat	288
Ala Glu Ala Glu Ala Gln Ala Ala Ala Glu Glu Lys Arg Arg Ala Asp	
85 90 95	
gag gct gct gca cag gca gcc gct gaa gct caa gaa gct gcc cag caa	336
Glu Ala Ala Ala Gln Ala Ala Ala Glu Ala Gln Glu Ala Ala Gln Gln	
100 105 110	
gct cag gcg gcg gag gaa gcc caa gcc gcg caa gca gct gag aca gca	384
Ala Gln Ala Ala Glu Glu Ala Gln Ala Ala Gln Ala Ala Glu Thr Ala	
115 120 125	
caa gcc caa gcc gcg caa gct gcg gaa acc caa gct gca caa gcc gcg	432
Gln Ala Gln Ala Ala Gln Ala Ala Glu Thr Gln Ala Ala Gln Ala Ala	
130 135 140	
caa gct cag gca gaa gcg aat gat cgt gcc gcc gcg caa cag cgt gct	480
Gln Ala Gln Ala Glu Ala Asn Asp Arg Ala Ala Ala Gln Gln Arg Ala	
145 150 155 160	
gca gag gct caa gca gca gcg gaa cag gcg caa cgt gag gct gac gct	528
Ala Glu Ala Gln Ala Ala Ala Glu Gln Ala Gln Arg Glu Ala Asp Ala	
165 170 175	
cag gcg gcc aac gat gcc caa gct cag gca ctg cgt gaa cag gcg ctc	576
Gln Ala Ala Asn Asp Ala Gln Ala Gln Ala Leu Arg Glu Gln Ala Leu	
180 185 190	
acc gca gcc tcc atc gct gcg gct gct cta att gcg gcg agc cag tcc	624
Thr Ala Ala Ser Ile Ala Ala Ala Leu Ile Ala Ala Ser Gln Ser	
195 200 205	
agc cat gcc act act caa aat cct tac cca act gat gaa gac gcg gat	672
Ser His Ala Thr Thr Gln Asn Pro Tyr Pro Thr Asp Glu Asp Ala Asp	
210 215 220	
ccg acc gat att gcg gac atc caa ggc cca acg cag cca ggt acg ggt	720
Pro Thr Asp Ile Ala Asp Ile Gln Gly Pro Thr Gln Pro Gly Thr Gly	
225 230 235 240	
gag tct gga gat tcc cag agc aac tcc agc gac aac gat tcc aca ggc	768
Glu Ser Gly Asp Ser Gln Ser Asn Ser Ser Asp Asn Asp Ser Thr Gly	
245 250 255	

aac gat tcc aca ggc tct gac tct tca gat tca gat tcc tcc ggc aac 816
 Asn Asp Ser Thr Gly Ser Asp Ser Ser Asp Ser Asp Ser Ser Gly Asn
 260 265 270

gat tct tca gag gtt att tcc ggc gat cgt tcc gct cag att gag act 864
 Asp Ser Ser Glu Val Ile Ser Gly Asp Arg Ser Ala Gln Ile Glu Thr
 275 280 285

gtg att gcg cgc gcc atg agc cag ttg ggt gtg cag tac gca tgg ggt 912
 Val Ile Ala Arg Ala Met Ser Gln Leu Gly Val Gln Tyr Ala Trp Gly
 290 295 300

ggc ggt aac gct aat ggc cca act ctg ggt atc cgt gac ggt ggc gtg 960
 Gly Gly Asn Ala Asn Gly Pro Thr Leu Gly Ile Arg Asp Gly Gly Val
 305 310 315 320

gcg gac tct tac ggc gat tac aac aag gtt ggc ttc gac tgc tct gga 1008
 Ala Asp Ser Tyr Gly Asp Tyr Asn Lys Val Gly Phe Asp Cys Ser Gly
 325 330 335

ctg acc ttg tat gcg ttt gcg ggt gtg gga att tca ctt cct cac tac 1056
 Leu Thr Leu Tyr Ala Phe Ala Gly Val Gly Ile Ser Leu Pro His Tyr
 340 345 350

acg ggc tac cag tac cag cac ggc acc aag gtg tcg cct tct gag atg 1104
 Thr Gly Tyr Gln Tyr Gln His Gly Thr Lys Val Ser Pro Ser Glu Met
 355 360 365

caa cgt ggc gat ctg atc ttc tat ggt ccg gga gcg tct cag cac gtg 1152
 Gln Arg Gly Asp Leu Ile Phe Tyr Gly Pro Gly Ala Ser Gln His Val
 370 375 380

gca att tac ctc ggt gat ggt cag atg att gag gct ccg aat tcg ggt 1200
 Ala Ile Tyr Leu Gly Asp Gly Gln Met Ile Glu Ala Pro Asn Ser Gly
 385 390 395 400

tct gtc gtg aag att tct cct gtt cgc tgg agc gga atg acc gag agc 1248
 Ser Val Val Lys Ile Ser Pro Val Arg Trp Ser Gly Met Thr Glu Ser
 405 410 415

gtg gta cgc ctc att tagtttcctc ctatgaatct tga 1286
 Val Val Arg Leu Ile
 420

<210> 408

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 408

Ala Arg Ile Val Ala Glu Gln Arg Glu Ala Glu Ala Val Glu Lys Lys
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Val Gln Thr Glu Ala Ala Ile Ala Ala Asn Ser Glu Gln Leu Asn Val
 20 25 30

Leu Thr Thr Asn Arg Ser Thr Leu Val Ala Gln Arg Asp Gly Ala Glu
 35 40 45

Arg Asn Leu Ala Ile Ala Arg Ala Gln Ala Asp Asn Leu Gln Gly Gln

50	55	60
Arg Ala Glu Tyr Glu Glu Phe Gln Gln Ala Glu Gln Ala Arg Ile Gln 65 70 75 80		
Ala Glu Ala Glu Ala Gln Ala Ala Ala Glu Glu Lys Arg Arg Ala Asp 85 90 95		
Glu Ala Ala Ala Gln Ala Ala Ala Glu Ala Gln Glu Ala Ala Gln Gln 100 105 110		
Ala Gln Ala Ala Glu Glu Ala Gln Ala Ala Gln Ala Ala Glu Thr Ala 115 120 125		
Gln Ala Gln Ala Ala Gln Ala Ala Glu Thr Gln Ala Ala Gln Ala Ala 130 135 140		
Gln Ala Gln Ala Glu Ala Asn Asp Arg Ala Ala Ala Gln Gln Arg Ala 145 150 155 160		
Ala Glu Ala Gln Ala Ala Ala Glu Gln Ala Gln Arg Glu Ala Asp Ala 165 170 175		
Gln Ala Ala Asn Asp Ala Gln Ala Gln Ala Leu Arg Glu Gln Ala Leu 180 185 190		
Thr Ala Ala Ser Ile Ala Ala Ala Ala Leu Ile Ala Ala Ser Gln Ser 195 200 205		
Ser His Ala Thr Thr Gln Asn Pro Tyr Pro Thr Asp Glu Asp Ala Asp 210 215 220		
Pro Thr Asp Ile Ala Asp Ile Gln Gly Pro Thr Gln Pro Gly Thr Gly 225 230 235 240		
Glu Ser Gly Asp Ser Gln Ser Asn Ser Ser Asp Asn Asp Ser Thr Gly 245 250 255		
Asn Asp Ser Thr Gly Ser Asp Ser Ser Asp Ser Asp Ser Ser Gly Asn 260 265 270		
Asp Ser Ser Glu Val Ile Ser Gly Asp Arg Ser Ala Gln Ile Glu Thr 275 280 285		
Val Ile Ala Arg Ala Met Ser Gln Leu Gly Val Gln Tyr Ala Trp Gly 290 295 300		
Gly Gly Asn Ala Asn Gly Pro Thr Leu Gly Ile Arg Asp Gly Gly Val 305 310 315 320		
Ala Asp Ser Tyr Gly Asp Tyr Asn Lys Val Gly Phe Asp Cys Ser Gly 325 330 335		
Leu Thr Leu Tyr Ala Phe Ala Gly Val Gly Ile Ser Leu Pro His Tyr 340 345 350		
Thr Gly Tyr Gln Tyr Gln His Gly Thr Lys Val Ser Pro Ser Glu Met 355 360 365		
Gln Arg Gly Asp Leu Ile Phe Tyr Gly Pro Gly Ala Ser Gln His Val 370 375 380		

Ala Ile Tyr Leu Gly Asp Gly Gln Met Ile Glu Ala Pro Asn Ser Gly
385 390 395 400

Ser Val Val Lys Ile Ser Pro Val Arg Trp Ser Gly Met Thr Glu Ser
405 410 415

Val Val Arg Leu Ile
420

<210> 409

<211> 972

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(949)

<223> RXA00208

<400> 409

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tgcctagggtc agttaagat atatcgataa gaggttttcc atg aac act cca gcg 115
Met Asn Thr Pro Ala
1 5

ccc cgc aaa cga cgc gaa atg aaa atc aag aca gca acc gtc act ggt 163
Pro Arg Lys Arg Arg Glu Met Lys Ile Lys Thr Ala Thr Val Thr Gly
10 15 20

gtg cgt caa att tcc ccc gat ctc atc cgc ttc agc ttc gac tgc cca 211
Val Arg Gln Ile Ser Pro Asp Leu Ile Arg Phe Ser Phe Asp Cys Pro
25 30 35

gaa atc gtt ggc gcc gac ctg ggg ttc acg gac cat tac atc aag atc 259
Glu Ile Val Gly Ala Asp Leu Gly Phe Thr Asp His Tyr Ile Lys Ile
40 45 50

ctc ttc gtg cca gca ggt gcg gat tac tcc tgg cct ttc gac atg gca 307
Leu Phe Val Pro Ala Gly Ala Asp Tyr Ser Trp Pro Phe Asp Met Ala
55 60 65

gaa att gcg gaa acc cag ccc cgt gag ctg caa cca gtg cgc cgc acc 355
Glu Ile Ala Glu Thr Gln Pro Arg Glu Leu Gln Pro Val Arg Arg Thr
70 75 80 85

tac act ttc cgc acg gtt gac act gtc gca ggc aca ttt gac ata gat 403
Tyr Thr Phe Arg Thr Val Asp Thr Val Ala Gly Thr Phe Asp Ile Asp
90 95 100

ttc gtt gcg cac ggc acc gat ggc ctt gcc ggt cct tgg gcg cag cag 451
Phe Val Ala His Gly Thr Asp Gly Leu Ala Gly Pro Trp Ala Gln Gln
105 110 115

gca cag gta ggt gat gtc atc gcg ttc ggc ggc cca ggt ggc gca tgg 499
Ala Gln Val Gly Asp Val Ile Ala Phe Gly Gly Pro Gly Gly Ala Trp
120 125 130

aag cca gaa acc acc tat gag cac tac gtt ctc gca ggc gat gaa gcc 547

Lys Pro Glu Thr Thr Tyr Glu His Tyr Val Leu Ala Gly Asp Glu Ala
 135 140 145
 gca gca ccc gca att ttc gca gcc tta gaa cac cta ccc gcc ggc acc 595
 Ala Ala Pro Ala Ile Phe Ala Ala Leu Glu His Leu Pro Ala Gly Thr
 150 155 160 165
 acc gcc aaa gcc ttc att gaa atc tcc tcc aac gaa gcg cgt ttc aac 643
 Thr Ala Lys Ala Phe Ile Glu Ile Ser Ser Asn Glu Ala Arg Phe Asn
 170 175 180
 gcc cca gcc agc gac aac atc gag gtt gtc tgg gtg ccc cgc gac ggc 691
 Ala Pro Ala Ser Asp Asn Ile Glu Val Val Trp Val Pro Arg Asp Gly
 185 190 195
 gcc acc cac ggt aca ttg ctt atc gac gcc ctc cgc cag gac ggc tac 739
 Ala Thr His Gly Thr Leu Leu Ile Asp Ala Leu Arg Gln Asp Gly Tyr
 200 205 210
 cca acc aag aaa act tcc tgg ttc atc cac gga gtc gcc gaa atg gtg 787
 Pro Thr Lys Lys Thr Ser Trp Phe Ile His Gly Val Ala Glu Met Val
 215 220 225
 aag gaa acc cgc aaa ttc ctc ttc gtg gaa ggc aac gta gac aaa gct 835
 Lys Glu Thr Arg Lys Phe Leu Phe Val Glu Gly Asn Val Asp Lys Ala
 230 235 240 245
 gat gca tcc att tcc gga tac tgg cgc ctt ggc atg acc gaa gac cag 883
 Asp Ala Ser Ile Ser Gly Tyr Trp Arg Leu Gly Met Thr Glu Asp Gln
 250 255 260
 tgg cag gcc tcc aag cgg gag ttc aat gag caa aat gag gca gaa gaa 931
 Trp Gln Ala Ser Lys Arg Glu Phe Asn Glu Gln Asn Glu Ala Glu Glu
 265 270 275
 ctc gcg ctc agc aag gca taagggcaag ggggttctaga aag 972
 Leu Ala Leu Ser Lys Ala
 280

<210> 410

<211> 283

<212> PRT

<213> Corynebacterium glutamicum

<400> 410

Met Asn Thr Pro Ala Pro Arg Lys Arg Arg Glu Met Lys Ile Lys Thr
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 Ala Thr Val Thr Gly Val Arg Gln Ile Ser Pro Asp Leu Ile Arg Phe
 20 25 30
 Ser Phe Asp Cys Pro Glu Ile Val Gly Ala Asp Leu Gly Phe Thr Asp
 35 40 45
 His Tyr Ile Lys Ile Leu Phe Val Pro Ala Gly Ala Asp Tyr Ser Trp
 50 55 60
 Pro Phe Asp Met Ala Glu Ile Ala Glu Thr Gln Pro Arg Glu Leu Gln
 65 70 75 80

Pro Val Arg Arg Thr Tyr Thr Phe Arg Thr Val Asp Thr Val Ala Gly
 85 90 95

Thr Phe Asp Ile Asp Phe Val Ala His Gly Thr Asp Gly Leu Ala Gly
 100 105 110

Pro Trp Ala Gln Gln Ala Gln Val Gly Asp Val Ile Ala Phe Gly Gly
 115 120 125

Pro Gly Gly Ala Trp Lys Pro Glu Thr Thr Tyr Glu His Tyr Val Leu
 130 135 140

Ala Gly Asp Glu Ala Ala Ala Pro Ala Ile Phe Ala Ala Leu Glu His
 145 150 155 160

Leu Pro Ala Gly Thr Thr Ala Lys Ala Phe Ile Glu Ile Ser Ser Asn
 165 170 175

Glu Ala Arg Phe Asn Ala Pro Ala Ser Asp Asn Ile Glu Val Val Trp
 180 185 190

Val Pro Arg Asp Gly Ala Thr His Gly Thr Leu Leu Ile Asp Ala Leu
 195 200 205

Arg Gln Asp Gly Tyr Pro Thr Lys Lys Thr Ser Trp Phe Ile His Gly
 210 215 220

Val Ala Glu Met Val Lys Glu Thr Arg Lys Phe Leu Phe Val Glu Gly
 225 230 235 240

Asn Val Asp Lys Ala Asp Ala Ser Ile Ser Gly Tyr Trp Arg Leu Gly
 245 250 255

Met Thr Glu Asp Gln Trp Gln Ala Ser Lys Arg Glu Phe Asn Glu Gln
 260 265 270

Asn Glu Ala Glu Glu Leu Ala Leu Ser Lys Ala
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<210> 411

<211> 411

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (26) .. (388)

<223> RXA00967

<400> 411

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5

aac aac aat gac cgg cca gtg atg ccg gga gag atc ctc cgt gag gaa 100

Asn Asn Asn Asp Arg Pro Val Met Pro Gly Glu Ile Leu Arg Glu Glu

10

15

20

25

ttc atg gag cct ttg ggg ctg tcc caa aac ggc ttg gcg cgg gca ata 148

Phe Met Glu Pro Leu Gly Leu Ser Gln Asn Gly Leu Ala Arg Ala Ile

	30		35		40	
gga gtg cca cca cgc agg att aat gag atc gtg cac ggc aaa cgc gca						196
Gly Val Pro Pro Arg Arg Ile Asn Glu Ile Val His Gly Lys Arg Ala						
	45		50		55	
atc acg gca gac act gcg ctg cgt tta gct gct tat tta ggt ccc gat						244
Ile Thr Ala Asp Thr Ala Leu Arg Leu Ala Ala Tyr Leu Gly Pro Asp						
	60		65		70	
cca cag ttt tgg ctc aac ttg cag acc cac tac gac ctg tcg gtg acg						292
Pro Gln Phe Trp Leu Asn Leu Gln Thr His Tyr Asp Leu Ser Val Thr						
	75		80		85	
tat tta gat gcg cgc aca ctg ttg gaa gcg atc aag cct tat gat cgt						340
Tyr Leu Asp Ala Arg Thr Leu Leu Glu Ala Ile Lys Pro Tyr Asp Arg						
	90		95		100	105
cag caa aat gtg gct cgg acc ctg aat ccg ctt cag gag agc tcg cag						388
Gln Gln Asn Val Ala Arg Thr Leu Asn Pro Leu Gln Glu Ser Ser Gln						
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<211> 121

<212> PRT

<213> Corynebacterium glutamicum

<400> 412

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	20					25						30		

Ser Gln Asn Gly Leu Ala Arg Ala Ile Gly Val Pro Pro Arg Arg Ile														
	35					40					45			

Asn Glu Ile Val His Gly Lys Arg Ala Ile Thr Ala Asp Thr Ala Leu														
	50					55					60			

Arg Leu Ala Ala Tyr Leu Gly Pro Asp Pro Gln Phe Trp Leu Asn Leu														
	65				70				75				80	

Gln Thr His Tyr Asp Leu Ser Val Thr Tyr Leu Asp Ala Arg Thr Leu														
			85					90					95	

Leu Glu Ala Ile Lys Pro Tyr Asp Arg Gln Gln Asn Val Ala Arg Thr														
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<211> 381

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(358)

<223> RXA01149

<400> 413

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ccccaccat cgggatccct gatccacgaa aggagtgttc gtg gta gct ccg cag 115
 Val Val Ala Pro Gln
 1 5

tcc cgg aaa ccg cag cac cct ggt gag att ttg agt gaa cgt ttc ctc 163
 Ser Arg Lys Pro Gln His Pro Gly Glu Ile Leu Ser Glu Arg Phe Leu
 10 15 20

gaa ccc cga gga atc agc cac tac gat ctc gcc aaa acc ctc cac atc 211
 Glu Pro Arg Gly Ile Ser His Tyr Asp Leu Ala Lys Thr Leu His Ile
 25 30 35

acc gaa gca acc atc gcc aat ttc gtt gaa ggt cgc acc gac ctc acc 259
 Thr Glu Ala Thr Ile Ala Asn Phe Val Glu Gly Arg Thr Asp Leu Thr
 40 45 50

atc gga ctt gca gta cgc ctc tcc cgc tca ttc gat ttg agc aca cag 307
 Ile Gly Leu Ala Val Arg Leu Ser Arg Ser Phe Asp Leu Ser Thr Gln
 55 60 65

gaa tgg atc gca ctg cag cgc acc ttt gat cag gct cat cgt cga tct 355
 Glu Trp Ile Ala Leu Gln Arg Thr Phe Asp Gln Ala His Arg Arg Ser
 70 75 80 85

gct taaaagtttt tagcttcacg gaa 381
 Ala

<210> 414

<211> 86

<212> PRT

<213> Corynebacterium glutamicum

<400> 414

Val Val Ala Pro Gln Ser Arg Lys Pro Gln His Pro Gly Glu Ile Leu
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Ser Glu Arg Phe Leu Glu Pro Arg Gly Ile Ser His Tyr Asp Leu Ala
 20 25 30

Lys Thr Leu His Ile Thr Glu Ala Thr Ile Ala Asn Phe Val Glu Gly
 35 40 45

Arg Thr Asp Leu Thr Ile Gly Leu Ala Val Arg Leu Ser Arg Ser Phe
 50 55 60

Asp Leu Ser Thr Gln Glu Trp Ile Ala Leu Gln Arg Thr Phe Asp Gln
 65 70 75 80

Ala His Arg Arg Ser Ala
 85


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<222> (101)..(1966)  
<223> RXA01305
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<400> 415																
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Met Arg Pro Ser Ser 5																
cgg cca ctt ggc ctc gtc cta tgc acc gca ctg gca tca acg atc atc 163																
Arg Pro Leu Gly Leu Val Leu Cys Thr Ala Leu Ala Ser Thr Ile Ile 20																
acc gtt ccc gca gcg tcc gcc cag gag cca gcg ctt ctc gat gcc tcc 211																
Thr Val Pro Ala Ala Ser Ala Gln Glu Pro Ala Leu Leu Asp Ala Ser 35																
gcc atc gcc cca cat acc gcc agc tac ggc tac tac gtt gat gca tgg 259																
Ala Ile Ala Pro His Thr Ala Ser Tyr Gly Tyr Tyr Val Asp Ala Trp 50																
gac acc aac gtt tcc act gat ctg aat cca tca agt aat gca gct gtt 307																
Asp Thr Asn Val Ser Thr Asp Leu Asn Pro Ser Ser Asn Ala Ala Val 65																
ggc gta ctg gag gaa atg ctt gag ctg tgg acc cca ggc gaa gaa tgg 355																
Gly Val Leu Glu Glu Met Leu Glu Leu Trp Thr Pro Gly Glu Glu Trp 85																
aac acc ggc gtc aag gtt gac ccc acc gtg ctg gat tcc aac atc gca 403																
Asn Thr Gly Val Lys Val Asp Pro Thr Val Leu Asp Ser Asn Ile Ala 100																
cag tct gtg gca atc tcc cag cag gcg acc gat gct cag caa gaa cgt 451																
Gln Ser Val Ala Ile Ser Gln Gln Ala Thr Asp Ala Gln Gln Glu Arg 115																
gct tgg gtt att gat cgc cgc aac cag aac tac acc gca acc gac ggt 499																
Ala Trp Val Ile Asp Arg Arg Asn Gln Asn Tyr Thr Ala Thr Asp Gly 130																
ctt ggc gca tac gca gat agt tac cgc gag acc gca cag gtg ggc acc 547																
Leu Gly Ala Tyr Ala Asp Ser Tyr Arg Glu Thr Ala Gln Val Gly Thr 145																
acc atc cct gac gtt gtt cca gct gat gcc acc acc gtg aag tac aac 595																
Thr Ile Pro Asp Val Val Pro Ala Asp Ala Thr Thr Val Lys Tyr Asn 165																
gat ggc ggc aat gtg aat ggc aat tgg gca gag acc ggt gga gaa ctc 643																
Asp Gly Gly Asn Val Asn Gly Asn Trp Ala Glu Thr Gly Gly Glu Leu 180																

gga tcc act gtt gat cta att gaa gct atc cgt cag cat gcc gca acc	691
Gly Ser Thr Val Asp Leu Ile Glu Ala Ile Arg Gln His Ala Ala Thr	
185 190 195	
agc aac aat gcc aag gcg tac tac caa tac cca cgc ccc tac cgc tgg	739
Ser Asn Asn Ala Lys Ala Tyr Tyr Gln Tyr Pro Arg Pro Tyr Arg Trp	
200 205 210	
act gaa tcc atc gaa cca gaa gcc tgg ggc gag ggc gtt gac atg cca	787
Thr Glu Ser Ile Glu Pro Glu Ala Trp Gly Glu Gly Val Asp Met Pro	
215 220 225	
gag tat gca aac cca ctg cgc aag gat gaa tcc gaa gct gcc agc gat	835
Glu Tyr Ala Asn Pro Leu Arg Lys Asp Glu Ser Glu Ala Ala Ser Asp	
230 235 240 245	
ggc ggt ttc cct tcc gga cac acc tcc gca ggc ggc atg gca acc aac	883
Gly Gly Phe Pro Ser Gly His Thr Ser Ala Gly Gly Met Ala Thr Asn	
250 255 260	
ggc ctg gct tac gct ttc cca cag caa tac gat aaa ctg ctc atg act	931
Gly Leu Ala Tyr Ala Phe Pro Gln Gln Tyr Asp Lys Leu Leu Met Thr	
265 270 275	
gca gcg gaa atc ggc gaa agc cgc atc cag ctg ggc atg cac tct ccg	979
Ala Ala Glu Ile Gly Glu Ser Arg Ile Gln Leu Gly Met His Ser Pro	
280 285 290	
ctt gat gtt att ggc ggc cgt gtt cta tcc acc gcg att act gca ggt	1027
Leu Asp Val Ile Gly Gly Arg Val Leu Ser Thr Ala Ile Thr Ala Gly	
295 300 305	
gca ctt aat gat ccg aat ctc gac tcg gtg aag gct gaa gcc ttc gat	1075
Ala Leu Asn Asp Pro Asn Leu Asp Ser Val Lys Ala Glu Ala Phe Asp	
310 315 320 325	
gat gct cag gca tgg atc agt aac cag agc gac atc acc acc aac act	1123
Asp Ala Gln Ala Trp Ile Ser Asn Gln Ser Asp Ile Thr Thr Asn Thr	
330 335 340	
cgc gat ttt gat gag caa ctc gcc gag tac acc aac ttc ctc acc ttc	1171
Arg Asp Phe Asp Glu Gln Leu Ala Glu Tyr Thr Asn Phe Leu Thr Phe	
345 350 355	
ggc ttc gag cag tcc ggc gac acc acc caa gac atg cgc gtg cca aag	1219
Gly Phe Glu Gln Ser Gly Asp Thr Thr Gln Asp Met Arg Val Pro Lys	
360 365 370	
gga gct gag gct ctg ctg gaa acc cgc ctt ccg tac ctt gat gac gaa	1267
Gly Ala Glu Ala Leu Leu Glu Thr Arg Leu Pro Tyr Leu Asp Asp Glu	
375 380 385	
cag cgc cgt tgg gtt cta cat tcc act ggc ctc gag tcc ggt ttc cca	1315
Gln Arg Arg Trp Val Leu His Ser Thr Gly Leu Glu Ser Gly Phe Pro	
390 395 400 405	
gta ctt gat gat gcc gaa ggt tgg ggc cgt ctc aac ctc tac gct gcc	1363
Val Leu Asp Asp Ala Glu Gly Trp Gly Arg Leu Asn Leu Tyr Ala Ala	
410 415 420	

cag gct ggc tac agt gca ttc gat acc aac gtt gac gtc acc atg aat 1411
 Gln Ala Gly Tyr Ser Ala Phe Asp Thr Asn Val Asp Val Thr Met Asn
 425 430 435

 gcc atc gac ggt ggc tac aac gcc aaa gac aac tgg caa aac gac atc 1459
 Ala Ile Asp Gly Gly Tyr Asn Ala Lys Asp Asn Trp Gln Asn Asp Ile
 440 445 450

 gag ggc gca gga tcc ctg acc aag aac ggt tcc ggt gaa ctc acc ctg 1507
 Glu Gly Ala Gly Ser Leu Thr Lys Asn Gly Ser Gly Glu Leu Thr Leu
 455 460 465

 tca ggt gac aac tcc tac acc ggt gga acc acc atc acc gcg ggc acc 1555
 Ser Gly Asp Asn Ser Tyr Thr Gly Gly Thr Thr Ile Thr Ala Gly Thr
 470 475 480 485

 ttg gtt gct gca act gag tca gct ctg gga gca ggc gat ctc acc atc 1603
 Leu Val Ala Ala Thr Glu Ser Ala Leu Gly Ala Gly Asp Leu Thr Ile
 490 495 500

 aac gat ggt gca acc ttg aag atc acc cag cct gtc acc gtg gat gga 1651
 Asn Asp Gly Ala Thr Leu Lys Ile Thr Gln Pro Val Thr Val Asp Gly
 505 510 515

 acc gca aac ctg gga gga act ctg cac gtt gcc ctt cct gtt ggc acc 1699
 Thr Ala Asn Leu Gly Gly Thr Leu His Val Ala Leu Pro Val Gly Thr
 520 525 530

 aac cac gtc acc gtg atc gat gct gca tca att tcc ggt gaa ttt gat 1747
 Asn His Val Thr Val Ile Asp Ala Ala Ser Ile Ser Gly Glu Phe Asp
 535 540 545

 gag gtt att gtt gat ggc gca gtt gac gct cag gtg agc tac gac aac 1795
 Glu Val Ile Val Asp Gly Ala Val Asp Ala Gln Val Ser Tyr Asp Asn
 550 555 560 565

 ggc tct gtc gtg att act aca ggc gca cct tct gat gac gta aag gaa 1843
 Gly Ser Val Val Ile Thr Thr Gly Ala Pro Ser Asp Asp Val Lys Glu
 570 575 580

 act ggc tct tct gct ggc gga att ctt gcc atc gtg gca gcc ctg ggt 1891
 Thr Gly Ser Ser Ala Gly Gly Ile Leu Ala Ile Val Ala Ala Leu Gly
 585 590 595

 ggc att gca gca ctg atc ttc ggt gca ttc acc cag ttt ggt ttc cca 1939
 Gly Ile Ala Ala Leu Ile Phe Gly Ala Phe Thr Gln Phe Gly Phe Pro
 600 605 610

 cca gca atc aag gaa atg ttc gac ctt taagccttcg ccaacccac 1986
 Pro Ala Ile Lys Glu Met Phe Asp Leu
 615 620

 ggc 1989

<210> 416

<211> 622

<212> PRT

<213> Corynebacterium glutamicum

<400> 416

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 20 25 30
 Leu Leu Asp Ala Ser Ala Ile Ala Pro His Thr Ala Ser Tyr Gly Tyr
 35 40 45
 Tyr Val Asp Ala Trp Asp Thr Asn Val Ser Thr Asp Leu Asn Pro Ser
 50 55 60
 Ser Asn Ala Ala Val Gly Val Leu Glu Glu Met Leu Glu Leu Trp Thr
 65 70 75 80
 Pro Gly Glu Glu Trp Asn Thr Gly Val Lys Val Asp Pro Thr Val Leu
 85 90 95
 Asp Ser Asn Ile Ala Gln Ser Val Ala Ile Ser Gln Gln Ala Thr Asp
 100 105 110
 Ala Gln Gln Glu Arg Ala Trp Val Ile Asp Arg Arg Asn Gln Asn Tyr
 115 120 125
 Thr Ala Thr Asp Gly Leu Gly Ala Tyr Ala Asp Ser Tyr Arg Glu Thr
 130 135 140
 Ala Gln Val Gly Thr Thr Ile Pro Asp Val Val Pro Ala Asp Ala Thr
 145 150 155 160
 Thr Val Lys Tyr Asn Asp Gly Gly Asn Val Asn Gly Asn Trp Ala Glu
 165 170 175
 Thr Gly Gly Glu Leu Gly Ser Thr Val Asp Leu Ile Glu Ala Ile Arg
 180 185 190
 Gln His Ala Ala Thr Ser Asn Asn Ala Lys Ala Tyr Tyr Gln Tyr Pro
 195 200 205
 Arg Pro Tyr Arg Trp Thr Glu Ser Ile Glu Pro Glu Ala Trp Gly Glu
 210 215 220
 Gly Val Asp Met Pro Glu Tyr Ala Asn Pro Leu Arg Lys Asp Glu Ser
 225 230 235 240
 Glu Ala Ala Ser Asp Gly Gly Phe Pro Ser Gly His Thr Ser Ala Gly
 245 250 255
 Gly Met Ala Thr Asn Gly Leu Ala Tyr Ala Phe Pro Gln Gln Tyr Asp
 260 265 270
 Lys Leu Leu Met Thr Ala Ala Glu Ile Gly Glu Ser Arg Ile Gln Leu
 275 280 285
 Gly Met His Ser Pro Leu Asp Val Ile Gly Gly Arg Val Leu Ser Thr
 290 295 300
 Ala Ile Thr Ala Gly Ala Leu Asn Asp Pro Asn Leu Asp Ser Val Lys
 305 310 315 320
 Ala Glu Ala Phe Asp Asp Ala Gln Ala Trp Ile Ser Asn Gln Ser Asp

325										330					335				
Ile	Thr	Thr	Asn	Thr	Arg	Asp	Phe	Asp	Glu	Gln	Leu	Ala	Glu	Tyr	Thr				
			340						345					350					
Asn	Phe	Leu	Thr	Phe	Gly	Phe	Glu	Gln	Ser	Gly	Asp	Thr	Thr	Gln	Asp				
		355					360					365							
Met	Arg	Val	Pro	Lys	Gly	Ala	Glu	Ala	Leu	Leu	Glu	Thr	Arg	Leu	Pro				
		370				375					380								
Tyr	Leu	Asp	Asp	Glu	Gln	Arg	Arg	Trp	Val	Leu	His	Ser	Thr	Gly	Leu				
385					390					395					400				
Glu	Ser	Gly	Phe	Pro	Val	Leu	Asp	Asp	Ala	Glu	Gly	Trp	Gly	Arg	Leu				
				405					410					415					
Asn	Leu	Tyr	Ala	Ala	Gln	Ala	Gly	Tyr	Ser	Ala	Phe	Asp	Thr	Asn	Val				
			420					425						430					
Asp	Val	Thr	Met	Asn	Ala	Ile	Asp	Gly	Gly	Tyr	Asn	Ala	Lys	Asp	Asn				
		435					440					445							
Trp	Gln	Asn	Asp	Ile	Glu	Gly	Ala	Gly	Ser	Leu	Thr	Lys	Asn	Gly	Ser				
	450					455					460								
Gly	Glu	Leu	Thr	Leu	Ser	Gly	Asp	Asn	Ser	Tyr	Thr	Gly	Gly	Thr	Thr				
465					470					475					480				
Ile	Thr	Ala	Gly	Thr	Leu	Val	Ala	Ala	Thr	Glu	Ser	Ala	Leu	Gly	Ala				
				485					490					495					
Gly	Asp	Leu	Thr	Ile	Asn	Asp	Gly	Ala	Thr	Leu	Lys	Ile	Thr	Gln	Pro				
		500						505						510					
Val	Thr	Val	Asp	Gly	Thr	Ala	Asn	Leu	Gly	Gly	Thr	Leu	His	Val	Ala				
		515					520					525							
Leu	Pro	Val	Gly	Thr	Asn	His	Val	Thr	Val	Ile	Asp	Ala	Ala	Ser	Ile				
	530					535					540								
Ser	Gly	Glu	Phe	Asp	Glu	Val	Ile	Val	Asp	Gly	Ala	Val	Asp	Ala	Gln				
545					550					555					560				
Val	Ser	Tyr	Asp	Asn	Gly	Ser	Val	Val	Ile	Thr	Thr	Gly	Ala	Pro	Ser				
			565					570						575					
Asp	Asp	Val	Lys	Glu	Thr	Gly	Ser	Ser	Ala	Gly	Gly	Ile	Leu	Ala	Ile				
		580						585					590						
Val	Ala	Ala	Leu	Gly	Gly	Ile	Ala	Ala	Leu	Ile	Phe	Gly	Ala	Phe	Thr				
		595					600					605							
Gln	Phe	Gly	Phe	Pro	Pro	Ala	Ile	Lys	Glu	Met	Phe	Asp	Leu						
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<210> 417

<211> 420

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(397)

<223> RXA01453

<400> 417

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gaaaacgtcg agatcgtgga ttatcactga ggaggagacg	atg gct cag aag ctc	115
	Met Ala Gln Lys Leu	
	1 5	

tac ccg ccg att cac cct ggt gag att ctc atg gag gac ttc atc aag	163
Tyr Pro Pro Ile His Pro Gly Glu Ile Leu Met Glu Asp Phe Ile Lys	
10 15 20	

ggc ttc ggc ctc aca cag aac aag gtc gcc gta tcg atc ggg gtg cct	211
Gly Phe Gly Leu Thr Gln Asn Lys Val Ala Val Ser Ile Gly Val Pro	
25 30 35	

ccg cga cgc atc aac gag atc gtg cac ggc aag cga tcc atc acg gcc	259
Pro Arg Arg Ile Asn Glu Ile Val His Gly Lys Arg Ser Ile Thr Ala	
40 45 50	

gat acg gct ctg cgt ctc ggg cgg tac ttc ggt atc gac ccg cag ttc	307
Asp Thr Ala Leu Arg Leu Gly Arg Tyr Phe Gly Ile Asp Pro Gln Phe	
55 60 65	

tgg ctg agc ctt cag act cag tac gag ttg gag ctc gat cgc gac gcc	355
Trp Leu Ser Leu Gln Thr Gln Tyr Glu Leu Glu Leu Asp Arg Asp Ala	
70 75 80 85	

ggg gca gcg act tac gca cag atc acg ccg ctg aag gtc gcg	397
Gly Ala Ala Thr Tyr Ala Gln Ile Thr Pro Leu Lys Val Ala	
90 95	

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<210> 418

<211> 99

<212> PRT

<213> Corynebacterium glutamicum

<400> 418

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Glu Asp Phe Ile Lys Gly Phe Gly Leu Thr Gln Asn Lys Val Ala Val
20 25 30

Ser Ile Gly Val Pro Pro Arg Arg Ile Asn Glu Ile Val His Gly Lys
35 40 45

Arg Ser Ile Thr Ala Asp Thr Ala Leu Arg Leu Gly Arg Tyr Phe Gly
50 55 60

Ile Asp Pro Gln Phe Trp Leu Ser Leu Gln Thr Gln Tyr Glu Leu Glu
65 70 75 80

Lys Val Ala

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<221> CDS
<222> (101)..(922)
<223> RXA01824
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aac cta ctg cgc gaa aac tcc cac gac cgc gac atc tct gaa atc gtc 163 Asn Leu Leu Arg Glu Asn Ser His Asp Arg Asp Ile Ser Glu Ile Val 20															
gcc acc atc act gcc ctt gac cac cca tca ccc tca ctt ctg cga ttc 211 Ala Thr Ile Thr Ala Leu Asp His Pro Ser Pro Ser Leu Leu Arg Phe 35															
aca gct ttt gtt cca gga tca gca aac aac cca gtg tgg gca gaa gcc 259 Thr Ala Phe Val Pro Gly Ser Ala Asn Asn Pro Val Trp Ala Glu Ala 50															
aac gtg gca atc agg ctt tac ctc agc gaa gaa ttc gac gac gcc acc 307 Asn Val Ala Ile Arg Leu Tyr Leu Ser Glu Glu Phe Asp Asp Ala Thr 65															
cgc gtc tac acc gtc cga tcc ttt gat gcc gca act gaa agc atc gtg 355 Arg Val Tyr Thr Val Arg Ser Phe Asp Ala Ala Thr Glu Ser Ile Val 85															
gtg gat gtg gtt caa cac cac cac gaa agc ccc atg atg cgc tgg tca 403 Val Asp Val Val Gln His His His Glu Ser Pro Met Met Arg Trp Ser 95															
gac acc gta aaa atc aac gac acc ctc gtg ctc acc gga ccc cgc cca 451 Asp Thr Val Lys Ile Asn Asp Thr Leu Val Leu Thr Gly Pro Arg Pro 115															
cac ttt gtc atc ccc gaa ggc gaa caa gca gca ctc ttc ctt gat gac 499 His Phe Val Ile Pro Glu Gly Glu Gln Ala Ala Leu Phe Leu Asp Asp 130															
acc gcc atc ccc gct ctc gcc gct att ttg gat caa tgg cca aca gat 547 Thr Ala Ile Pro Ala Leu Ala Ala Ile Leu Asp Gln Trp Pro Thr Asp 145															
ctt cgt ggc aaa gga tgg gtt gtc act gac gat ccc gca gcc ttc gat 595															

Leu Arg Gly Lys Gly Trp Val Val Thr Asp Asp Pro Ala Ala Phe Asp
 150 155 160 165
 gaa cta ccc agc atc gac gga ctg gaa ctg aac ctg ctc gcg ccg gga 643
 Glu Leu Pro Ser Ile Asp Gly Leu Glu Leu Asn Leu Leu Ala Pro Gly
 170 175 180
 tca gat cca act gtt cag cca ctt gcc caa cag gca tat gac ctg gaa 691
 Ser Asp Pro Thr Val Gln Pro Leu Ala Gln Gln Ala Tyr Asp Leu Glu
 185 190 195
 aac cca gaa act tac gtg gtg tgg gca gcc ggc gag cga gat gaa ata 739
 Asn Pro Glu Thr Tyr Val Val Trp Ala Ala Gly Glu Arg Asp Glu Ile
 200 205 210
 aaa tcc atc cgc agg cac ttc cgc aag cag gtg gga ttg gaa aaa gat 787
 Lys Ser Ile Arg Arg His Phe Arg Lys Gln Val Gly Leu Glu Lys Asp
 215 220 225
 gca gtg gcc gtg ttt ggg tac tgg aaa tac aac acc acc aac act cag 835
 Ala Val Ala Val Phe Gly Tyr Trp Lys Tyr Asn Thr Thr Asn Thr Gln
 230 235 240 245
 atc gat gca gtc cgc aaa gaa aac tac atg aag atg ctc tct gaa ggg 883
 Ile Asp Ala Val Arg Lys Glu Asn Tyr Met Lys Met Leu Ser Glu Gly
 250 255 260
 cta cag ctg gaa aac ttc gac gac ctc tca ttg gag att taaggggtcg 932
 Leu Gln Leu Glu Asn Phe Asp Asp Leu Ser Leu Glu Ile
 265 270
 agtttttaga atg 945

<210> 420

<211> 274

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

Met Lys Glu Thr Asp Asn Leu Leu Arg Glu Asn Ser His Asp Arg Asp
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 Ile Ser Glu Ile Val Ala Thr Ile Thr Ala Leu Asp His Pro Ser Pro
 20 25 30
 Ser Leu Leu Arg Phe Thr Ala Phe Val Pro Gly Ser Ala Asn Asn Pro
 35 40 45
 Val Trp Ala Glu Ala Asn Val Ala Ile Arg Leu Tyr Leu Ser Glu Glu
 50 55 60
 Phe Asp Asp Ala Thr Arg Val Tyr Thr Val Arg Ser Phe Asp Ala Ala
 65 70 75 80
 Thr Glu Ser Ile Val Val Asp Val Val Gln His His His Glu Ser Pro
 85 90 95
 Met Met Arg Trp Ser Asp Thr Val Lys Ile Asn Asp Thr Leu Val Leu
 100 105 110

Thr Gly Pro Arg Pro His Phe Val Ile Pro Glu Gly Glu Gln Ala Ala
 115 120 125
 Leu Phe Leu Asp Asp Thr Ala Ile Pro Ala Leu Ala Ala Ile Leu Asp
 130 135 140
 Gln Trp Pro Thr Asp Leu Arg Gly Lys Gly Trp Val Val Thr Asp Asp
 145 150 155 160
 Pro Ala Ala Phe Asp Glu Leu Pro Ser Ile Asp Gly Leu Glu Leu Asn
 165 170 175
 Leu Leu Ala Pro Gly Ser Asp Pro Thr Val Gln Pro Leu Ala Gln Gln
 180 185 190
 Ala Tyr Asp Leu Glu Asn Pro Glu Thr Tyr Val Val Trp Ala Ala Gly
 195 200 205
 Glu Arg Asp Glu Ile Lys Ser Ile Arg Arg His Phe Arg Lys Gln Val
 210 215 220
 Gly Leu Glu Lys Asp Ala Val Ala Val Phe Gly Tyr Trp Lys Tyr Asn
 225 230 235 240
 Thr Thr Asn Thr Gln Ile Asp Ala Val Arg Lys Glu Asn Tyr Met Lys
 245 250 255
 Met Leu Ser Glu Gly Leu Gln Leu Glu Asn Phe Asp Asp Leu Ser Leu
 260 265 270

Glu Ile

<210> 421
 <211> 1017
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(994)
 <223> RXA01832

<400> 421
 tttcagtcac agggagggac aaagccatgc ccttaggcgt tttctaggag aagacactta 60
 tggaacaccc aacttattga gaaaaggagg tcgcaaagtt atg gct act tcg aat 115
 Met Ala Thr Ser Asn
 1 5
 cgg ata gct aat gct atg aac agt ttg gcc aag ctg gac agt tct atg 163
 Arg Ile Ala Asn Ala Met Asn Ser Leu Ala Lys Leu Asp Ser Ser Met
 10 15 20
 caa cgc ggc ctt gat aat gcg ttg gcg ttt gtt ttc cgt ggt cgc gtt 211
 Gln Arg Gly Leu Asp Asn Ala Leu Ala Phe Val Phe Arg Gly Arg Val
 25 30 35
 gtt ccg gct gag ctt gag gag ctt ttg aag caa gag gct gag gac aat 259
 Val Pro Ala Glu Leu Glu Glu Leu Leu Lys Gln Glu Ala Glu Asp Asn

40	45	50	
gtg gtt cat act gag ttt ggc tat gtt gag gcg ccg aat gtt ttt aag Val Val His Thr Glu Phe Gly Tyr Val Glu Ala Pro Asn Val Phe Lys 55 60 65			307
gtt tgc gtg agc ccg aac gat ttt agt aat ctt gtc gat cgt ttt cct Val Ser Val Ser Pro Asn Asp Phe Ser Asn Leu Val Asp Arg Phe Pro 70 75 80 85			355
gat cag ccg gct cgt ttt ggt gat cag atg atg agg ttc tgc agg aac Asp Gln Pro Ala Arg Phe Gly Asp Gln Met Met Arg Phe Cys Arg Asn 90 95 100			403
agt ggc tgg acg ttg gtt ggg ccg gtg att gtg ttg att gaa gag gat Ser Gly Trp Thr Leu Val Gly Pro Val Ile Val Leu Ile Glu Glu Asp 105 110 115			451
tct tgc ttg cac acg ggc cag ttg aag tgc gtt tgc gag aag gat ccg Ser Ser Leu His Thr Gly Gln Leu Lys Ser Val Ser Glu Lys Asp Pro 120 125 130			499
gat ccg gag tta agt agc ggt tat ctg cct ttg gaa ggc gac ggc atc Asp Pro Glu Leu Ser Ser Gly Tyr Leu Pro Leu Glu Gly Asp Gly Ile 135 140 145			547
ctg cct gtc gca gaa agt gag tct aag aac gtg tct gac agt tcc cct Leu Pro Val Ala Glu Ser Glu Ser Lys Asn Val Ser Asp Ser Ser Pro 150 155 160 165			595
tac act ggt acg gag ttt ttg ccg gcg caa tca gcg gat cgc cct ttg Tyr Thr Gly Thr Glu Phe Leu Pro Ala Gln Ser Ala Asp Arg Pro Leu 170 175 180			643
gtt cag ggt gtg ccg cag tct cag gtt gat gcg aat cgc cag gct gcg Val Gln Gly Val Pro Gln Ser Gln Val Asp Ala Asn Arg Gln Ala Ala 185 190 195			691
atg aag ccc gcg ggc cct acg gtg act ttg ctg ctg cag gat ggt tgc Met Lys Pro Ala Gly Pro Thr Val Thr Leu Leu Leu Gln Asp Gly Ser 200 205 210			739
agc cgg act tat ttg gtt cgg gag ggt tgc aac atc att ggt cgt agt Ser Arg Thr Tyr Leu Val Arg Glu Gly Ser Asn Ile Ile Gly Arg Ser 215 220 225			787
aat gat gcg gat ctt cgt ttg ccg gat act ggt gtg tct cgt cag cat Asn Asp Ala Asp Leu Arg Leu Pro Asp Thr Gly Val Ser Arg Gln His 230 235 240 245			835
gtg gag atc acg tgg gat ggc cgg gat gcc att ttg gtt gat ttg aag Val Glu Ile Thr Trp Asp Gly Arg Asp Ala Ile Leu Val Asp Leu Lys 250 255 260			883
tgc act aat ggc acc acg gtg aat gac act cct gtg gat aat tgg ttg Ser Thr Asn Gly Thr Thr Val Asn Asp Thr Pro Val Asp Asn Trp Leu 265 270 275			931
ttg gct gat ggt gat gtc att acg gtg ggt cat tcc aat atc gaa gtt Leu Ala Asp Gly Asp Val Ile Thr Val Gly His Ser Asn Ile Glu Val 280 285 290			979

cgt att gtt agt ccc tagagggaga ggttgatcaa tgg
 Arg Ile Val Ser Pro
 295

1017

<210> 422

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 422

Met Ala Thr Ser Asn Arg Ile Ala Asn Ala Met Asn Ser Leu Ala Lys
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Leu Asp Ser Ser Met Gln Arg Gly Leu Asp Asn Ala Leu Ala Phe Val
 20 25 30

Phe Arg Gly Arg Val Val Pro Ala Glu Leu Glu Glu Leu Leu Lys Gln
 35 40 45

Glu Ala Glu Asp Asn Val Val His Thr Glu Phe Gly Tyr Val Glu Ala
 50 55 60

Pro Asn Val Phe Lys Val Ser Val Ser Pro Asn Asp Phe Ser Asn Leu
 65 70 75 80

Val Asp Arg Phe Pro Asp Gln Pro Ala Arg Phe Gly Asp Gln Met Met
 85 90 95

Arg Phe Cys Arg Asn Ser Gly Trp Thr Leu Val Gly Pro Val Ile Val
 100 105 110

Leu Ile Glu Glu Asp Ser Ser Leu His Thr Gly Gln Leu Lys Ser Val
 115 120 125

Ser Glu Lys Asp Pro Asp Pro Glu Leu Ser Ser Gly Tyr Leu Pro Leu
 130 135 140

Glu Gly Asp Gly Ile Leu Pro Val Ala Glu Ser Glu Ser Lys Asn Val
 145 150 155 160

Ser Asp Ser Ser Pro Tyr Thr Gly Thr Glu Phe Leu Pro Ala Gln Ser
 165 170 175

Ala Asp Arg Pro Leu Val Gln Gly Val Pro Gln Ser Gln Val Asp Ala
 180 185 190

Asn Arg Gln Ala Ala Met Lys Pro Ala Gly Pro Thr Val Thr Leu Leu
 195 200 205

Leu Gln Asp Gly Ser Ser Arg Thr Tyr Leu Val Arg Glu Gly Ser Asn
 210 215 220

Ile Ile Gly Arg Ser Asn Asp Ala Asp Leu Arg Leu Pro Asp Thr Gly
 225 230 235 240

Val Ser Arg Gln His Val Glu Ile Thr Trp Asp Gly Arg Asp Ala Ile
 245 250 255

Leu Val Asp Leu Lys Ser Thr Asn Gly Thr Thr Val Asn Asp Thr Pro

260

265

270

Val Asp Asn Trp Leu Leu Ala Asp Gly Asp Val Ile Thr Val Gly His
 275 280 285

Ser Asn Ile Glu Val Arg Ile Val Ser Pro
 290 295

<210> 423

<211> 690

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(667)

<223> RXA02533

<400> 423

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tagtagataa aattgttctt aaagcgacat tattgtctgc atg gaa gac gat ctc 115
 Met Glu Asp Asp Leu
 1 5

agt gct gct ctc gtc aaa gcg ctt ttc gac gcg cga acc caa cgc agg 163
 Ser Ala Ala Leu Val Lys Ala Leu Phe Asp Ala Arg Thr Gln Arg Arg
 10 15 20

ctc tct atc tcg gcg tta gct gaa tcc tcc ggt gtg tcg cga gca atg 211
 Leu Ser Ile Ser Ala Leu Ala Glu Ser Ser Gly Val Ser Arg Ala Met
 25 30 35

att tcc cgc gtg gaa aac gca gag gcg caa cca agc gct gca tta ctt 259
 Ile Ser Arg Val Glu Asn Ala Glu Ala Gln Pro Ser Ala Ala Leu Leu
 40 45 50

gga cgc ctt tcc ggt gca ttg ggt atg acg ctt tcg gag ctc att gca 307
 Gly Arg Leu Ser Gly Ala Leu Gly Met Thr Leu Ser Glu Leu Ile Ala
 55 60 65

cag gct gaa ggt ggc tat gac cgg ggc gct cgg cgg tca aag cag tct 355
 Gln Ala Glu Gly Gly Tyr Asp Arg Gly Ala Arg Ser Lys Gln Ser
 70 75 80 85

gta tgg aca gat cca gct acc ggt tac aca cgg cgt gca gtg tca cag 403
 Val Trp Thr Asp Pro Ala Thr Gly Tyr Thr Arg Arg Ala Val Ser Gln
 90 95 100

ccg tca gaa tcc cca cta gaa cta gtg gaa gta atg ctg cct cct ggg 451
 Pro Ser Glu Ser Pro Leu Glu Leu Val Glu Val Met Leu Pro Pro Gly
 105 110 115

gcg gaa gtt ggc tac cca gct gat gct tat cgt ttc atg gat cag gtg 499
 Ala Glu Val Gly Tyr Pro Ala Asp Ala Tyr Arg Phe Met Asp Gln Val
 120 125 130

gtc tgg gta ctc gaa ggg gcc gtt cgt att act gaa ggt gaa gag gtc 547
 Val Trp Val Leu Glu Gly Ala Val Arg Ile Thr Glu Gly Glu Glu Val
 135 140 145

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<210> 425
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum
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<220>

<221> CDS

<222> (101)..(1012)

<223> RXN02727

<400> 425

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ctaaagcagc	aggtcgaaga	gctagaggcg	caggttgccg	gtg	gtc	ctt	ctt	ccg	115
				Val	Val	Leu	Leu	Pro	
				1				5	

ctg	cta	gtt	cct	caa	ctg	cag	gtg	cag	cca	cag	ttg	cag	ctt	cca	agt	163
Leu	Leu	Val	Pro	Gln	Leu	Gln	Val	Gln	Pro	Gln	Leu	Gln	Leu	Pro	Ser	
			10					15						20		

ctg	ttg	acg	agg	cag	cgc	tgc	gca	agg	aaa	tca	aag	aga	agc	tgc	gct	211
Leu	Leu	Thr	Arg	Gln	Arg	Cys	Ala	Arg	Lys	Ser	Lys	Arg	Ser	Cys	Ala	
			25					30					35			

ccg	aat	acg	gca	tcc	aag	ctc	gat	gat	gcc	tcc	aag	gcc	gct	cag	aag	259
Pro	Asn	Thr	Ala	Ser	Lys	Leu	Asp	Asp	Ala	Ser	Lys	Ala	Ala	Gln	Lys	
			40				45					50				

gct	caa	aac	gat	gcg	aag	tcc	gct	caa	gat	cag	cta	cag	cgt	gca	caa	307
Ala	Gln	Asn	Asp	Ala	Lys	Ser	Ala	Gln	Asp	Gln	Leu	Gln	Arg	Ala	Gln	
	55					60					65					

gct	gac	gca	aag	gca	gct	cgc	gac	gaa	gct	gaa	aag	gcc	aag	gct	gaa	355
Ala	Asp	Ala	Lys	Ala	Ala	Arg	Asp	Glu	Ala	Glu	Lys	Ala	Lys	Ala	Glu	
	70				75				80						85	

gct	aag	tca	gca	gca	tcc	tcc	agc	acc	act	aag	gca	gca	gcg	gtt	ggc	403
Ala	Lys	Ser	Ala	Ala	Ser	Ser	Ser	Thr	Thr	Lys	Ala	Ala	Ala	Val	Gly	
			90						95					100		

gct	gtc	ggc	gct	ggc	acc	gga	gca	gca	gtt	gct	aca	ggt	gct	gca	aat	451
Ala	Val	Gly	Ala	Gly	Thr	Gly	Ala	Ala	Val	Ala	Thr	Gly	Ala	Ala	Asn	
		105						110					115			

gtg	gac	acc	cac	atg	cag	gca	gcg	aag	gtt	ctg	gga	ctc	gca	cag	gaa	499
Val	Asp	Thr	His	Met	Gln	Ala	Ala	Lys	Val	Leu	Gly	Leu	Ala	Gln	Glu	
		120					125					130				

atg	gca	gac	cgc	ctg	acc	tca	gag	gct	cgc	tcc	gaa	tcc	aag	tcc	atg	547
Met	Ala	Asp	Arg	Leu	Thr	Ser	Glu	Ala	Arg	Ser	Glu	Ser	Lys	Ser	Met	
		135				140					145					

ctg	gac	gag	gct	cgc	gaa	gca	gca	gag	aag	cag	atc	gag	gaa	gca	aac	595
Leu	Asp	Glu	Ala	Arg	Glu	Ala	Ala	Glu	Lys	Gln	Ile	Glu	Glu	Ala	Asn	
	150			155					160						165	

agc	acc	tcc	aac	cgc	act	ctg	gaa	gat	gct	cgc	gca	aac	gct	gag	aag	643
Ser	Thr	Ser	Asn	Arg	Thr	Leu	Glu	Asp	Ala	Arg	Ala	Asn	Ala	Glu	Lys	
			170					175						180		

cag	atc	gct	gaa	gcg	cag	aac	cgc	gct	gac	act	ctg	gtc	aac	gaa	gct	691
Gln	Ile	Ala	Glu	Ala	Gln	Asn	Arg	Ala	Asp	Thr	Leu	Val	Asn	Glu	Ala	
		185					190						195			

gac gct aag gct aag aac ctg gtt tcc gaa gcc gag aag aag tcc gca 739
 Asp Ala Lys Ala Lys Asn Leu Val Ser Glu Ala Glu Lys Lys Ser Ala
 200 205 210

gcc acc ctg gcc gca tcc acc tct cgt gca gaa gct cag atc cgt caa 787
 Ala Thr Leu Ala Ala Ser Thr Ser Arg Ala Glu Ala Gln Ile Arg Gln
 215 220 225

gcc gag gac aag gca aac gcc ctc cag gca gac gca gag cgc aag cac 835
 Ala Glu Asp Lys Ala Asn Ala Leu Gln Ala Asp Ala Glu Arg Lys His
 230 235 240 245

acc gaa acc atg gct gca gtc aag gaa cag cag aat gct ctg gag acc 883
 Thr Glu Thr Met Ala Ala Val Lys Glu Gln Gln Asn Ala Leu Glu Thr
 250 255 260

cgc atc gcg gaa ctg cag acc ttc gag cgt gag tac cgc acc cgt ctg 931
 Arg Ile Ala Glu Leu Gln Thr Phe Glu Arg Glu Tyr Arg Thr Arg Leu
 265 270 275

aag tcc ctc ctc gag ggc cag ctg gaa gaa ctc cac gca cgt ggc tcc 979
 Lys Ser Leu Leu Glu Gly Gln Leu Glu Glu Leu His Ala Arg Gly Ser
 280 285 290

tct gca cca acc aac aac aag cca tct ggt gag taaaaagaaa gattagttat 1032
 Ser Ala Pro Thr Asn Asn Lys Pro Ser Gly Glu
 295 300

ctt 1035

<210> 426
 <211> 304
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 426
 Val Val Leu Leu Pro Leu Leu Val Pro Gln Leu Gln Val Gln Pro Gln
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Leu Gln Leu Pro Ser Leu Leu Thr Arg Gln Arg Cys Ala Arg Lys Ser
 20 25 30

Lys Arg Ser Cys Ala Pro Asn Thr Ala Ser Lys Leu Asp Asp Ala Ser
 35 40 45

Lys Ala Ala Gln Lys Ala Gln Asn Asp Ala Lys Ser Ala Gln Asp Gln
 50 55 60

Leu Gln Arg Ala Gln Ala Asp Ala Lys Ala Ala Arg Asp Glu Ala Glu
 65 70 75 80

Lys Ala Lys Ala Glu Ala Lys Ser Ala Ala Ser Ser Ser Thr Thr Lys
 85 90 95

Ala Ala Ala Val Gly Ala Val Gly Ala Gly Thr Gly Ala Ala Val Ala
 100 105 110

Thr Gly Ala Ala Asn Val Asp Thr His Met Gln Ala Ala Lys Val Leu
 115 120 125

Gly Leu Ala Gln Glu Met Ala Asp Arg Leu Thr Ser Glu Ala Arg Ser
 130 135 140
 Glu Ser Lys Ser Met Leu Asp Glu Ala Arg Glu Ala Ala Glu Lys Gln
 145 150 155 160
 Ile Glu Glu Ala Asn Ser Thr Ser Asn Arg Thr Leu Glu Asp Ala Arg
 165 170 175
 Ala Asn Ala Glu Lys Gln Ile Ala Glu Ala Gln Asn Arg Ala Asp Thr
 180 185 190
 Leu Val Asn Glu Ala Asp Ala Lys Ala Lys Asn Leu Val Ser Glu Ala
 195 200 205
 Glu Lys Lys Ser Ala Ala Thr Leu Ala Ala Ser Thr Ser Arg Ala Glu
 210 215 220
 Ala Gln Ile Arg Gln Ala Glu Asp Lys Ala Asn Ala Leu Gln Ala Asp
 225 230 235 240
 Ala Glu Arg Lys His Thr Glu Thr Met Ala Ala Val Lys Glu Gln Gln
 245 250 255
 Asn Ala Leu Glu Thr Arg Ile Ala Glu Leu Gln Thr Phe Glu Arg Glu
 260 265 270
 Tyr Arg Thr Arg Leu Lys Ser Leu Leu Glu Gly Gln Leu Glu Glu Leu
 275 280 285
 His Ala Arg Gly Ser Ser Ala Pro Thr Asn Asn Lys Pro Ser Gly Glu
 290 295 300

<210> 427
 <211> 1143
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1120)
 <223> RXN01575

<400> 427
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 gtttagtgcc accgacccca gtgatgataa cttgattgtc atg aaa tcc att gat 115
 Met Lys Ser Ile Asp
 1 5
 ctt gag cag ctg gcg ggc acg caa tcg cgc acg tat caa tcg cga aag 163
 Leu Glu Gln Leu Ala Gly Thr Gln Ser Arg Thr Tyr Gln Ser Arg Lys
 10 15 20
 atc acc gat gag atg gtc gcc cgg ccg gtg cat gtg gcg atc gcg ctg 211
 Ile Thr Asp Glu Met Val Ala Arg Pro Val His Val Ala Ile Ala Leu
 25 30 35

tgg gaa gtg ccg tgg gag tcg gca aaa tcc ggc aag att gag ggt tgg	259
Trp Glu Val Pro Trp Glu Ser Ala Lys Ser Gly Lys Ile Glu Gly Trp	
40 45 50	
gtc att gcc gtg gat tcg ccg cgt ggg cgg ttt gtg cgc agc ggg cag	307
Val Ile Ala Val Asp Ser Pro Arg Gly Arg Phe Val Arg Ser Gly Gln	
55 60 65	
acc aaa aat ggc gac gcc gtc aac cgg act gtg tcg atg ctg aaa tca	355
Thr Lys Asn Gly Asp Ala Val Asn Arg Thr Val Ser Met Leu Lys Ser	
70 75 80 85	
gcg ttg aaa ggg gtc cgc ggg aag gcg tgg att gta act ggg cgt cga	403
Ala Leu Lys Gly Val Arg Gly Lys Ala Trp Ile Val Thr Gly Arg Arg	
90 95 100	
caa gca gct tta cgc gca gcc ctg gtg cgc gaa aac tac ctg gtc acc	451
Gln Ala Ala Leu Arg Ala Ala Leu Val Arg Glu Asn Tyr Leu Val Thr	
105 110 115	
gga agc ttc gcc gag caa aat agg gcc ggc gtg aag gcg tcg gcg atc	499
Gly Ser Phe Ala Glu Gln Asn Arg Ala Gly Val Lys Ala Ser Ala Ile	
120 125 130	
tcg cgc cgc gcc gaa caa tcc gcg ctc tac aag gcg aaa aaa atc ggc	547
Ser Arg Arg Ala Glu Gln Ser Ala Leu Tyr Lys Ala Lys Lys Ile Gly	
135 140 145	
gaa ttc gcc gag cgc gcc cca cgc gtc aaa gag cgg caa gag gca cat	595
Glu Phe Ala Glu Arg Ala Pro Arg Val Lys Glu Arg Gln Glu Ala His	
150 155 160 165	
tgg tgg cca cgg ttg tca cgc acg caa ggc acc gca ggc gtt tta cgc	643
Trp Trp Pro Arg Leu Ser Arg Thr Gln Gly Thr Ala Gly Val Leu Arg	
170 175 180	
tta gcg acg gac gcc tct acc gat ggg gtc ttc cgc ggc gcc atg tgc	691
Leu Ala Thr Asp Ala Ser Thr Asp Gly Val Phe Arg Gly Ala Met Cys	
185 190 195	
ttc gta gcc tca aac ggc gac tac ctc ctg gag acc caa gac acc acc	739
Phe Val Ala Ser Asn Gly Asp Tyr Leu Leu Glu Thr Gln Asp Thr Thr	
200 205 210	
gca agc tcc gac gaa tta gaa ctc gaa agc atc acc cac gcc ctg atc	787
Ala Ser Ser Asp Glu Leu Glu Leu Glu Ser Ile Thr His Ala Leu Ile	
215 220 225	
tac ctc aaa acc atc ggc gcg acc caa gcc atc atc gaa tcc gac agc	835
Tyr Leu Lys Thr Ile Gly Ala Thr Gln Ala Ile Ile Glu Ser Asp Ser	
230 235 240 245	
aaa gcc gca ctt gaa gcc atc gac ttc atc ctc aac aac cga ccg cgc	883
Lys Ala Ala Leu Glu Ala Ile Asp Phe Ile Leu Asn Asn Arg Pro Arg	
250 255 260	
cgg ggc agg tgg cgc ggc atc acc gca tgc gcc cgc aac cgg ttc cgg	931
Arg Gly Arg Trp Arg Gly Ile Thr Ala Cys Ala Arg Asn Arg Phe Arg	
265 270 275	

gat gcc tgg gaa gcg ctt atc gac gac tgc gtt gtg gaa tta tcc cgc 979
 Asp Ala Trp Glu Ala Leu Ile Asp Asp Cys Val Val Glu Leu Ser Arg
 280 285 290
 gta cta ggg cac gcc ggg gat cca ctg aac caa gca gcc gac caa atc 1027
 Val Leu Gly His Ala Gly Asp Pro Leu Asn Gln Ala Ala Asp Gln Ile
 295 300 305
 gca tac atg ggc atg cgc gcc gta att ttt gaa caa aaa tcc gca cac 1075
 Ala Tyr Met Gly Met Arg Ala Val Ile Phe Glu Gln Lys Ser Ala His
 310 315 320 325
 ccc aca ttg ctc aaa gga att gac aag gcg ctt cgc aag gcc gag 1120
 Pro Thr Leu Leu Lys Gly Ile Asp Lys Ala Leu Arg Lys Ala Glu
 330 335 340
 taaggtgggc aacgagtcgg tga 1143

<210> 428

<211> 340

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 428

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 Tyr Gln Ser Arg Lys Ile Thr Asp Glu Met Val Ala Arg Pro Val His
 20 25 30
 Val Ala Ile Ala Leu Trp Glu Val Pro Trp Glu Ser Ala Lys Ser Gly
 35 40 45
 Lys Ile Glu Gly Trp Val Ile Ala Val Asp Ser Pro Arg Gly Arg Phe
 50 55 60
 Val Arg Ser Gly Gln Thr Lys Asn Gly Asp Ala Val Asn Arg Thr Val
 65 70 75 80
 Ser Met Leu Lys Ser Ala Leu Lys Gly Val Arg Gly Lys Ala Trp Ile
 85 90 95
 Val Thr Gly Arg Arg Gln Ala Ala Leu Arg Ala Ala Leu Val Arg Glu
 100 105 110
 Asn Tyr Leu Val Thr Gly Ser Phe Ala Glu Gln Asn Arg Ala Gly Val
 115 120 125
 Lys Ala Ser Ala Ile Ser Arg Arg Ala Glu Gln Ser Ala Leu Tyr Lys
 130 135 140
 Ala Lys Lys Ile Gly Glu Phe Ala Glu Arg Ala Pro Arg Val Lys Glu
 145 150 155 160
 Arg Gln Glu Ala His Trp Trp Pro Arg Leu Ser Arg Thr Gln Gly Thr
 165 170 175
 Ala Gly Val Leu Arg Leu Ala Thr Asp Ala Ser Thr Asp Gly Val Phe
 180 185 190

Arg Gly Ala Met Cys Phe Val Ala Ser Asn Gly Asp Tyr Leu Leu Glu
 195 200 205
 Thr Gln Asp Thr Thr Ala Ser Ser Asp Glu Leu Glu Leu Glu Ser Ile
 210 215 220
 Thr His Ala Leu Ile Tyr Leu Lys Thr Ile Gly Ala Thr Gln Ala Ile
 225 230 235 240
 Ile Glu Ser Asp Ser Lys Ala Ala Leu Glu Ala Ile Asp Phe Ile Leu
 245 250 255
 Asn Asn Arg Pro Arg Arg Gly Arg Trp Arg Gly Ile Thr Ala Cys Ala
 260 265 270
 Arg Asn Arg Phe Arg Asp Ala Trp Glu Ala Leu Ile Asp Asp Cys Val
 275 280 285
 Val Glu Leu Ser Arg Val Leu Gly His Ala Gly Asp Pro Leu Asn Gln
 290 295 300
 Ala Ala Asp Gln Ile Ala Tyr Met Gly Met Arg Ala Val Ile Phe Glu
 305 310 315 320
 Gln Lys Ser Ala His Pro Thr Leu Leu Lys Gly Ile Asp Lys Ala Leu
 325 330 335
 Arg Lys Ala Glu
 340

<210> 429

<211> 780

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(757)

<223> RXN01966

<400> 429

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 Val Ser Glu Ser Glu
 1 5

aac aac aca aca cca gca gtc gca gct cgc gat gac cgt ctg gtc tgg 163
 Asn Asn Thr Thr Pro Ala Val Ala Ala Arg Asp Asp Arg Leu Val Trp
 10 15 20

gtc gat ctg gaa atg act ggt cta gat ttg aag cgc cac gtg atc gtg 211
 Val Asp Leu Glu Met Thr Gly Leu Asp Leu Lys Arg His Val Ile Val
 25 30 35

gag gtt gcg gcg ttg gtc act gac gct aac ctc aac gtt ttg ggc gag 259
 Glu Val Ala Ala Leu Val Thr Asp Ala Asn Leu Asn Val Leu Gly Glu
 40 45 50

ggc gtg gac ttg gtt gtt cac gca act gaa gaa gag ctc gcg cag atg 307

Gly Val Asp Leu Val Val His Ala Thr Glu Glu Glu Leu Ala Gln Met
 55 60 65
 gat gat ttt gtc acc aac atg cac gaa tcc tct ggg ctg act gag cag 355
 Asp Asp Phe Val Thr Asn Met His Glu Ser Ser Gly Leu Thr Glu Gln
 70 75 80 85
 atc cgg gaa tcc gcg gtc acg ttg aag gaa gcc gaa gat gct gtg ctc 403
 Ile Arg Glu Ser Ala Val Thr Leu Lys Glu Ala Glu Asp Ala Val Leu
 90 95 100
 gca ttg att gaa aag cac tgc gat cca gcc cat cct gca ccg cta gct 451
 Ala Leu Ile Glu Lys His Cys Asp Pro Ala His Pro Ala Pro Leu Ala
 105 110 115
 ggt aac tcc att gcc act gac cgc gcg ttt atc cgc gaa cat atg cca 499
 Gly Asn Ser Ile Ala Thr Asp Arg Ala Phe Ile Arg Glu His Met Pro
 120 125 130
 cgt ctt gat gag gcc ctg cat tac cgc atg gtg gat gtg tcc tcg gtg 547
 Arg Leu Asp Glu Ala Leu His Tyr Arg Met Val Asp Val Ser Ser Val
 135 140 145
 aag gaa ttg gcg cgt cgc tgg tac cca cgc gtg tac tac aag cag ccg 595
 Lys Glu Leu Ala Arg Arg Trp Tyr Pro Arg Val Tyr Tyr Lys Gln Pro
 150 155 160 165
 gag aag ggt ttg gcg cac cgc gcg ttg gcg gac att gtg gag tcg att 643
 Glu Lys Gly Leu Ala His Arg Ala Leu Ala Asp Ile Val Glu Ser Ile
 170 175 180
 cgg gag ttg gat tac tac cgt cgc tca ttt ttt gtt gca gag cct ggt 691
 Arg Glu Leu Asp Tyr Tyr Arg Arg Ser Phe Phe Val Ala Glu Pro Gly
 185 190 195
 cct acc tct gag cag tgc gca gat gat gcg cag gca gcg gtg gac cgt 739
 Pro Thr Ser Glu Gln Cys Ala Asp Asp Ala Gln Ala Ala Val Asp Arg
 200 205 210
 ttt gca ccc tac ttt gat tagagggttt taagcagcct ggt 780
 Phe Ala Pro Tyr Phe Asp
 215

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<212> PRT

<213> Corynebacterium glutamicum

<400> 430

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 Asp Arg Leu Val Trp Val Asp Leu Glu Met Thr Gly Leu Asp Leu Lys
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 Arg His Val Ile Val Glu Val Ala Ala Leu Val Thr Asp Ala Asn Leu
 35 40 45
 Asn Val Leu Gly Glu Gly Val Asp Leu Val Val His Ala Thr Glu Glu
 50 55 60

Sub-21

Glu Leu Ala Gln Met Asp Asp Phe Val Thr Asn Met His Glu Ser Ser
65 70 75 80

Gly Leu Thr Glu Gln Ile Arg Glu Ser Ala Val Thr Leu Lys Glu Ala
85 90 95

Glu Asp Ala Val Leu Ala Leu Ile Glu Lys His Cys Asp Pro Ala His
100 105 110

Pro Ala Pro Leu Ala Gly Asn Ser Ile Ala Thr Asp Arg Ala Phe Ile
115 120 125

Arg Glu His Met Pro Arg Leu Asp Glu Ala Leu His Tyr Arg Met Val
130 135 140

Asp Val Ser Ser Val Lys Glu Leu Ala Arg Arg Trp Tyr Pro Arg Val
145 150 155 160

Tyr Tyr Lys Gln Pro Glu Lys Gly Leu Ala His Arg Ala Leu Ala Asp
165 170 175

Ile Val Glu Ser Ile Arg Glu Leu Asp Tyr Tyr Arg Arg Ser Phe Phe
180 185 190

Val Ala Glu Pro Gly Pro Thr Ser Glu Gln Cys Ala Asp Asp Ala Gln
195 200 205

Ala Ala Val Asp Arg Phe Ala Pro Tyr Phe Asp
210 215